

Knot Theory

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Unit 1 – Knot Theory Basics: Intro & Definitions

1.1 History and development of knot theory

Knots aren't just for tying shoelaces. In the late 1800s, scientists realized they could use knot theory to understand how molecules twist and turn. This sparked a whole new field of math, with big names like Gauss and Tait laying the groundwork.

Knot theory isn't just abstract math – it's super useful in real life. It helps biologists figure out how DNA and proteins fold, which is crucial for understanding how our bodies work. It even helps scientists design new drugs and materials.

Historical Context and Early Development of Knot Theory

Origins of knot theory

- Knot theory originated from the study of molecules and their behavior in physics and chemistry
- Physicists and chemists in the late 19th century recognized the importance of understanding the entanglement and linking of molecules (DNA, proteins)
- Knots were used to describe the complex structures formed by intertwined molecules
- Knot theory emerged as a distinct mathematical discipline in the early 20th century
- Mathematicians formalized the concepts and techniques used to study knots
- Topology, the study of geometric properties preserved under continuous deformations, provided a framework for rigorous analysis of knots

Key figures in knot theory

- Carl Friedrich Gauss (1777-1855) introduced the concept of linking number, a measure of how two closed curves are linked together, laying the foundation for the mathematical study of knots and links
- Peter Guthrie Tait (1831-1901) compiled the first systematic tabulation of knots (Tait knot table) and developed the concept of knot invariants, quantities that remain unchanged under continuous deformations of the knot
- James Clerk Maxwell (1831-1879) applied knot theory to the study of electromagnetic fields, recognizing the potential of knot theory in understanding the behavior of physical systems
- Max Dehn (1878-1952) introduced the concept of knot complement, the space surrounding a knot, and developed algorithms for determining the equivalence of knots

Applications and Connections

Knot theory in molecular structures

- Knot theory plays a crucial role in studying molecular structures and their properties
- DNA molecules often form complex knots and links, affecting their biological function

1. Entanglement of DNA strands can influence processes such as replication and transcription
2. Knot theory provides tools for analyzing and classifying these structures
 - Proteins exhibit knotted and linked conformations, impacting their stability and activity
1. Folding of protein chains into specific three-dimensional structures is essential for their biological function
2. Knot theory helps in understanding the topological constraints and properties of protein knots
 - Applying knot theory to molecular biology has led to significant advances in fields such as
 - Drug design and development by understanding the topological properties of drug targets to aid in rational design of therapeutic compounds
 - Nanotechnology and materials science by guiding the design and synthesis of novel materials with desired properties based on their molecular topology

Connections to other mathematical fields

- Knot theory is closely related to topology, the study of geometric properties preserved under continuous deformations
- Knots are studied as embeddings of circles in three-dimensional space, a fundamental concept in topology
- Topological invariants (knot group, Alexander polynomial) are used to classify and distinguish different knots
- Graph theory, the study of graphs and their properties, has connections to knot theory
- Knot diagrams, two-dimensional representations of knots, can be viewed as planar graphs
- Crossings in a knot diagram correspond to the vertices of the graph
- Arcs between crossings correspond to the edges of the graph
- Graph-theoretic techniques (computation of graph genus) can be applied to the study of knots and their properties
- Knot theory also has links to other areas of mathematics, including
 - Algebra through the study of knot polynomials and their properties
 - Combinatorics in the enumeration and classification of knots and links
 - Mathematical physics, where knots arise in the study of quantum field theories and statistical mechanics

1.2 Basic definitions: knots, links, and embeddings

Knots and links are fundamental concepts in knot theory. Knots are closed curves in 3D space, while links are collections of intertwined knots. Understanding their definitions and differences is crucial for grasping the basics of this field.

Embeddings play a key role in knot theory, mapping objects into higher-dimensional spaces. Knot projections help visualize 3D knots in 2D, preserving crossing information. These concepts form the foundation for studying knot behavior and classification.

Knots and Links

Definition of knots

- A knot is a closed curve in 3D space without endpoints forming a continuous loop
- The curve must be non-self-intersecting or simple at any point
- Examples include the trefoil knot, figure-eight knot, and unknot (a simple loop)

Knots vs links

- A link is a collection of multiple intertwined or linked knots, each called a component
- Links are classified by the number of components they contain (2-component link, 3-component link, etc.)
- Examples of links include the Hopf link (2 components), Borromean rings (3 components), and Whitehead link (2 components)

Embeddings in knot theory

- An embedding maps an object into a higher-dimensional space without self-intersection
- In knot theory, an embedding maps a 1D curve into 3D space
- Knots and links are images of embeddings of circles into 3D space
- A knot is the image of an embedding of a single circle
- A link is the image of an embedding of multiple circles
- Studying embedding properties helps understand knot and link behavior and classification

Knots and their projections

- A knot projection is a 2D representation of a 3D knot obtained by projecting onto a plane
- The projection may contain crossings where the curve appears to pass over or under itself
- In a knot projection, over and under information at each crossing is preserved using breaks in the underpass to reconstruct the original 3D knot
- A knot projection may not accurately represent the 3D structure, as different projections of the same knot may appear visually distinct
- Knot invariants (crossing number, Jones polynomial) can distinguish between different knots based on their projections

1.3 Ambient isotopy and knot equivalence

Ambient isotopy is a key concept in knot theory. It's all about smoothly deforming one knot into another without cutting or gluing. This idea helps us understand when two knots are essentially the same.

Reidemeister moves are the building blocks of ambient isotopy. These simple twists, pokes, and slides let us change knot diagrams without changing the knot itself. They're crucial for figuring out if knots are equivalent.

Ambient Isotopy and Knot Equivalence

Ambient isotopy in knot equivalence

- Continuous deformation of the ambient space (usually $\mathbb{R}^3$) that transforms one knot into another
- Family of homeomorphisms $h_t : \mathbb{R}^3 \rightarrow \mathbb{R}^3$, where $t \in [0, 1]$, with h_0 being the identity map and h_1 mapping the first knot onto the second knot
- Defines an equivalence relation on the set of all knots
- Reflexive property: every knot is ambient isotopic to itself
- Symmetric property: if knot K_1 is ambient isotopic to K_2 , then K_2 is ambient isotopic to K_1
- Transitive property: if K_1 is ambient isotopic to K_2 , and K_2 is ambient isotopic to K_3 , then K_1 is ambient isotopic to K_3
- Fundamental concept in determining whether two knots are of the same knot type (trefoil knot, figure-eight knot)

Significance of Reidemeister moves

- Local modifications of a knot diagram that do not change the underlying knot type
- Three types of Reidemeister moves: 1. Type I (Twist): adds or removes a twist in a strand 2. Type II (Poke): moves one strand over another, creating or removing two crossings 3. Type III (Slide): moves a strand over or under a crossing
- Reidemeister's theorem: two knots are ambient isotopic if and only if their diagrams are related by a finite sequence of Reidemeister moves
- Provide a systematic way to manipulate knot diagrams while preserving the knot type

Application of Reidemeister moves

- Determine if two knots are equivalent by transforming one knot diagram into the other using Reidemeister moves
- If a sequence of Reidemeister moves exists that transforms one diagram into the other, the knots are equivalent
- Examples:
 - The unknot (trivial knot) and the trefoil knot are not equivalent, as no sequence of Reidemeister moves can transform the unknot diagram into the trefoil knot diagram
 - The left-handed and right-handed trefoil knots are equivalent, as a sequence of Reidemeister moves can be used to transform one into the other
- Practical tool for studying knot equivalence and classifying knots

Challenges in knot equivalence

- Determining knot equivalence using Reidemeister moves can be difficult and time-consuming
- No general algorithm exists to determine the minimum number of moves required to transform one knot diagram into another

- Knot invariants (crossing number, unknotting number) can help distinguish between non-equivalent knots but are not always conclusive
- Reidemeister moves are sufficient but not always necessary for determining knot equivalence
- Some equivalent knots may have diagrams that are not related by Reidemeister moves alone
- Other methods (Jones polynomial, Khovanov homology) may be needed to establish equivalence in such cases
- Ongoing research in knot theory aims to develop more efficient and comprehensive methods for determining knot equivalence

1.4 Orientation and chirality of knots

Knots can be oriented, giving them direction and distinguishing mirror images. This affects their properties and classification. Orientation is key in understanding knot behavior and relationships between different knots.

Chirality in knots refers to their "handedness" - whether they're equivalent to their mirror image. This concept is crucial in molecular biology and chemistry, impacting DNA topology and drug design.

Orientation and Chirality in Knot Theory

Concept of knot orientation

- Orientation of a knot specifies the direction in which the knot is traversed (clockwise or counterclockwise)
- Assigning a direction to each strand of the knot determines its overall orientation
- Distinguishes between knots that are mirror images of each other and affects their properties and invariants
- Plays a crucial role in the classification and tabulation of knots (trefoil knot, figure-eight knot)

Chirality and knot equivalence

- Chirality is the property of an object being non-superimposable on its mirror image due to lack of symmetry and distinct "handedness" (left and right hands, DNA helices, certain molecules)
- Two knots are equivalent if they can be continuously deformed into each other without cutting or passing through itself
- Chiral knots are not equivalent to their mirror images, while achiral knots are equivalent to their mirror images (trefoil knot, unknot)

Determining knot chirality

- Examine the knot diagram for symmetry or lack thereof in the crossings and overall structure
- Use invariants such as the Jones polynomial or HOMFLY-PT polynomial to determine chirality
- If the invariants differ for the knot and its mirror image, the knot is chiral
- Obtain the mirror image of a knot by: 1. Reversing all crossings in the knot diagram 2. Reflecting the knot diagram across a plane

Applications of knot chirality

- Molecular biology: DNA molecules can form knots during replication and recombination processes, and the chirality of DNA knots affects their biological properties and interactions (DNA topology, cellular processes)
- Chemistry: Chirality is a fundamental property of many molecules (amino acids, sugars) and affects their chemical and physical properties
- Knot theory models and studies the chirality of complex molecular structures
- Chirality plays a crucial role in drug design and synthesis, as different chiral forms of a molecule can have different biological activities (thalidomide, ibuprofen)

Unit 2 – Knot Diagrams and Reidemeister Moves

2.1 Knot diagrams and projections

Knot diagrams are 2D representations of 3D knots, essential for studying knot structure and equivalence. They capture crucial information like crossing numbers and symmetries, enabling the computation of knot invariants and the application of Reidemeister moves.

Creating knot diagrams involves projecting the knot onto a plane, assigning over/under information at crossings, and considering different types of crossings. Properties like crossing number and alternating knots provide insights into a knot's complexity and unique characteristics.

Knot Diagrams

Role of knot diagrams

- Knot diagrams are 2D representations of 3D knots obtained by projecting a knot onto a plane (trefoil knot, figure-eight knot)
- Capture essential information about the knot's structure such as crossing number and knot symmetries
- Knot diagrams are used to study knot equivalence where two knots are equivalent if their diagrams can be transformed into each other through a sequence of Reidemeister moves (Type I, Type II, Type III)
- Allow for the computation of knot invariants which are quantities that remain unchanged under Reidemeister moves (crossing number, Jones polynomial, Alexander polynomial)

Construction of knot diagrams

- Choose a projection plane that is generic with respect to the knot ensuring the resulting diagram has a finite number of crossings and no self-tangencies (xy-plane, yz-plane)
- Project the knot onto the chosen plane by mapping each point on the knot to a corresponding point on the plane
- Assign over/under information at each crossing indicating which strand passes over the other at each intersection (right-handed crossing, left-handed crossing)
- Different projection planes may result in different knot diagrams for the same knot with some projections yielding simpler or more complex diagrams depending on the knot's structure (minimal crossing diagram, alternating diagram)

Types of knot crossings

- Crossings occur when two strands of the knot intersect in the projection
- Positive (right-handed) crossings where the over-strand passes from top-left to bottom-right and are assigned a value of +1

- Negative (left-handed) crossings where the over-strand passes from top-right to bottom-left and are assigned a value of -1
- The writhe of a knot diagram is the sum of the crossing values calculated using the formula

$$Writhe = \sum_{i=1}^n sign(c_i)$$

, where c_i is the i -th crossing and n is the total number of crossings

Properties of knot diagrams

- Crossing number is the minimum number of crossings among all possible diagrams of a knot and provides a lower bound on the knot's complexity (trefoil knot has crossing number 3, figure-eight knot has crossing number 4)
- Alternating knots have diagrams where over and under crossings alternate along the knot and possess special properties such as the crossing number being additive under connected sum (alternating prime knots, alternating composite knots)
- Minimal diagrams are knot diagrams with the least number of crossings for a given knot but may not be unique as some knots have multiple minimal diagrams
- Reidemeister moves can be applied to knot diagrams without changing the underlying knot: 1. Type I: twisting or untwisting a single strand 2. Type II: overlapping or separating two strands 3. Type III: moving a strand over or under a crossing

2.2 Reidemeister moves and their significance

Reidemeister moves are the building blocks of knot manipulation. These three types of moves allow us to twist, uncross, and slide strands without changing the knot's fundamental structure.

By applying Reidemeister moves, we can simplify knot diagrams and prove knot equivalence. This powerful tool is essential for studying knot properties and has applications in physics, chemistry, and biology.

Reidemeister Moves

Types of Reidemeister moves

- Reidemeister move I (RI) adds or removes a twist in a strand without changing the knot type (trefoil knot, figure-eight knot)
- Reidemeister move II (RII) adds or removes two crossings between two strands without changing the knot type (Hopf link, Whitehead link)
- Reidemeister move III (RIII) slides a strand over or under a crossing without changing the knot type (Borromean rings, Kinoshita-Terasaka knot)

Application of Reidemeister moves

- Simplifying knot diagrams involves using Reidemeister moves to reduce the number of crossings and obtain the minimal crossing number representation of a knot (unknot, trefoil knot)
- Manipulating knot diagrams involves using Reidemeister moves to alter the appearance of a knot diagram while maintaining the knot type (figure-eight knot, cinquefoil knot)

Proof of knot equivalence

- Two knots are equivalent if their diagrams can be transformed into each other using a sequence of Reidemeister moves (trefoil knot, mirror image trefoil knot)
- Proving knot equivalence involves finding a sequence of Reidemeister moves that transforms one knot diagram into the other and demonstrating that the knot type remains unchanged throughout the transformation (figure-eight knot, Listing's knot)

Importance in knot theory

- Reidemeister moves play a fundamental role in knot theory by providing a way to manipulate and compare knot diagrams, enabling the study of knot equivalence and classification (knot invariants, knot polynomials)
- Reidemeister moves have applications in various fields: 1. Topology and geometry: Study properties of knots and links (linking number, writhe), and investigate 3-dimensional manifolds (Seifert surfaces, Dehn surgery) 2. Physics: Model physical systems, such as polymer chains and DNA (statistical mechanics, quantum field theory), and study the behavior of entangled objects (fluid dynamics, magnetohydrodynamics) 3. Chemistry and molecular biology: Analyze the structure and properties of molecules (molecular knots, catenanes), and understand the behavior of DNA and proteins (DNA topology, protein folding)

2.3 Planar isotopy and regular isotopy

Planar and regular isotopy are crucial concepts in knot theory. Planar isotopy involves continuous deformations of knot diagrams without changing crossings, while regular isotopy allows Reidemeister moves too. These tools help simplify and compare knot diagrams.

Understanding isotopy types is key for classifying knots and determining equivalence. Planar isotopy preserves knot type, while regular isotopy defines a broader notion of knot equivalence. These concepts are fundamental for studying knot properties and developing invariants.

Planar and Regular Isotopy

Planar isotopy in knot diagrams

- Planar isotopy continuously deforms a knot diagram in the plane by stretching, shrinking, and bending without changing the crossing structure (over/under relationships)
- Preserves the knot type as planar isotopic diagrams represent the same knot (trefoil knot, figure-eight knot)
- Key tool in determining knot equivalence by simplifying diagrams and reducing complexity
- Helps compute knot invariants (crossing number, writhe) and compare knots

Planar vs regular isotopy

- Regular isotopy generalizes planar isotopy by allowing Reidemeister moves on the knot diagram in addition to continuous deformations
- Reidemeister move I twists or untwists a strand in either direction
- Reidemeister move II overlaps or separates two strands

- Reidemeister move III moves a strand over or under a crossing
- Regular isotopic diagrams represent the same knot as Reidemeister moves preserve the underlying knot type (unknot, trefoil knot)
- Planar isotopy is a special case of regular isotopy where all planar isotopies are regular isotopies, but not vice versa

Isotopy types of knot diagrams

- Check for planar isotopy by continuously deforming one diagram into the other without changing crossings (unknot diagrams)
- Check for regular isotopy using a sequence of Reidemeister moves and planar isotopy to transform one diagram into the other (left-handed and right-handed trefoil knots)
- Planar isotopic diagrams are always regular isotopic, but regular isotopic diagrams may not be planar isotopic

Isotopy's role in knot classification

- Fundamental tools for identifying equivalent knot diagrams and classifying knots up to regular isotopy
- Planar isotopy simplifies diagrams by removing unnecessary crossings and reducing complexity (alternating knot diagrams)
- Regular isotopy defines knot equivalence where two knots are equivalent if their diagrams are regular isotopic, providing a rigorous mathematical definition of sameness
- Crucial for studying knot properties, developing invariants (Jones polynomial, HOMFLY polynomial), and understanding knot structure and behavior in three-dimensional space

Unit 3 – Knot Equivalence and Knot Invariants

3.1 Concept of knot invariants

Knot invariants are mathematical properties that remain constant when a knot is deformed. They help distinguish different knots and include crossing numbers, tricolorability, and knot polynomials. These tools are crucial for understanding knot equivalence.

While knot invariants are powerful for differentiating knots, they have limitations. No single invariant can classify all knots, and knots with the same invariants aren't necessarily equivalent. This ongoing challenge keeps mathematicians searching for new methods to understand knots.

Knot Invariants

Definition of knot invariants

- Mathematical properties or quantities associated with a knot that remain constant under continuous deformations (ambient isotopy)
- Help distinguish different knots from one another even if they appear similar
- Two knots with different invariants cannot be equivalent
- Examples include:
 - Crossing number represents the minimum number of crossings in any diagram of the knot
 - Tricolorability determines whether a knot diagram can be colored with three colors while following certain rules
 - Knot polynomial is a polynomial associated with a knot (Jones polynomial, Alexander polynomial)

Invariance under ambient isotopy

- Ambient isotopy is a continuous deformation of the 3-dimensional space containing a knot without allowing the knot to pass through itself
- Can be visualized as manipulating a knotted rope without cutting or gluing it
- Knot invariants are designed to be unaffected by ambient isotopy
- If two knots have different invariants, they cannot be transformed into each other through ambient isotopy
- If two knots have the same invariants, they may be equivalent but additional invariants might be needed to confirm this

Types of knot invariants

- Crossing number:
 - Determines the minimum complexity of a knot

- Can quickly rule out the equivalence of knots with different crossing numbers
- Tricolorability:
 - A knot is tricolorable if its diagram can be colored with three colors following the rule that at each crossing, either all three colors are present or only one color is present
 - Non-tricolorable knots cannot be equivalent to tricolorable knots
- Knot polynomials:
 - Algebraic expressions associated with knots obtained through specific rules and calculations
 - Different knot polynomials (Jones polynomial, Alexander polynomial) can distinguish between knots that other invariants might not
 - Reveal connections between knot theory and other areas of mathematics (statistical mechanics, quantum field theory)

Limitations in knot classification

- Knot invariants are powerful tools for distinguishing knots but have limitations in providing a complete classification
- Two knots with the same invariants are not necessarily equivalent; they may be distinguished by other, more sensitive invariants
- No known single invariant or finite set of invariants can distinguish all knots from one another
- Mutant knots have the same polynomial invariants but are not equivalent highlighting the need for additional invariants or techniques to fully classify knots
- Classification of knots remains an ongoing area of research in knot theory
- Mathematicians continue to develop new invariants and methods to better understand and distinguish knots

3.2 Crossing number and bridge number

Crossing numbers and bridge numbers are crucial measures of knot complexity. They help us distinguish between different knots and understand their structure. These invariants remain constant regardless of how we represent the knot.

Calculating these numbers involves examining all possible diagrams of a knot and finding the minimum. We can simplify diagrams using Reidemeister moves to reduce crossings and bridges. Examples like the trefoil and figure-eight knots illustrate these concepts.

Crossing Number

Crossing number of knots

- Minimum number of crossings in any diagram of the knot
- Invariant of the knot remains the same regardless of representation
- Measure of knot complexity higher crossing numbers indicate more complex knots
- Helps distinguish between different knots knots with different crossing numbers are distinct

- Used in knot tabulation and classification knots organized by crossing numbers in tables and databases

Calculation of crossing numbers

- Find crossing number by examining all possible diagrams and counting crossings
- Crossing number is the minimum number of crossings among all diagrams
- Simplify knot diagrams to reduce crossings using Reidemeister moves
- Reidemeister move I untwists a twist in the diagram
- Reidemeister move II overlaps two strands and then separates them
- Reidemeister move III moves a strand over or under a crossing
- Examples of knots and their crossing numbers
- Unknot (trivial knot) $c(Unknot) = 0$
- Trefoil knot $c(Trefoil) = 3$
- Figure-eight knot $c(Figure - eight) = 4$
- Cinquefoil knot $c(Cinquefoil) = 5$

Bridge Number

Bridge number in knot theory

- Minimum number of local maxima (bridges) in any diagram of the knot when projected onto a plane
- Bridge portion of the knot that goes over at a local maximum in the projection
- Invariant of the knot remains the same regardless of representation
- Measure of knot complexity higher bridge numbers indicate more complex knots
- Provides a lower bound for the crossing number $b(K) \leq c(K)$ for any knot K
- Useful in studying topology of knot complements complement of knot with bridge number n can be decomposed into n trivial tangles

Determination of bridge numbers

- Find bridge number by examining all possible diagrams and counting local maxima (bridges) when projected onto a plane
- Bridge number is the minimum number of bridges among all diagrams
- Simplify knot diagrams using Reidemeister moves to minimize bridge number
- Examples of knots and their bridge numbers
- Unknot (trivial knot) $b(Unknot) = 1$
- Trefoil knot $b(Trefoil) = 2$
- Figure-eight knot $b(Figure - eight) = 2$

- Cinquefoil knot $b(\text{Cinquefoil}) = 2$
- Determine bridge number by considering knot's presentation in bridge position
- Knot in bridge position is positioned with respect to a plane so that the plane intersects the knot transversely and the knot has a minimal number of local maxima (bridges) above the plane

3.3 Tricolorability and other coloring invariants

Tricolorability is a cool way to tell knots apart. It's all about coloring knot diagrams with three colors, following specific rules at each crossing. This simple idea helps us figure out if knots are different or the same.

But tricolorability is just the beginning. We can expand this concept to use more colors or even algebraic structures called quandles. These advanced coloring methods give us powerful tools to study and classify knots.

Tricolorability and Coloring Invariants

Concept of tricolorability

- Tricolorability represents a property of knots and links where the knot or link can be colored using three distinct colors (red, green, blue) in a specific manner
- At each crossing in a tricolorable knot or link, either all three colors must be present or only one color should appear
- Tricolorability serves as a knot invariant, meaning if two knots are equivalent and can be transformed into each other through a series of Reidemeister moves, they will exhibit the same tricolorability
- Tricolorability helps distinguish between different knots, as knots with different tricolorability cannot be equivalent

Application of tricolorability test

- To determine if a knot is tricolorable, assign colors to the strands of the knot diagram starting with one strand and a chosen color
- Follow the strand through the crossings and assign colors to the other strands based on the following rules:
 - When the strand goes over another strand at a crossing, the crossed strand must have a different color
 - When the strand goes under another strand at a crossing, the crossed strand must have the same color
- Continue the color assignment process until all strands have been colored or a contradiction arises
- If a contradiction occurs, such as a strand requiring two different colors, the knot is not tricolorable
- If all strands can be consistently colored without contradictions, the knot is considered tricolorable

Generalizations of tricolorability

- p -colorability extends the concept of tricolorability, where p represents a prime number

- A knot is considered p -colorable if it can be colored using p colors, ensuring that at each crossing, the sum of the colors of the undercrossing strands equals twice the color of the overcrossing strand modulo p
- The tricolorability test can be modified for p -colorability by assigning colors from the set $0, 1, \dots, p-1$ to the strands and verifying the crossing condition using modulo p arithmetic
- p -colorability also serves as a knot invariant, meaning equivalent knots will have the same p -colorability for all prime numbers p

Properties of coloring invariants

- Fox n -colorability generalizes the concept further, allowing a knot to be colored with n colors, where n is any integer greater than or equal to 2
- In Fox n -colorability, the sum of the colors of the undercrossing strands must equal twice the color of the overcrossing strand modulo n at each crossing
- Fox n -colorability acts as a knot invariant for all integers $n \geq 2$
- Quandle coloring utilizes an algebraic structure called a quandle, which captures the properties of Reidemeister moves
- A knot is quandle colorable if it can be colored with elements of a quandle while satisfying the quandle axioms at each crossing
- Quandle coloring proves to be a powerful knot invariant capable of distinguishing many knots that other invariants cannot

3.4 Unknotting number and slice genus

The unknotting number reveals a knot's complexity by counting the minimum crossing changes needed to untangle it. It's like measuring how many steps it takes to untie a shoelace. This concept helps us compare knots and understand their structure.

Slice genus takes knots to the next level, exploring how they behave in four dimensions. It's about finding the simplest surface a knot can bound in 4D space. This idea connects to the unknotting number and helps classify knots in a whole new way.

Unknotting Number

Definition of unknotting number

- Minimum number of crossing changes needed to transform a knot into the unknot (trivial knot)
- Crossing change involves switching an overcrossing to an undercrossing or vice versa at a single crossing (trefoil knot, figure-eight knot)
- Knot invariant remains constant under ambient isotopy (Reidemeister moves)
- Provides insight into knot complexity
- Higher unknotting number indicates more complex knot (Kinoshita-Terasaka knot, Conway knot)
- Lower unknotting number suggests simpler knot (unknot, trefoil knot)
- Upper bound for other knot invariants (4-ball genus, slice genus)

Calculation of unknotting numbers

- Unknot has unknotting number 0 requires no crossing changes to become unknot
- Trefoil knot has unknotting number 1
- One crossing change sufficient to transform trefoil into unknot
- Figure-eight knot has unknotting number 1
- Despite having four crossings, only one crossing change needed to unknot figure-eight knot
- Kinoshita-Terasaka knot and Conway knot have unknotting number 1, even with 11 and 12 crossings, respectively
- Determining unknotting number for complex knots can be challenging, upper and lower bounds often used (torus knots, satellite knots)

Slice Genus

Concept of slice genus

- Minimum genus of smooth, oriented surface properly embedded in 4-ball B^4 with boundary given knot
- 4-ball is unit ball in 4-dimensional Euclidean space, $B^4 = \{x \in \mathbb{R}^4 : ||x|| \leq 1\}$
- Knot is slice if slice genus is 0
- Slice knots bound smooth, oriented disk in 4-ball (unknot, figure-eight knot)
- Slice genus is concordance invariant preserved under knot concordance
- Two knots concordant if they cobound smooth, oriented, properly embedded annulus in $S^3 \times [0, 1]$
- Slice genus provides lower bound for unknotting number, $g_s(K) \leq u(K)$

Determination of slice genus

- Unknot has slice genus 0 bounds smooth, oriented disk in 4-ball
- Trefoil knot has slice genus 1
- Trefoil does not bound disk in 4-ball, but bounds Möbius band with genus 1
- Figure-eight knot has slice genus 0, making it slice knot
- Figure-eight knot bounds smooth, oriented disk in 4-ball
- Slice genus is subadditive under connected sum, $g_s(K_1 \# K_2) \leq g_s(K_1) + g_s(K_2)$
- Determining slice genus for complex knots and links involves knot invariants and obstructions to sliceness (Alexander polynomial, Levine-Tristram signatures)

Unit 4 – The Fundamental Group and the Knot Group

4.1 Introduction to the fundamental group

The fundamental group is a powerful tool in knot theory, helping us classify knots and links. It captures information about loops and paths in a space, remaining unchanged under continuous deformations. This makes it invaluable for distinguishing between different knots.

Computing the fundamental group involves choosing a basepoint and considering loops. For simple spaces, we can use properties like contractibility and product spaces. In knot theory, we focus on the fundamental group of a knot's complement to determine its uniqueness.

Fundamental Group and Knot Theory

Fundamental group of topological spaces

- The fundamental group $\pi_1(X)$ is a group associated with a topological space X that captures information about loops and paths in the space
- Elements of the fundamental group are equivalence classes of loops, where two loops are equivalent if they can be continuously deformed into each other (homotopic)
- The fundamental group is a topological invariant, meaning it remains unchanged under continuous deformations (homeomorphisms) of the space
- In knot theory, the fundamental group is used to study and classify knots and links by examining the fundamental group of the complement of a knot or link (the space obtained by removing the knot or link from the 3-dimensional space $\mathbb{R}^3$ or S^3)
- Knots and links with different fundamental groups of their complements are considered distinct

Computation of fundamental groups

- To compute the fundamental group, choose a basepoint X_0 in the space X and consider loops based at X_0
- For simple spaces, the fundamental group can be computed using the following properties:
- The fundamental group of a contractible space is trivial: $\pi_1(X) = \{e\}$ (point, disk)
- The fundamental group of a circle S^1 is isomorphic to the integers: $\pi_1(S^1) \cong \mathbb{Z}$
- If X is the product of two spaces X_1 and X_2 , then $\pi_1(X) \cong \pi_1(X_1) \times \pi_1(X_2)$
- If X is the wedge sum of two spaces X_1 and X_2 , then $\pi_1(X) \cong \pi_1(X_1) * \pi_1(X_2)$ (free product of groups)
- The fundamental group of a torus $T = S^1 \times S^1$ is $\pi_1(T) \cong \mathbb{Z} \times \mathbb{Z}$
- The fundamental group of a figure-eight space (wedge sum of two circles) is $\pi_1(X) \cong \mathbb{Z} * \mathbb{Z}$ (free group on two generators)

Homotopy vs fundamental group

- Two continuous functions $f, g : X \rightarrow Y$ are homotopic if there exists a continuous function $H : X \times [0, 1] \rightarrow Y$ such that $H(x, 0) = f(x)$ and $H(x, 1) = g(x)$ for all $x \in X$
- Homotopy is an equivalence relation on the set of continuous functions from X to Y
- If two loops α and β based at x_0 are homotopic, then they represent the same element in the fundamental group $\pi_1(X, x_0)$
- Homotopy invariance: If $f : X \rightarrow Y$ is a continuous function and $f_* : \pi_1(X, x_0) \rightarrow \pi_1(Y, f(x_0))$ is the induced homomorphism, then homotopic maps induce the same homomorphism on fundamental groups

Applications in knot classification

- The fundamental group of the complement of a knot or link can be used to distinguish between different knots and links
- The unknot (trivial knot) has a complement with fundamental group isomorphic to $\mathbb{Z}$
- The trefoil knot has a complement with fundamental group presented by $\langle a, b | a^3 = b^2 \rangle$
- The Hopf link has a complement with fundamental group presented by $\langle a, b | [a, b] = 1 \rangle$ (free abelian group of rank 2)
- If two knots or links have complements with non-isomorphic fundamental groups, then the knots or links are distinct
- However, the converse is not true: there exist distinct knots and links with complements having isomorphic fundamental groups (square knot, granny knot)

4.2 Knot group and Wirtinger presentation

Knot groups are a powerful tool for understanding knots. They're defined as the fundamental group of the knot complement, capturing essential topological information. Even though equivalent knots have isomorphic knot groups, the reverse isn't always true.

Wirtinger presentations offer a way to compute knot groups from knot diagrams. By assigning generators to arcs and relations to crossings, we can create a group presentation. Simplifying these presentations helps us compare and analyze different knots more easily.

The Knot Group and Its Presentation

Knot groups and fundamental groups

- The knot group of a knot K is defined as the fundamental group of the knot complement $S^3 \setminus K$
- The knot complement is obtained by removing the knot K from the 3-dimensional sphere S^3
- The fundamental group captures information about the loops and holes in a topological space (knot complement)
- The knot group encodes essential topological information about the knot
- Equivalent knots (trefoil and its mirror image) have isomorphic knot groups

- Non-equivalent knots (trefoil and figure-eight) may have isomorphic knot groups, but the converse does not hold

Wirtinger presentations from knot diagrams

- Assign an orientation to the knot and label the arcs of the diagram with generators $X_1, X_2, \dots, X_n$
- At each crossing, assign the relation $X_k = X_i^{-1}X_jX_i$ or $X_k = X_iX_jX_i^{-1}$ depending on the orientation and crossing type
- X_i represents the generator for the arc passing under the crossing
- X_j represents the generator for the arc passing over the crossing
- X_k represents the generator for the outgoing arc
- The Wirtinger presentation is written as $\langle X_1, X_2, \dots, X_n \mid r_1, r_2, \dots, r_m \rangle$
- $X_1, X_2, \dots, X_n$ are the generators, one for each arc in the diagram
- $r_1, r_2, \dots, r_m$ are the relations, one for each crossing in the diagram

Simplification of Wirtinger presentations

- Apply Tietze transformations to modify the presentation without changing the group
- Add or remove a generator that can be expressed using other generators
- Add or remove a relation that follows from other relations
- Eliminate redundant generators and relations by substituting generators
- Identify patterns or symmetries in the presentation to further simplify it
- Use algebraic manipulations to rewrite relations in simpler forms

Computation of knot groups

- Unknot (trivial knot): $\langle x \mid \rangle \cong \mathbb{Z}$
- Trefoil knot: $\langle x, y \mid xyx = yxy \rangle$
- Figure-eight knot: $\langle x, y \mid xy^{-1}xy^{-1} = y^{-1}xyx \rangle$
- Hopf link: $\langle x, y \mid xy = yx \rangle \cong \mathbb{Z} \oplus \mathbb{Z}$
- Whitehead link: $\langle x, y \mid xyx^{-1}yxy^{-1} = y^{-1}xyx^{-1}yx \rangle$
- Borromean rings: $\langle x, y, z \mid xy = yz, yz = zx, zx = xy \rangle$

4.3 Applications of knot groups in distinguishing knots

Knot groups are powerful tools for distinguishing knots. They capture the essential structure of a knot's topology, allowing mathematicians to prove that certain knots are distinct. This algebraic approach to knot classification provides a bridge between geometry and algebra.

However, knot groups have limitations. They can't always differentiate between non-equivalent knots or detect chirality. This has led mathematicians to develop additional invariants and techniques for a more comprehensive understanding of knot classification and properties.

Knot Groups and Knot Classification

Knot groups for distinction

- The knot group is the fundamental group of the knot complement
- Knot complement is the 3-dimensional space obtained by removing the knot from $\mathbb{R}^3$ or S^3 ($\mathbb{R}^3$ is 3D Euclidean space, S^3 is the 3-sphere)
- Knot groups capture essential information about the knot's structure and entanglements
- Provide an algebraic encoding of the knot's topology (crossings, twists, and loops)
- If two knots have different knot groups, they must be distinct knots
- Knot group is a knot invariant, remains unchanged under ambient isotopy (continuous deformation without cutting or passing through itself)
- Examples of distinct knots with different knot groups:
 - Trefoil knot (simplest nontrivial knot) and unknot (simple loop with no crossings)
 - Figure-eight knot (4 crossings) and cinquefoil knot (5 crossings)

Application of knot group techniques

- To show that two knots are distinct using knot groups: 1. Calculate the knot group for each knot using a knot diagram and the Wirtinger presentation (method for presenting the knot group based on the knot diagram) 2. Simplify the presentations using Tietze transformations (operations that modify group presentations without changing the group) or other methods 3. If the resulting groups are not isomorphic (have the same structure), the knots must be distinct
- Example: The trefoil knot and the unknot have different knot groups
- Trefoil knot group has a presentation $\langle a, b \mid a^3 = b^2 \rangle$, while the unknot group is isomorphic to $\mathbb{Z}$ (the group of integers under addition)
- Knot groups can be used to prove the existence of non-equivalent knots with the same number of crossings
- 5_1 and 5_2 knots (two distinct 5-crossing knots) have different knot groups

Limitations of knot groups

- Knot groups are not complete invariants, non-equivalent knots can have isomorphic knot groups
- Square knot (two trefoil knots linked together) and granny knot (two trefoil knots linked with opposite handedness) have isomorphic knot groups but are distinct knots
- There exist infinitely many prime knots with isomorphic knot groups
- Limits the effectiveness of using knot groups alone for classification
- Prime knots cannot be decomposed into simpler knots (analogous to prime numbers)
- Knot groups cannot always detect the chirality (handedness) of a knot
- A knot and its mirror image have isomorphic knot groups, but they may not be equivalent knots (cannot be deformed into each other)

- Chirality is important in applications such as chemistry and biology

Knot groups vs other invariants

- The abelianization (making the group commutative) of the knot group yields the first homology group of the knot complement
- Related to the linking number (measure of how two knots are linked) and the Alexander polynomial (polynomial invariant of knots)
- Knot group is related to the peripheral subgroup, which encodes information about the knot's meridian (loop around the knot) and longitude (loop along the knot)
- This information is used in the construction of other invariants, such as the A-polynomial (polynomial invariant that captures the $SL(2, \mathbb{C})$ representation space of the knot group)
- Knot group can be used to construct representations into other groups
- Braid group (group of braids, which are intertwined strings) or symmetric group (group of permutations)
- These representations give rise to additional knot invariants and provide connections to other areas of mathematics (algebra, topology, and representation theory)

Unit 5 – Seifert Surfaces and Genus

5.1 Seifert surfaces and their construction

Seifert surfaces are a crucial tool in knot theory, providing a bridge between knots and surfaces. These oriented surfaces, whose boundaries are knots or links, allow us to study knot properties and compute important invariants like genus and Alexander polynomials.

Constructing Seifert surfaces is a straightforward process using Seifert's algorithm. By smoothing crossings, filling in circles, and connecting disks, we create a surface that reveals deep insights into knot structure and complexity, helping us better understand knot classification and properties.

Seifert Surfaces

Seifert surfaces in knot theory

- Oriented surface whose boundary is a given knot or link (trefoil knot, figure-eight knot)
- Exists for every knot and link proven by Herbert Seifert in 1934
- Provides a way to study properties of knots and links such as genus and Alexander polynomial
- Allows for the computation of knot and link invariants
- Genus of the knot measures complexity (genus-1 surface for trefoil knot)
- Alexander polynomial encodes topological information ($\Delta(t) = t^2 - t + 1$ for trefoil knot)
- Seifert matrix used to compute signature and determinant of knots (Seifert matrix for figure-eight knot)

Construction of Seifert surfaces

- Seifert's algorithm constructs a Seifert surface from a knot diagram (trefoil knot diagram)
- Steps: 1. Orient the knot diagram by assigning a direction to each strand (clockwise orientation) 2. Smooth each crossing according to the orientation by connecting strands of the same orientation (smoothing a crossing) 3. Fill in the resulting set of circles with disks (Seifert circles) 4. Connect the disks with twisted bands corresponding to the crossings (half-twisted bands)
- The resulting surface is a Seifert surface for the given knot (Seifert surface for the trefoil knot)
- Different choices of orientation may lead to different Seifert surfaces (Seifert surfaces for the figure-eight knot)

Properties of Seifert surfaces

- Orientable surface meaning it has a consistent choice of normal vector at each point (Möbius strip is non-orientable)
- Genus is a knot invariant defined as the minimal genus of all Seifert surfaces for the knot
- Formula: $g = \frac{1}{2}(2 - \chi(S))$, where $\chi(S)$ is the Euler characteristic ($\chi = V - E + F$ for a triangulation)
- Genus measures the complexity of the knot (unknot has genus 0, trefoil knot has genus 1)
- Seifert matrix encodes linking information of the surface

- Computed using a basis for the first homology group of the surface (generators and relations)
- Used to compute Alexander polynomial $\Delta_K(t) = \det(tV - V^T)$ and signature $\sigma(K) = \text{sign}(V + V^T)$ (Seifert matrix for the figure-eight knot)

Seifert surfaces vs knot diagrams

- Every knot diagram gives rise to a Seifert surface via Seifert's algorithm (trefoil knot diagram and its Seifert surface)
- Different knot diagrams of the same knot may yield different Seifert surfaces (figure-eight knot diagrams)
- These surfaces are related by Reidemeister moves and surface modifications (Reidemeister moves on knot diagrams)
- The minimal genus of a Seifert surface is independent of the choice of knot diagram (genus is a knot invariant)
- The crossing number $c(K)$ of a knot K provides an upper bound for the genus of its Seifert surfaces
- Inequality: $g \leq \frac{1}{2}(c(K) - 1)$ (trefoil knot has crossing number 3 and genus 1)
- This bound is not always sharp (knots with genus lower than the bound)

5.2 Genus of a knot and its properties

Knot genus is a key measure of knot complexity. It's defined as the smallest genus among all surfaces bounded by the knot. This non-negative integer remains unchanged under ambient isotopy, making it useful for classifying knots.

Calculating knot genus involves Seifert surfaces. These are oriented surfaces with the knot as their boundary. By applying Seifert's algorithm to a knot diagram, we can construct these surfaces and use them to determine the knot's genus.

Genus of a Knot

Definition of knot genus

- Non-negative integer measuring complexity of knot denoted as $g(K)$
- Defined as minimal genus among all oriented surfaces bounded by knot
- Knot invariant remains unchanged under ambient isotopy
- Knots with different genera not equivalent useful for knot classification
- Genus 0 knot is unknot bounds a disk (surface with genus 0)
- Higher genus knots more complex cannot be unknotted without cutting and reconnecting (trefoil knot, figure-eight knot)

Calculation using Seifert surfaces

- Seifert surface oriented surface whose boundary is given knot
- Constructed by applying Seifert's algorithm to knot diagram

- Knot genus is minimal genus among all possible Seifert surfaces for knot
- Calculate genus using Seifert surface: 1. Construct Seifert surface from knot diagram 2. Count number of crossings (c) in knot diagram 3. Count number of Seifert circles (s) in constructed surface 4. Apply genus formula: $g = \frac{1}{2}(2 - s + c)$
- Genus obtained from specific Seifert surface may not always be minimal provides upper bound for knot's actual genus (trefoil knot, figure-eight knot)

Properties of Knot Genus

Additivity under connected sum

- Connected sum of two knots $K_1 \# K_2$ formed by removing small arc from each knot and joining resulting endpoints
- Theorem: For any two knots K_1 and K_2 , genus of connected sum equals sum of individual genera
- In other words, $g(K_1 \# K_2) = g(K_1) + g(K_2)$
- Proof: 1. Let S_1 and S_2 be minimal genus Seifert surfaces for K_1 and K_2 , respectively 2. Remove small disk from each surface and connect surfaces along boundaries of removed disks 3. Resulting surface S is Seifert surface for $K_1 \# K_2$ 4. Genus of S equals $g(S_1) + g(S_2)$ connecting surfaces does not change total genus 5. Since S_1 and S_2 are minimal genus surfaces, $g(S)$ also minimal for $K_1 \# K_2$ 6. Therefore, $g(K_1 \# K_2) = g(S) = g(S_1) + g(S_2) = g(K_1) + g(K_2)$

Relationship to other invariants

- Crossing number $c(K)$ minimum number of crossings among all diagrams of knot
- For any knot K , $g(K) \leq \frac{1}{2}(c(K) - 1)$
- Inequality provides lower bound for crossing number in terms of genus (trefoil knot, figure-eight knot)
- Unknotting number $u(K)$ minimum number of crossing changes needed to transform knot into unknot
- For any knot K , $g(K) \leq u(K)$
- Changing crossing can be thought of as performing band surgery on Seifert surface increases genus by at most 1 (trefoil knot, figure-eight knot)
- Signature $\sigma(K)$ knot invariant derived from knot's Seifert matrix
- For any knot K , $|\sigma(K)| \leq 2g(K)$
- Inequality relates signature and genus of knot (trefoil knot, figure-eight knot)

5.3 Seifert matrices and their applications

Seifert matrices are powerful tools in knot theory, encoding crucial information about knots and links. They represent the linking data of a Seifert surface, providing a way to compute important knot invariants like the Alexander polynomial and signature.

These matrices are computed through a step-by-step process involving Seifert surfaces and homology groups. While not unique, they offer valuable insights into knot properties and help bridge the gap between geometric and algebraic aspects of knot theory.

Seifert Matrices

Seifert matrices and surfaces

- Seifert matrix represents linking information of a Seifert surface associated with a knot or link
- Seifert surface is an oriented surface bounded by the knot or link (Möbius band, punctured torus)
- Encodes topological data about the knot or link and its Seifert surface
- Depends on the choice of basis for the first homology group of the Seifert surface and its orientation
- Non-unique but provides a powerful tool for studying knots and links

Computation of Seifert matrices

- Algorithmic process to compute Seifert matrix for a given knot or link: 1. Construct a Seifert surface bounded by the knot or link (checkerboard coloring, Seifert's algorithm) 2. Select a basis for the first homology group of the surface (generators, closed loops) 3. Calculate linking numbers between each pair of basis elements and their positive pushoffs
- Positive pushoff is a slightly shifted copy of the curve in the positive normal direction 4. Organize the linking numbers into a square matrix
- Concrete examples help understand the computation process:
- Trefoil knot:

$$\begin{bmatrix} -1 & 0 \\ 1 & -1 \end{bmatrix}$$

(disk with three twisted bands)

- Figure-eight knot:

$$\begin{bmatrix} -1 & 1 \\ 0 & -1 \end{bmatrix}$$

(punctured torus)

Invariance under S-equivalence

- S-equivalence (Seifert equivalence) relates Seifert matrices representing the same knot or link
- Theorem states S-equivalent matrices share invariants like determinant and signature
- Determinant: product of eigenvalues, $\det(S)$
- Signature: number of positive minus negative eigenvalues, $\sigma(S)$
- Proof relies on showing S-equivalence is generated by matrix operations preserving these invariants
- Elementary row/column operations, transposition, direct sum with

$$\pm \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix}$$

- Establishes determinant and signature as knot invariants derivable from any Seifert matrix

Applications to knot invariants

- Seifert matrices enable computation of various knot invariants
- Alexander polynomial $\Delta_K(t)$ is defined via the Seifert matrix S :
- $\Delta_K(t) = \det(tS - S^T)$
- Symmetric: $\Delta_K(t) = \Delta_K(t^{-1})$
- Evaluates to 1 at $t = 1$
- Multiplicative under connected sum of knots
- Other invariants expressible using Seifert matrices:
- Knot determinant: $\det(K) = |\Delta_K(-1)|$ (unknot has determinant 1)
- Knot signature: $\sigma(K) = \text{signature}(S + S^T)$ (unknot has signature 0)
- Seifert matrices provide a bridge between the geometric and algebraic aspects of knot theory

Unit 6 – The Alexander Polynomial

6.1 Definition and properties of the Alexander polynomial

The Alexander polynomial is a powerful tool in knot theory, assigning a unique polynomial to each knot or link. It's calculated from a knot diagram and remains constant under deformation, making it useful for distinguishing between different knots.

This polynomial has interesting properties, like symmetry and reversibility. Its degree and coefficients provide insights into the knot's structure, including a lower bound for the knot's genus. However, it's not a perfect classifier, as different knots can share the same polynomial.

Alexander Polynomial

Definition of Alexander polynomial

- Associates a polynomial invariant $\Delta_K(t)$ with a knot or link K computed from a diagram of the knot or link
- Constructed by creating the Alexander matrix and calculating its determinant
- Laurent polynomial in the variable t with integer coefficients
- Lowest degree term has a positive power of t
- Highest degree term has a negative power of t (trefoil knot, figure-eight knot)

Invariance under ambient isotopy

- Remains constant under ambient isotopy, continuous deformation without self-intersection (Reidemeister moves)
- Knots or links with identical polynomials may not be equivalent as different knots can share the same Alexander polynomial (knot 5_1 and knot 10_132)
- Knots or links with distinct polynomials are definitely not equivalent (trefoil knot and figure-eight knot)

Symmetry and reversibility properties

- Symmetry property: $\Delta_K(t) = \Delta_K(t^{-1})$ meaning coefficients are the same read from left to right or right to left due to the determinant of the Alexander matrix
- Reversibility property: $\Delta_{K^r}(t) = \Delta_K(t^{-1})$, where K^r is the reverse of knot K
- Obtained by substituting t^{-1} for t in the original polynomial
- Results from the symmetry property and reversing a knot preserves its type (trefoil knot and its reverse)

Interpretation of degree and coefficients

- Degree of $\Delta_K(t)$ gives a lower bound for the genus $g(K)$ of knot K , the minimum number of handles needed to construct a surface bounded by the knot
- $\deg(\Delta_K(t)) \leq 2g(K)$ (trefoil knot has genus 1, degree 2)

- Coefficients alternate in sign with the constant term (coefficient of t^0) and leading/trailing coefficients (coefficients of highest/lowest degree terms) always ± 1
- Absolute values of coefficients do not necessarily decrease from the center (figure-eight knot polynomial $t^{-1} - 3 + t$)

6.2 Computation techniques for the Alexander polynomial

The Alexander polynomial is a powerful tool for distinguishing knots. It's calculated using a knot's diagram, assigning variables to arcs and creating a matrix based on crossings. The determinant of this matrix gives us the polynomial, which uniquely characterizes the knot.

Skein relations offer a way to simplify knot calculations. By relating different crossing types, we can break down complex knots into simpler ones. This method, along with Fox calculus and computer algorithms, provides multiple approaches to compute the Alexander polynomial efficiently.

Computation Techniques for the Alexander Polynomial

Computation of Alexander polynomial

- Obtain knot diagram representing the knot visually depicts crossings and loops
- Label arcs of knot diagram with variables (a, b, c) to track each segment
- Assign matrix entry for each crossing in knot diagram encodes over/under information
- Positive crossing uses t for over-arc and $1 - t$ for under-arc (right-handed)
- Negative crossing uses $1 - t$ for over-arc and t for under-arc (left-handed)
- Construct Alexander matrix using assigned matrix entries captures knot structure
- Matrix has one less row than number of arcs since one arc is redundant
- Each row corresponds to crossing and each column to arc establishing relationships
- Calculate determinant of any minor of Alexander matrix by deleting one column
- Resulting determinant is Alexander polynomial $\Delta(t)$ characterizing knot

Skein relations for simplification

- Skein relations provide recursive method to compute Alexander polynomial by simplifying knot
- Three basic skein relations for Alexander polynomial:
 - $\Delta_{L_+}(t) = \Delta_{L_-}(t) + (t^{1/2} - t^{-1/2})\Delta_{L_0}(t)$ relates positive, negative, and no crossing
 - $\Delta_{L_-}(t) = \Delta_{L_+}(t) - (t^{1/2} - t^{-1/2})\Delta_{L_0}(t)$ expresses negative in terms of positive and no crossing
 - $\Delta_{L_0}(t) = \frac{\Delta_{L_+}(t) - \Delta_{L_-}(t)}{t^{1/2} - t^{-1/2}}$ calculates no crossing from positive and negative
- L_+, L_-, L_0 represent link diagrams differing only in small region
- L_+ has positive crossing, L_- negative crossing, L_0 no crossing (unknot)
- Apply skein relations repeatedly to simplify knot diagram by reducing crossings
- Continue until diagram reduced to simple unknot or split link

- Alexander polynomial of unknot is 1 (trivial knot)
- Alexander polynomial of split link is 0 (unlinked components)

Fox calculus for Alexander polynomial

- Consider knot group presentation associated with knot diagram algebraically
- Assign generator to each arc in knot diagram labeling segments
- Write relations at each crossing using assigned generators expressing connectivity
- Positive crossing with generators a, b, c has relation $a = c^{-1}bc$ (right-hand rule)
- Negative crossing with generators a, b, c has relation $a = bcb^{-1}$ (left-hand rule)
- Apply Fox derivative to each relation wrt each generator
- Fox derivative is linear operator satisfying specific properties (product rule, chain rule)
- Construct Jacobian matrix using Fox derivatives encoding knot group info
- Each row corresponds to relation and each column to generator mapping presentation
- Substitute t for one generator and 1 for others in Jacobian matrix
- Calculate determinant of resulting matrix
- Determinant is Alexander polynomial $\Delta(t)$ derived from knot group

Algorithms in computer algebra systems

- Utilize computer algebra systems (Mathematica, Maple, SageMath) to automate computation
- Implement algorithms based on Alexander matrix method
- Represent knot diagram as data structure capturing crossings and arcs
- Assign variables to arcs and construct Alexander matrix programmatically
- Calculate determinant of minor of Alexander matrix using built-in functions
- Implement algorithms based on skein relation method
- Recursively apply skein relations to simplify knot diagram until base case reached
- Handle base cases (unknot and split link) appropriately returning known values
- Implement algorithms based on Fox calculus method
- Represent knot group presentation and assign generators to arcs as symbols
- Apply Fox derivative to relations and construct Jacobian matrix using symbolic math
- Substitute variables and calculate determinant leveraging matrix operations
- Verify correctness of implemented algorithms using known examples (3_1 knot, 4_1 knot) and properties of Alexander polynomial (symmetry, normalization)

6.3 Applications and limitations of the Alexander polynomial

The Alexander polynomial is a powerful tool in knot theory, helping us tell different knots apart. It's calculated using knot diagrams and has cool properties like being multiplicative for connected sums. This makes it super useful for studying knots and links.

But it's not perfect. Some different knots can have the same Alexander polynomial, and it can't tell apart a knot from its mirror image. Still, it's connected to other important concepts in knot theory and has real-world applications in biology, physics, and chemistry.

Applications and Properties of the Alexander Polynomial

Alexander polynomial for knot distinction

- Powerful knot invariant distinguishes between different knots and links
- Different Alexander polynomials prove knots are distinct (trefoil knot $\Delta(t) = t^2 - t + 1$, figure-eight knot $\Delta(t) = t^2 - 3t + 1$)
- Calculated using knot diagram and determinant formula
- Independent of chosen diagram for a given knot, making it well-defined invariant
- Multiplicative under connected sum operation
- Connected sum $K_1 \# K_2$ has Alexander polynomial $\Delta_{K_1 \# K_2}(t) = \Delta_{K_1}(t) \cdot \Delta_{K_2}(t)$
- Distinguishes between different links
- Links with different numbers of components have different Alexander polynomials (Hopf link $\Delta(t) = t^{1/2} - t^{-1/2}$, unlink $\Delta(t) = 0$)

Limitations of Alexander polynomial

- Not a complete invariant, distinct knots can have same Alexander polynomial
- Conway knot and Kinoshita-Terasaka knot both have $\Delta(t) = 1$ but are distinct
- Cannot detect chirality of a knot
- Knot and its mirror image have same Alexander polynomial (right-handed and left-handed trefoil knots $\Delta(t) = t^2 - t + 1$)
- Does not provide information about genus of a knot
- Knots with different genera can have same Alexander polynomial
- Cannot detect unknotting number of a knot
- Minimum number of crossings changed to transform knot into unknot
- Knots with different unknotting numbers can have same Alexander polynomial

Alexander polynomial vs other invariants

- Related to Jones polynomial, another important knot invariant
- Jones polynomial obtained from Alexander polynomial by variable substitution and normalization

- Jones polynomial is stronger invariant, can distinguish knots with same Alexander polynomial
- Connected to knot group, fundamental group of knot complement
- Alexander polynomial derived from Alexander matrix, obtained from presentation of knot group
- Knot group contains more information than Alexander polynomial but more difficult to compute and compare
- Related to signature of a knot, another numerical invariant
- Signature obtained from Alexander polynomial by evaluating at $t = -1$
- Signature provides information about cobordism class of the knot

Applications of Alexander polynomial

- Biology: studies topology of DNA molecules
- DNA forms knots and links during replication and recombination
- Classifies and distinguishes different DNA knot types
- Analyzes knotting probability and complexity of DNA in viral capsids
- Physics: appears in quantum knot invariants and topological quantum field theories
- Quantum knot invariants generalize classical knot polynomials (Alexander and Jones) in quantum mechanics context
- Related to Chern-Simons theory, describes behavior of knots and links in 3D space
- Chemistry: applications in molecular knots and links
- Molecules (catenanes, rotaxanes) exhibit non-trivial topological structures described using knot theory
- Characterizes and distinguishes different molecular knot types
- Studies synthesis and properties of molecular Borromean rings (link of three interlocked rings)

Unit 7 – The Jones Polynomial and Kauffman Bracket

7.1 Introduction to the Jones polynomial

The Jones polynomial is a game-changer in knot theory. Discovered in 1984, it's a powerful tool that can tell apart knots that other methods couldn't. It assigns a unique polynomial to each knot, staying the same even when you twist and turn the knot around.

Calculating the Jones polynomial is like solving a puzzle. You start with a knot diagram and use special rules to break it down into simpler pieces. Keep going until you reach the simplest knot, then work backwards to get the final answer.

Introduction to the Jones Polynomial

Jones polynomial in knot theory

- Knot invariant discovered by Vaughan Jones in 1984 remains unchanged under continuous deformations of the knot (Reidemeister moves)
- Polynomial in the variable t associated with each knot or link
- Distinguishes many knots previously indistinguishable by other invariants (Alexander polynomial)
- Has connections to statistical mechanics and quantum field theory

Construction of Jones polynomial

- Defined recursively using skein relations which relate the polynomials of different knot diagrams
- Skein relation for the Jones polynomial: $t^{-1}V_{L_+}(t) - tV_{L_-}(t) = (t^{1/2} - t^{-1/2})V_{L_0}(t)$
- L_+ , L_- , and L_0 represent link diagrams differing only in a small region with a positive crossing, negative crossing, and no crossing, respectively
- Jones polynomial of the unknot defined as $V_{\text{unknot}}(t) = 1$
- Calculating the Jones polynomial of a knot or link: 1. Choose a crossing in the diagram and apply the skein relation 2. Continue applying the skein relation to the resulting diagrams until the unknot is reached 3. Combine the results using the skein relation to obtain the final polynomial

Calculation for simple knots

- Trefoil knot:
 - Applying skein relation to a crossing results in the unknot and the Hopf link
 - Jones polynomial of the trefoil knot: $V_{\text{trefoil}}(t) = t + t^3 - t^4$
- Figure-eight knot:
 - Applying skein relation to a crossing results in the unknot and a link with two components
 - Jones polynomial of the figure-eight knot: $V_{\text{figure-eight}}(t) = t^{-2} - t^{-1} + 1 - t + t^2$

- Hopf link:
- Applying skein relation to a crossing results in two unknots
- Jones polynomial of the Hopf link: $V_{\text{Hopf}}(t) = -t^{5/2} - t^{1/2}$

Invariance under Reidemeister moves

- Jones polynomial invariant under Reidemeister moves which are local moves on a knot diagram not changing the underlying knot type
- Reidemeister move I: Adds or removes a twist from the diagram
- Reidemeister move II: Moves two strands over or under each other
- Reidemeister move III: Moves a strand over or under a crossing
- Proving invariance under Reidemeister moves requires showing the polynomial remains unchanged when each move is applied
- Achieved by applying the skein relation to relevant parts of the diagram and showing the resulting polynomials are equal

7.2 The Kauffman bracket and its relation to the Jones polynomial

The Kauffman bracket is a powerful tool in knot theory. It assigns a polynomial to unoriented link diagrams, providing a way to distinguish between different knots and links. This invariant forms the foundation for the Jones polynomial.

Calculating the Kauffman bracket involves applying skein relations to simplify link diagrams. Its invariance under Reidemeister moves ensures it remains consistent regardless of how a knot is drawn, making it a reliable method for knot classification.

The Kauffman Bracket

Kauffman bracket properties

- Polynomial invariant of unoriented link diagrams assigns Laurent polynomial in variable A to each unoriented link diagram
- Unknot $\bigcirc$ has Kauffman bracket $\langle \bigcirc \rangle = 1$
- Disjoint union of link L and unknot $L \sqcup \bigcirc$ satisfies $\langle L \sqcup \bigcirc \rangle = (-A^2 - A^{-2})\langle L \rangle$
- Skein relation for overcrossing  expressed as $\langle \text{overcrossing} \rangle = A \langle \text{smoothing}_A \rangle + A^{-1} \langle \text{smoothing}_B \rangle$

Kauffman bracket vs Jones polynomial

- Jones polynomial $V_L(t)$ obtained from Kauffman bracket by variable substitution $t = A^{-4}$ and normalization factor $(-A)^{-3w(L)}$
- $w(L)$ represents writhe of oriented link L
- Relationship between Kauffman bracket and Jones polynomial: $V_L(t) = (-A)^{-3w(L)} \langle L \rangle|_{A=t^{-1/4}}$

Calculating Jones polynomials

1. Obtain unoriented diagram of knot or link
2. Apply Kauffman bracket skein relation recursively until diagram reduced to linear combination of unknots
3. Evaluate resulting polynomial in variable A
4. Substitute $t = A^{-4}$ and multiply by normalization factor $(-A)^{-3w(L)}$ to obtain Jones polynomial $V_L(t)$

Invariance of the Kauffman Bracket

Invariance under Reidemeister moves

- Kauffman bracket invariant under three Reidemeister moves, local modifications of link diagrams not changing underlying link
- Reidemeister move I:
 - $\langle \text{\includegraphics[height=0.4cm]{R1_before.png}} \rangle = (-A^3) \langle \text{\includegraphics[height=0.4cm]{R1_after.png}} \rangle$ (positive twist)
 - $\langle \text{\includegraphics[height=0.4cm]{R1_mirror_before.png}} \rangle = (-A^{-3}) \langle \text{\includegraphics[height=0.4cm]{R1_mirror_after.png}} \rangle$ (negative twist)
- Reidemeister move II: $\langle \text{\includegraphics[height=0.4cm]{R2_before.png}} \rangle = \langle \text{\includegraphics[height=0.4cm]{R2_after.png}} \rangle$
- Reidemeister move III: $\langle \text{\includegraphics[height=0.4cm]{R3_before.png}} \rangle = \langle \text{\includegraphics[height=0.4cm]{R3_after.png}} \rangle$
- Invariance under Reidemeister moves ensures Kauffman bracket well-defined link invariant independent of chosen diagram representation

7.3 Properties and applications of the Jones polynomial

The Jones polynomial is a powerful tool in knot theory, helping us tell knots apart. It's like a unique fingerprint for knots, staying the same even when we twist or move the knot around without cutting it.

This polynomial has some cool tricks up its sleeve. It can spot differences between knots, works well with combined knots, and even tells us about mirror images. But it's not perfect – sometimes different knots can have the same polynomial.

Properties of the Jones Polynomial

Properties of Jones polynomial

- Remains unchanged under ambient isotopy of the knot (knot invariant)
- Satisfies multiplicative property for connected sum of two knots K_1 and K_2 :
 $V_{K_1 \# K_2}(t) = V_{K_1}(t) \cdot V_{K_2}(t)$
- For mirror image of knot K , denoted as K^* , satisfies: $V_{K^*}(t) = V_K(t^{-1})$
- Equal to 1 for the unknot

- For empty link with n components, equal to $(-t^{\frac{1}{2}} - t^{-\frac{1}{2}})^{n-1}$

Jones polynomial for knot distinction

- Distinguishes between certain knots and links with different polynomials
- Different Jones polynomials imply necessarily distinct knots
- Examples of knots with distinct Jones polynomials:
 - Unknot: Jones polynomial of 1
 - Trefoil knot: Jones polynomial of $t + t^3 - t^4$
 - Figure-eight knot: Jones polynomial of $t^{-2} - t^{-1} + 1 - t + t^2$

Limitations in knot equivalence detection

- Same Jones polynomial does not guarantee equivalent knots
- Infinitely many distinct knots exist with the same Jones polynomial
- Conway knot and Kinoshita-Terasaka knot: same Jones polynomial but not equivalent
- Not a complete invariant, cannot always determine knot equivalence

Applications of the Jones Polynomial

Applications beyond knot theory

- Connections to statistical mechanics and quantum field theory
- Interpreted as partition function in certain statistical mechanical models
- Related to Witten-Reshetikhin-Turaev invariant in quantum field theory
- Related to representation theory of quantum group $U_q(sl_2)$
- Describes behavior of certain anyons in topological quantum computation
- Anyons: quasi-particles with exotic braiding statistics used for quantum computation
- Applications in DNA topology and study of enzyme action on DNA knots and links

Unit 8 – Polynomial Invariants: HOMFLY and Kauffman

8.1 The HOMFLY polynomial: definition and properties

The HOMFLY polynomial is a powerful tool in knot theory, generalizing both the Alexander and Jones polynomials. It's defined using skein relations, which relate polynomials of links differing at a single crossing, allowing us to compute it for various knots and links.

Calculating the HOMFLY polynomial involves applying skein relations recursively until a link is reduced to a combination of unknots. This process helps distinguish between different knots and links, making it a valuable invariant in the study of knot theory.

Definition and Computation of the HOMFLY Polynomial

Definition of HOMFLY polynomial

- Denoted as $P(L)$, two-variable polynomial invariant of oriented links (knots and links)
- Generalizes Alexander polynomial and Jones polynomial
- Defined using skein relations relate polynomials of links differing at a single crossing
- Skein relations for HOMFLY polynomial:
 - $lP(L_+) + l^{-1}P(L_-) + mP(L_0) = 0$
 - L_+ , L_- , L_0 represent links differing at a single crossing
 - l and m are variables in the polynomial
 - $P(U) = 1$, where U is the unknot (simplest knot)

Computation for simple knots

- Apply skein relations recursively until link is reduced to combination of unknots
- At each crossing, use skein relation to express polynomial in terms of simpler links
- Continue process until link is fully simplified
- Trefoil knot (3_1) example: 1. Apply skein relation at one of the crossings 2. Express polynomial in terms of unknot and Hopf link (two linked circles) 3. Use skein relation again on Hopf link to express it in terms of unknots 4. Simplify resulting expression to obtain HOMFLY polynomial for trefoil knot

Relationship to other polynomials

- HOMFLY polynomial generalizes both Alexander and Jones polynomials
- Setting $l = i$ and $m = i(t^{1/2} - t^{-1/2})$ yields Jones polynomial
- Setting $l = i$ and $m = i(t^{1/2} - t^{-1/2})$, then substituting $t = -s^{-2}$, yields Alexander polynomial multiplied by $(-1)^{w(L)}s^{-w(L)}$, where $w(L)$ is writhe of link L (sum of crossing signs)

- HOMFLY polynomial distinguishes more links than Alexander or Jones polynomials individually (figure-eight knot and its mirror image)

Invariance under Reidemeister moves

- To prove invariance, show polynomial remains unchanged under each move
- Reidemeister move I:
 - Use skein relation to express polynomial of link with twist in terms of polynomial of link without twist
 - Show resulting expression is equal to original polynomial
- Reidemeister move II:
 - Apply skein relation twice to link with two overlapping strands
 - Show resulting expression is equal to polynomial of link without overlapping strands
- Reidemeister move III:
 - Apply skein relation to each side of move
 - Show resulting expressions are equal, demonstrating invariance of polynomial under move

8.2 The Kauffman polynomial: definition and properties

The Kauffman polynomial is a powerful tool in knot theory, offering a two-variable approach to distinguishing knots and links. It builds on the Kauffman bracket, incorporating writhe normalization to create a more robust invariant than its predecessors.

This polynomial's strength lies in its ability to differentiate between certain knots that simpler invariants can't. It's also closely related to the Jones polynomial, showcasing the interconnected nature of knot invariants in this fascinating field of mathematics.

The Kauffman Polynomial

Definition of Kauffman polynomial

#####

- Two-variable polynomial invariant for knots and links denoted as $F(L, a, x)$
- L represents the link or knot being studied
- a and x are variables used in the polynomial
- Defined using the Kauffman bracket $\langle L \rangle$, a Laurent polynomial in the variable A that is a state sum invariant of unoriented link diagrams
- Obtained from the Kauffman bracket by substituting $A = a^{-1/4}$ and introducing a writhe normalization factor $a^{-w(L)/4}$
- Writhe $w(L)$ measures the self-linking of a knot or link diagram, with each positive crossing contributing +1 and each negative crossing contributing -1
- The Kauffman polynomial is defined as: $F(L, a, x) = a^{-w(L)/4} \langle L \rangle|_{A=a^{-1/4}}$

Calculation for simple knots

- Compute the Kauffman bracket of the link diagram using the following rules: 1. $\langle \bigcirc \rangle = 1$ for the unknot $\bigcirc$ 2. $\langle L \sqcup \bigcirc \rangle = (-A^2 - A^{-2})\langle L \rangle$ for disjoint union $\sqcup$ 3. $\langle \text{raisebox-2pt\includegraphics[height=0.4cm]{L+.png}} \rangle = A \langle \text{raisebox-2pt\includegraphics[height=0.4cm]{L0.png}} \rangle + A^{-1} \langle \text{raisebox-2pt\includegraphics[height=0.4cm]{Linf.png}} \rangle$ for link diagrams differing only at one crossing
- Calculate the writhe of the link diagram by summing the contributions of each crossing
- Substitute $A = a^{-1/4}$ in the Kauffman bracket and multiply by the writhe normalization factor $a^{-w(L)/4}$ to obtain the Kauffman polynomial

Kauffman vs Jones polynomials

- The Kauffman polynomial is a generalization of the Jones polynomial $V(L, t)$, a one-variable polynomial invariant for knots and links
- The Kauffman polynomial can be specialized to the Jones polynomial by setting $x = -A^3$ and $a = A^4$: $V(L, t) = F(L, t^{-1/4}, -t^{-3/4})|_{t=A^{-4}}$
- Both polynomials are invariant under Reidemeister moves and can distinguish certain knots and links

Invariance under Reidemeister moves

- The Kauffman polynomial is invariant under Reidemeister moves, local modifications of link diagrams that do not change the underlying knot or link
- Reidemeister move I: A twist can be added or removed from a strand
- Reidemeister move II: Two strands can be moved over or under each other
- Reidemeister move III: A strand can be moved over or under a crossing

Knot Theory Study Guide

- The Kauffman polynomial is invariant under Reidemeister moves, local modifications of link diagrams that do not change the underlying knot or link
- Reidemeister move I: A twist can be added or removed from a strand
- Reidemeister move II: Two strands can be moved over or under each other
- Reidemeister move III: A strand can be moved over or under a crossing

Invariance under Reidemeister move I:

Consider a link diagram with a single twist [positive twist] and its Kauffman bracket:

$$\langle [\text{positive twist}] \rangle = A \langle [\text{straight strand}] \rangle + A^{-1} \langle [\text{straight strand}] \rangle = (-A^3 - A^{-3}) \langle [\text{straight strand}] \rangle$$

1. The writhe of [positive twist] is 1, so the Kauffman polynomial is:

$$F([\text{positive twist}], a, x) = a^{-1/4}(-a^{-3/4} - a^{3/4}) \langle [\text{straight strand}] \rangle = (-a^{-1} - a)F([\text{straight strand}], a, x)$$

1. Similarly, for a negative twist [negative twist], the Kauffman polynomial is:

$$F([\text{negative twist}], a, x) = (-a^{-1} - a)F([\text{straight strand}], a, x)$$

1. This shows that the Kauffman polynomial is invariant under Reidemeister move I, up to multiplication by $(-a^{-1} - a)$

- Similar arguments demonstrate invariance under Reidemeister moves II and III

8.3 Comparisons and relationships between polynomial invariants

Polynomial invariants are powerful tools in knot theory, helping us distinguish and classify knots. The HOMFLY, Kauffman, Alexander, and Jones polynomials each have unique strengths and weaknesses in differentiating knots and capturing their properties.

While the HOMFLY polynomial is the most general, encompassing both Alexander and Jones, no universal polynomial invariant exists yet. Researchers continue to explore new invariants and their connections to other areas of math, seeking a more comprehensive understanding of knots.

Polynomial Invariants in Knot Theory

Strengths vs weaknesses of polynomial invariants

- HOMFLY polynomial
 - Strengths
 - Distinguishes a wide range of knots and links (trefoil knot, figure-eight knot)
 - Generalizes both the Alexander and Jones polynomials unifying them under one framework
 - Sensitive to the orientation of the knot or link captures directional information
 - Weaknesses
 - Computationally more complex than the Alexander and Jones polynomials requires more computational resources
 - Does not distinguish all knots fails to differentiate mutant knots
- Kauffman polynomial
 - Strengths
 - Distinguishes a wide range of knots and links (Kinoshita-Terasaka knot, Conway knot)
 - Sensitive to the framing of the knot or link detects twisting and linking
 - Generalizes the Jones polynomial extending its capabilities
 - Weaknesses
 - Computationally more complex than the Jones polynomial demands more computational power
 - Does not distinguish all knots unable to distinguish mutant knots
- Alexander polynomial
 - Strengths
 - Relatively simple to compute easier to calculate than HOMFLY and Kauffman polynomials
 - Distinguishes a significant number of knots (trefoil knot, figure-eight knot)

- Provides information about the knot group and the Alexander module offers algebraic insights
- Weaknesses
 - Less powerful than the HOMFLY and Kauffman polynomials in distinguishing knots has limitations in classification
 - Not sensitive to the orientation of the knot does not capture directional information
 - Does not distinguish all knots cannot differentiate the unknot and the trefoil knot
- Jones polynomial
- Strengths
 - Relatively simple to compute more efficient than HOMFLY and Kauffman polynomials
 - Distinguishes a significant number of knots (trefoil knot, figure-eight knot)
 - Sensitive to the orientation of the knot captures directional information
- Weaknesses
 - Less powerful than the HOMFLY and Kauffman polynomials in distinguishing knots has limitations in classification
 - Does not distinguish all knots fails to differentiate mutant knots

Relationships between polynomial invariants

- The HOMFLY polynomial generalizes both the Alexander and Jones polynomials
- Setting a variable in the HOMFLY polynomial to a specific value yields the Alexander polynomial ($z = 1$)
- Setting another variable in the HOMFLY polynomial to a specific value yields the Jones polynomial ($a = t^{-1}, z = \sqrt{t}$)
- The Kauffman polynomial generalizes the Jones polynomial
- Setting a variable in the Kauffman polynomial to a specific value yields the Jones polynomial ($a = 1$)
- The Alexander and Jones polynomials are not directly related but both are special cases of the HOMFLY polynomial
- All polynomial invariants are derived from the skein relations describe how the polynomial changes under certain modifications of the knot or link diagram (Reidemeister moves)

Suitability of invariants for classification

- Consider the computational complexity of the polynomial invariant
- For large knots or links, the HOMFLY and Kauffman polynomials may be more time-consuming to compute than the Alexander and Jones polynomials due to their increased complexity
- Assess the level of distinction required between knots
- If the knots in question are known to be distinguishable by the Alexander or Jones polynomials, these may be sufficient for classification purposes

- For more challenging classification problems, the HOMFLY or Kauffman polynomials may be necessary to achieve the required level of distinction
- Evaluate the sensitivity to orientation and framing required
- If orientation or framing is crucial to the classification problem, choose a polynomial invariant that is sensitive to these properties (HOMFLY, Kauffman, or Jones)
- Consider the potential for additional insights
- The Alexander polynomial provides information about the knot group and the Alexander module may be valuable for certain classification problems offering algebraic insights

Possibility of universal polynomial invariant

- The HOMFLY polynomial is the most general polynomial invariant currently known encompassing both the Alexander and Jones polynomials
- However, the HOMFLY polynomial does not distinguish all knots fails to differentiate mutant knots
- The existence of a truly universal polynomial invariant that distinguishes all knots remains an open question in knot theory an active area of research
- Research in this area focuses on: 1. Discovering new polynomial invariants that generalize existing ones seeking more powerful invariants 2. Investigating the relationships between polynomial invariants and other knot invariants exploring connections with Vassiliev invariants and Khovanov homology 3. Exploring the connections between polynomial invariants and other areas of mathematics uncovering links to quantum field theory and representation theory

Unit 9 – Knot Tabulation and Classification

9.1 Historical development of knot tables

Knot tables have come a long way since Tait's first attempt in 1877. From manual tabulation to computerized databases, these tables have grown to include knots with up to 19 crossings, revolutionizing how we study and classify knots.

The development of knot tables has faced challenges like distinguishing between knots and computational limitations. However, these tables have become crucial for classification, developing invariants, and applications in physics and chemistry, connecting knot theory to various mathematical disciplines.

Historical Development of Knot Tables

Progression of knot tabulation

- Early attempts at knot tabulation
- Tait's knot tables (1877) first systematic attempt to classify knots included knots up to 10 crossings
- Little's knot tables (1885) extended Tait's work to include knots up to 11 crossings
- Modern comprehensive knot tables
- Rolfsen's knot table (1976) included knots up to 10 crossings with detailed diagrams and invariants
- Hoste-Thistlethwaite-Weeks (HTW) knot table (1998) computerized table of prime knots up to 16 crossings
- Knot Atlas (2005-present) online database of knots and links includes knots up to 19 crossings and links up to 12 crossings

Contributors to knot tabulation

- Peter Guthrie Tait (1831-1901)
- Scottish physicist and mathematician pioneered the systematic study of knots
- Created the first knot tables up to 10 crossings
- Charles Newton Little (1858-1923)
- American mathematician extended Tait's work to include knots up to 11 crossings
- Introduced the concept of knot invariants
- Dale Rolfsen (1940-present)
- Canadian mathematician created a comprehensive knot table with detailed diagrams and invariants
- Author of the influential book "Knots and Links"
- Jim Hoste, Morwen Thistlethwaite, and Jeff Weeks collaborated to create the computerized HTW knot table extended the tabulation of prime knots up to 16 crossings

- Dror Bar-Natan and Scott Morrison creators of the online Knot Atlas database continuously update and maintain the database with contributions from the knot theory community

Challenges in early tabulation

- Distinguishing between different knots
- Early tabulators relied on visual inspection and manual manipulation of knot diagrams
- Development of knot invariants (Alexander polynomial, Jones polynomial) provided more reliable methods for distinguishing knots
- Computational limitations
- Manual tabulation was time-consuming and error-prone
- Advances in computer technology and algorithms allowed for automated generation and analysis of knot diagrams
- Incomplete or inconsistent notation
- Early knot tables lacked a standardized notation system
- Introduction of Dowker-Thistlethwaite notation and Gauss code provided a consistent way to represent knots
- Limited scope
- Early tables only included knots up to a certain number of crossings
- Collaborative efforts and use of computers enabled tabulation of knots with higher crossing numbers

Significance of knot tables

- Classification and organization of knots
- Knot tables provide a systematic way to categorize and study knots
- Enable researchers to identify patterns and relationships between different knots
- Development of knot invariants
- Knot tables serve as a testing ground for new knot invariants
- Help in evaluating the effectiveness and discriminatory power of invariants
- Applications in physics
- Knot tables are used to study the behavior of knotted structures in polymer physics and statistical mechanics
- Help in understanding the properties of DNA and other biological molecules
- Applications in chemistry
- Knot tables are used to classify and study molecular knots and links
- Aid in the design and synthesis of novel knotted molecules with potential applications in materials science and drug delivery
- Connections to other areas of mathematics

- Knot tables provide insights into the relationships between knot theory and other mathematical disciplines (group theory, topology, combinatorics)
- Stimulate cross-disciplinary research and the development of new mathematical tools and techniques

9.2 Classification of knots up to certain crossing numbers

Crossing number is a crucial concept in knot classification. It's the minimum number of crossings in any diagram of a knot, helping determine complexity. Knots with the same crossing number are grouped together in knot tables.

Up to 10 crossings, there are 165 distinct knots. These include familiar examples like the trefoil knot (3_1) and figure-eight knot (4_1). Prime knots can't be decomposed, while composite knots are formed by combining prime knots.

Knot Classification by Crossing Number

Crossing number in knot classification

- Minimum number of crossings in any diagram of a knot K denoted as $c(K)$
- Determines knot complexity and serves as primary means of classification
- Knots with same crossing number grouped together in knot tables
- Invariant property remains constant under ambient isotopy (continuous deformations)

Knot classification up to 10 crossings

- Knots denoted by n_m , where n is crossing number and m is index within that crossing number
- Trefoil knot (3_1) first knot with 3 crossings
- 165 distinct knots up to 10 crossings (not including mirror images)
- 0 crossings: unknot (0_1)
- 3 crossings: trefoil knot (3_1)
- 4 crossings: figure-eight knot (4_1)
- 5 crossings: 5_1 and 5_2
- 6 crossings: 6_1 , 6_2 , and 6_3
- 7 crossings: 7_1 to 7_7
- 8 crossings: 8_1 to 8_{21}
- 9 crossings: 9_1 to 9_{49}
- 10 crossings: 10_1 to 10_{165}

Prime vs composite knots

- Prime knots cannot be decomposed into sum (connected sum) of two non-trivial knots
- All knots up to 7 crossings are prime (trefoil knot 3_1 , figure-eight knot 4_1)

- Composite knots formed by connected sum of two or more prime knots
- Denoted by prime knots used in composition (square knot $3_1 \# 3_1$ composed of two trefoil knots)
- First appear in knot tables at 8 crossings (8_{20} and 8_{21})
- Knot tables typically list prime knots first followed by composite knots

Knot Invariants and Symmetries

Knot invariants for differentiation

- Properties that remain constant under ambient isotopy used to distinguish knots with same crossing number
- Tricolorability: knot diagram can be colored with three colors such that at each crossing either all three colors are present or only one color is present
- Trefoil knot (3_1) is tricolorable, figure-eight knot (4_1) is not
- Knot polynomials: algebraic expressions associated with knot that are invariant under ambient isotopy (Alexander polynomial, Jones polynomial, HOMFLY-PT polynomial)
- Knot signature: integer invariant derived from knot's Seifert matrix
- Trefoil knot (3_1) has signature -2, figure-eight knot (4_1) has signature 0

Symmetries and chirality of knots

- Symmetries are transformations that preserve knot type
- Rotational symmetry: knot unchanged by rotations about an axis
- Trefoil knot (3_1) has no rotational symmetry, figure-eight knot (4_1) has 180-degree rotational symmetry
- Mirror symmetry: knot unchanged by reflection across a plane
- Amphichiral knots equivalent to their mirror image (figure-eight knot 4_1)
- Chiral knots not equivalent to their mirror image (trefoil knot 3_1 with distinct left-handed and right-handed forms)
- Knot tables often include information about symmetries and chirality of each knot

9.3 Computational methods in knot tabulation

Computational methods have revolutionized knot tabulation, enabling faster classification and analysis of complex knots. These techniques leverage algorithms and computer power to generate, classify, and study knots with higher crossing numbers, pushing the boundaries of what's possible in knot theory.

Knot databases and visualization tools have emerged as crucial resources for researchers. These digital platforms allow for easy access to comprehensive knot information, fostering collaboration and knowledge sharing among knot theorists worldwide. They're changing how we approach and understand knots.

Computational Methods in Knot Tabulation

Computational methods in knot tabulation

- Computational methods have revolutionized knot tabulation and classification by:
- Utilizing algorithms that can generate and classify knots much faster than manual methods
- Leveraging computers to handle complex calculations and large datasets efficiently
- Computational approaches have extended the limits of knot tabulation enabling:
- Tabulation and classification of knots with higher crossing numbers
- Discovery and analysis of new knot invariants and properties
- Computational methods enable the creation and maintenance of comprehensive knot databases that:
- Allow researchers to access and study a wide range of knots and their properties
- Facilitate collaboration and knowledge sharing among knot theorists (KnotInfo, KnotAtlas)

Algorithms for knot classification

- Knot generation algorithms involve:
- Systematic generation of knot diagrams based on crossing number
- Recursive algorithms that build knots from simpler components (tangles, braids)
- Random knot generation using statistical methods (Gaussian random polygons)
- Knot classification algorithms include:
- Calculation of knot invariants, such as polynomial invariants (Jones polynomial) and hyperbolic volume
- Comparison of invariants to determine knot equivalence
- Application of machine learning techniques for pattern recognition and classification (neural networks)
- Efficient data structures and algorithms for representing and manipulating knots utilize:
- Planar diagram representations, such as Gauss codes and Dowker-Thistlethwaite codes
- Graph-based representations, such as the knot complement and the fundamental group

Computational vs manual tabulation

- Advantages of computational methods:
- Faster and more efficient than manual tabulation
- Can handle larger datasets and higher crossing numbers
- Enable the discovery of new knot properties and relationships
- Facilitate collaboration and data sharing among researchers
- Limitations of computational methods:

- Dependent on the quality and completeness of the underlying algorithms
- May miss subtle geometric or topological properties that human intuition can detect
- Computational complexity can limit the feasibility of certain calculations (NP-hard problems)
- Require specialized knowledge in programming and algorithm design

Knot databases and visualization tools

- Knot databases:
 - KnotInfo: A comprehensive database of knots and their properties
 - KnotAtlas: An interactive database with visualizations and invariant data
 - LinkInfo: A database focused on links and their properties
- Software tools for knot manipulation and visualization:
 - KnotPlot: A program for creating and manipulating knot diagrams
 - SnapPy: A software package for studying the topology and geometry of 3-manifolds
 - KnotTheory package for Mathematica: A set of tools for symbolic computation in knot theory
- Visualization techniques:
 - 2D projections and diagrams (knot diagrams, Reidemeister moves)
 - 3D models and interactive visualizations (virtual knots, knotted surfaces)
 - Virtual reality and augmented reality applications for immersive knot exploration

Extending tabulation through computation

- Pushing the boundaries of knot tabulation by:
 - Developing more efficient algorithms for generating and classifying knots
 - Exploiting parallel computing and distributed systems to handle larger datasets
 - Applying machine learning and artificial intelligence techniques to discover new patterns and relationships
- Exploring new frontiers in knot theory through:
 - Investigating higher-dimensional knots and their properties (knotted spheres, tori)
 - Studying the relationships between knots and other mathematical objects, such as 3-manifolds and braids
 - Applying knot theory to problems in physics (quantum entanglement), chemistry (molecular knots), and biology (DNA topology)
- Collaborative efforts to extend knot tabulation involve:
 - International research projects and consortia
 - Open-source software development and data sharing initiatives (GitHub repositories)
 - Interdisciplinary collaborations with experts in computer science, data analysis, and visualization

Unit 10 – Braids and the Braid Group

10.1 Introduction to braids and the braid group

Braids are fascinating mathematical objects that intertwine strands in 3D space. They form a group structure, allowing us to combine and manipulate them in unique ways. This concept bridges geometry and algebra, offering a visual and intuitive approach to abstract mathematical ideas.

Understanding braids and braid groups is crucial for grasping more advanced topics in knot theory. These structures provide powerful tools for analyzing knots and links, and their applications extend to various fields, including physics and cryptography.

Introduction to Braids and the Braid Group

Definition of braids and braid groups

- A braid on n strands consists of n non-intersecting paths in 3D space connecting n points on a horizontal plane to n points directly below on another horizontal plane
- Paths may intertwine but never turn back upward (monotonic in the vertical direction)
- Braids are equivalent if they can be continuously deformed into one another without intersecting the paths (ambient isotopy)
- The braid group on n strands, B_n , is the set of all equivalence classes of braids on n strands with the composition operation
- Composition of braids is performed by stacking one braid on top of the other and connecting the endpoints (vertical stacking)
- Identity element is the braid with n straight vertical strands (trivial braid)
- Every braid has an inverse obtained by reflecting the braid across a horizontal plane (mirror image)

Representation of braids

- Braid diagrams are 2D representations of braids viewed from the top
- Each crossing represents a strand passing over or under another strand (over/under information)
- Crossings are labeled with numbers to indicate the order in which they occur (crossing labels)
- Braid words are algebraic representations of braids using generators and their inverses
- Generator σ_i represents a crossing where the i -th strand passes over the $(i + 1)$ -th strand (positive crossing)
- Inverse of a generator, σ_i^{-1} , represents a crossing where the i -th strand passes under the $(i + 1)$ -th strand (negative crossing)
- A braid word is a sequence of generators and their inverses read from left to right (product of generators)
- Example: the braid word $\sigma_1\sigma_2^{-1}\sigma_1$ represents a braid with three crossings (2 positive, 1 negative)

Operations on braids

- Composition of braids is performed by stacking one braid diagram on top of the other and connecting the endpoints
- For braid words, composition is achieved by concatenating the words (juxtaposition)
- Example: if $\alpha = \sigma_1\sigma_2$ and $\beta = \sigma_2^{-1}\sigma_1$, then $\alpha\beta = \sigma_1\sigma_2\sigma_2^{-1}\sigma_1$
- The inverse of a braid is obtained by reflecting the braid diagram across a horizontal line and reversing the direction of each crossing
- For braid words, the inverse is obtained by reversing the order of the generators and replacing each generator with its inverse (reverse order and invert generators)
- Example: if $\alpha = \sigma_1\sigma_2^{-1}\sigma_1$, then $\alpha^{-1} = \sigma_1^{-1}\sigma_2\sigma_1^{-1}$

Properties of braid groups

- The braid group B_n is a group under the composition operation
- Composition of braids is associative: $(\alpha\beta)\gamma = \alpha(\beta\gamma)$ for all braids α, β, γ (associativity)
- Identity element is the braid with n straight vertical strands (identity)
- Every braid has an inverse as described in the previous section (inverses)
- The braid group is non-commutative for $n \geq 3$
- Shown by considering the generators σ_1 and σ_2
- $\sigma_1\sigma_2 \neq \sigma_2\sigma_1$ as the resulting braids are not equivalent (non-commutativity)
- The braid group B_n is generated by the elements $\sigma_1, \sigma_2, \dots, \sigma_{n-1}$
- These generators satisfy the braid relations:
 1. $\sigma_i\sigma_j = \sigma_j\sigma_i$ for $|i - j| > 1$ (far commutativity)
 2. $\sigma_i\sigma_{i+1}\sigma_i = \sigma_{i+1}\sigma_i\sigma_{i+1}$ for $1 \leq i \leq n - 2$ (braid relation)
- Any braid in B_n can be expressed as a product of these generators and their inverses (generated group)

10.2 Artin's braid theory and Markov's theorem

Artin's braid theory bridges geometry and algebra in knot theory. It provides a framework for studying braids and their relationships to knots and links. This approach simplifies many problems in knot theory by allowing the use of algebraic techniques.

Markov's theorem is a key tool for classifying links using braids. It states that two braids have ambient isotopic closures if and only if they're related by Markov moves. This theorem enables the classification of links by studying braids under specific equivalence relations.

Artin's Braid Theory

Significance of Artin's braid theory

- Provides mathematical framework studying braids and their relationships to knots and links
- Braid is collection of intertwining strands starting and ending at fixed points (typically arranged in two parallel rows)
- Braids can be combined by concatenation forming group structure known as braid group B_n where n is number of strands
- Offers algebraic approach to study and classify knots and links
- Every link can be represented as closure of braid establishing connection between geometric and algebraic aspects of knot theory (Alexander's theorem)
- Allows use of algebraic techniques to study and classify links simplifying many problems in knot theory (word problem, conjugacy problem)

Braids and links through closure

- Closure operation obtains link from braid by connecting corresponding endpoints of braid strands
- To perform closure top endpoints of braid are connected to their corresponding bottom endpoints without introducing new crossings
- Resulting link is called closure of braid denoted as $\hat{\beta}$ for braid β
- Alexander's theorem states every link can be represented as closure of some braid
- Establishes surjective map from set of braids to set of links
- Map is not injective as different braids can have same link as their closure (Markov's theorem)

Markov's Theorem

Markov's theorem for link classification

- Provides way to classify links up to ambient isotopy using braids and Markov moves
- Ambient isotopy is equivalence relation on links capturing notion of continuous deformation without cutting or passing through itself
- Theorem states two braids have ambient isotopic closures if and only if they are related by finite sequence of Markov moves
- Markov moves are specific operations performed on braids without changing ambient isotopy type of their closures
- Two types of Markov moves:
 1. Type I (conjugation): $\beta \sim \alpha\beta\alpha^{-1}$ where α and β are braids
 2. Type II (stabilization/destabilization): $\beta \sim \beta\sigma_n^{\pm 1}$ where σ_n is generator of braid group B_{n+1}
- Proof involves showing any two braids with ambient isotopic closures can be related by sequence of Markov moves and that Markov moves preserve ambient isotopy type of closure

- Allows classification of links up to ambient isotopy by studying braids modulo equivalence relation generated by Markov moves

Markov moves and link transformations

- Markov moves can be applied to braids to obtain equivalent braids with ambient isotopic closures
- Type I moves (conjugation) correspond to sliding strand over or under other strands not changing link type of closure
- Type II moves (stabilization/destabilization) involve adding or removing single crossing at end of braid also preserving link type of closure
- When applying Markov moves to braid corresponding link obtained by closure operation remains unchanged up to ambient isotopy
- Allows simplification and manipulation of braids while maintaining link type of their closures
- Can be used to find minimal braid representation for given link
- By applying sequence of Markov moves one can potentially reduce number of crossings in braid while preserving link type of its closure
- Finding minimal braid representations is important problem in knot theory with applications in various fields (molecular biology, quantum computation)

10.3 Relationships between braids and knots

Braid representations offer a powerful way to study knots. By transforming knots into braids and back, we gain new insights into their structure and properties. This technique opens up exciting avenues for computing knot invariants and polynomials.

Alexander's theorem tells us every knot can be represented as a closed braid. This allows us to apply braid theory tools to knot problems, leading to breakthroughs in understanding knot complexity and developing new invariants.

Braid Representations of Knots

Knots as braid closures

- Alexander's theorem establishes every knot or link represents the closure of a braid
- Braid consists of strings running top to bottom with finitely many crossings between adjacent strings
- Closure of a braid obtained by connecting top and bottom endpoints of each string (trefoil knot, figure-eight knot)
- Representing a knot as a braid involves choosing a projection plane, selecting a perpendicular "vertical" direction, and manipulating the knot diagram to consist of monotonic strands with crossings only between adjacent strands
- Markov moves (conjugation, stabilization/destabilization) applied to a braid yield equivalent braids representing the same knot

Braid representation via Alexander's theorem

- Begin with a regular knot diagram

- Select a basepoint and direction of travel on the knot diagram
- Number the crossings sequentially while following the knot diagram in the chosen direction
- Construct a braid by creating straight strands corresponding to regions between crossings 1. Each crossing in the knot diagram maps to a crossing between two adjacent strands in the braid 2. Over/under information at each crossing is preserved in the braid representation
- Closing the resulting braid by connecting top and bottom endpoints represents the original knot (trefoil knot, cinquefoil knot)

Braid index vs knot complexity

- Braid index of a knot is the minimum number of strands needed to represent the knot as a closed braid
- Braid index provides a lower bound on the crossing number (minimum crossings in any knot diagram)
- Higher crossing numbers generally correspond to higher braid indices, but knots with the same crossing number can have different braid indices (5_1 and 5_2 knots)
- Braid index is not a complete knot invariant; non-equivalent knots can have the same braid index (6_1 and 6_2 knots)
- No general algorithm exists for determining the minimum braid index of a given knot

Applications of braid theory

- Braid representations enable computation of knot invariants and polynomials
- Jones polynomial defined using Kauffman bracket, interpreted in terms of braids
- Kauffman bracket of a braid closure is a weighted sum over all possible smoothings of the crossings
- Jones polynomial obtained from Kauffman bracket by normalizing and accounting for writhe of the knot diagram
- HOMFLY-PT polynomial computed using skein relation applied to braid representations, generalizing Jones and Alexander polynomials
- Khovanov homology, a categorification of the Jones polynomial, studied using braid representations and a cube of resolutions construction
- Knot invariants defined using representations of the braid group (Bureau representation, Lawrence-Krammer representation)

Unit 11 – Links and Link Invariants

11.1 Multi-component links and their properties

Multi-component links expand our understanding beyond single knots. They involve multiple intertwined curves, like the Hopf link and Borromean rings. Each component can have its own orientation, and links can be classified as splittable or non-splittable.

Link equivalence and ambient isotopy are key concepts in analyzing multi-component links. These ideas help us determine when two links are essentially the same, sharing properties like component count, linking number, and individual knot types.

Multi-Component Links

Types of multi-component links

- Hopf link consists of two linked circles that cannot be separated without cutting one of them
- Borromean rings are three linked circles where removing any one of them leaves the other two unlinked
- Whitehead link has two linked circles that are not splittable but become splittable after removing one full twist from either component
- Other examples include the Brunnian link, Solomon's knot, and the Star of David link

Components and orientations of links

- Identify the components of a link by visually inspecting the link diagram and locating each separate simple closed curve
- Each separate curve in the diagram represents one component of the link
- Determine the orientation of a component by assigning a direction (clockwise or counterclockwise) to each component
- Indicate orientations using arrows on the link diagram
- The choice of orientation for each component is arbitrary but must remain consistent throughout the analysis of the link

Link equivalence and ambient isotopy

- Link equivalence is a relation between two links that can be transformed into each other through continuous deformations without cutting or passing through itself
- Ambient isotopy refers to continuously deforming the link in 3-dimensional space
- Equivalent links are related by an ambient isotopy and share the same topological properties
- These properties include the number and type of components, the linking number between components, and the knot type of each component

Splittable vs non-splittable links

- A link is splittable if its components can be separated into two or more subsets without cutting or passing through any component
- In a splittable link, a 2-sphere embedded in $\mathbb{R}^3$ or S^3 separates the components into two or more subsets
- The subsets of components in a splittable link are not linked with each other (Hopf link is an example of a splittable link)
- A link is non-splittable if its components cannot be separated into subsets without cutting or passing through any component
- In a non-splittable link, no 2-sphere can separate the components into subsets
- Non-splittable links have components that are inherently linked with each other (Borromean rings and Whitehead link are examples of non-splittable links)
- The splittability of a link is a topological property that remains invariant under ambient isotopy

11.2 Linking number and other numerical link invariants

Linking numbers are a powerful tool for measuring how intertwined two components of a link are. By assigning values to crossings and summing them up, we can quantify the degree of linkage between oriented components.

This numerical invariant remains unchanged under Reidemeister moves, making it a reliable measure of link equivalence. While not perfect, linking numbers provide a solid foundation for understanding more complex polynomial invariants in knot theory.

Linking Number

Calculation of linking numbers

- Computes $lk(L_1, L_2)$, a numerical invariant measuring the linkage between two oriented link components
- Considers a regular link projection and identifies crossings where one component passes over the other
- Assigns +1 or -1 to each crossing based on orientation using the right-hand rule
- +1 if the top strand aligns with the bottom strand by a counterclockwise rotation $< 180^\circ$
- -1 otherwise
- Sums the assigned values and divides by 2 to obtain the linking number (always an integer)
- $lk(L_1, L_2) = 0$ indicates unlinked components
- $|lk(L_1, L_2)| > 0$ indicates linked components, with the absolute value representing the degree of linkage

Linking number as invariant

- Proves the linking number remains unchanged under Reidemeister moves (local deformations preserving link type)
- Reidemeister move I (twist): Adding/removing a twist in a single component does not affect the linking number (no crossings between components)
- Reidemeister move II (overlapping): Adding/removing two same-sign crossings between components does not change the linking number (sum of assigned values is zero)
- Reidemeister move III (triangle): Moving a strand over/under a crossing between two other strands preserves the linking number (sum of assigned values remains the same)
- Invariance under Reidemeister moves implies the linking number is a link invariant under ambient isotopy

Link equivalence via linking numbers

- Different linking numbers imply non-equivalent links under ambient isotopy (equivalent links must have the same linking number)
- Same linking number does not guarantee link equivalence (Whitehead link and unlink with two components are non-equivalent with the same linking number)
- Additional invariants or techniques may be necessary to definitively determine link equivalence

Introduction to polynomial invariants

- Alexander polynomial $\Delta_L(t)$: Polynomial invariant defined using the Alexander matrix from a link diagram
- Invariant under ambient isotopy
- Distinguishes some links that the linking number cannot
- Jones polynomial $V_L(t)$: Polynomial invariant defined using a skein relation relating polynomials of links differing by a single crossing change
- Invariant under ambient isotopy
- Distinguishes some links that the Alexander polynomial cannot
- Alexander and Jones polynomials are more powerful than the linking number but still have limitations (non-equivalent links with the same polynomials exist)
- HOMFLY-PT polynomial and Kauffman polynomial generalize the Alexander and Jones polynomials, respectively

11.3 Milnor invariants and higher-order linking

Milnor invariants reveal hidden complexities in links with three or more components. They go beyond simple pairwise linking, capturing intricate relationships between multiple strands that traditional methods might miss.

These invariants are crucial for distinguishing seemingly similar links. By measuring higher-order linking, they can tell apart links that look identical at first glance, like the Borromean rings and a simple

three-component unlink.

Milnor Invariants

Milnor invariants for multi-component links

- Capture higher-order linking information for links with three or more components beyond pairwise linking
- Denoted as $\tilde{\mu}_{i_1 i_2 \dots i_k}(L)$, where L is a link and $i_1, i_2, \dots, i_k$ are indices representing the components of the link (Borromean rings, Whitehead link)
- Defined using the lower central series of the link group and the Magnus expansion, which encodes the structure of the link complement
- The first non-vanishing Milnor invariant is the linking number, measuring the pairwise linking between two components (linking number of Hopf link is ± 1)
- Vanishing of lower-order Milnor invariants does not necessarily imply the link is trivial, as higher-order invariants may still be non-zero (Borromean rings have zero pairwise linking but non-trivial triple linking)

Computation of Milnor invariants

- For the Borromean rings, a link with three components: 1. Compute all pairwise linking numbers (all zero for Borromean rings) 2. Compute the triple Milnor invariant $\tilde{\mu}_{123}$ (equal to ± 1 for Borromean rings)
- For the Whitehead link, a link with two components: 1. Compute the linking number (zero for Whitehead link) 2. Higher-order Milnor invariants vanish, as the link has only two components
- Computed using the Magnus expansion and the Wirtinger presentation of the link group, which relates the link complement to a group presentation

Higher-order linking information

- Generalize the concept of pairwise linking to multiple components, capturing "linking of linking" (Borromean rings, Brunnian links)
- Detect how the linking between two components is affected by the presence of other components (Whitehead link, Bing double)
- Related to the lower central series of the link group, which captures the "nilpotency" of the linking, or how quickly the linking information vanishes under repeated commutators

Relationships among link invariants

- Related to the Alexander polynomial:
- Alexander polynomial can be derived from the Milnor invariants
- Coefficients of the Alexander polynomial contain information about the Milnor invariants (Conway polynomial, Jones polynomial)
- Related to the Massey products in cohomology, which are higher-order cohomological operations capturing similar higher-order linking information

- The Kontsevich integral, a universal finite-type invariant, can be used to compute Milnor invariants (Vassiliev invariants, chord diagrams)

Application in link distinction

- Distinguish between links with the same pairwise linking numbers but different higher-order linking (Borromean rings vs. unlink with three components)
- Distinguish between links with the same Alexander polynomial (Whitehead link vs. unlink with two components, due to non-vanishing $\tilde{\mu}_{1122}$ for Whitehead link)
- Determine if two links are equivalent (have the same link type) by comparing their Milnor invariants (link classification, link table)

Unit 12 – Khovanov Homology and Categorification

12.1 Introduction to homology theories in knot theory

Homology theories are powerful tools in knot theory, assigning algebraic structures to knots that remain unchanged under deformation. These theories provide a richer understanding of knots compared to polynomial invariants, offering more detailed information about their properties.

Chain complexes form the backbone of homology theories in knot theory. By assigning algebraic objects to knot diagram crossings and defining boundary maps, we create a structure whose homology groups serve as knot invariants, capturing essential topological information.

Homology Theories and Knot Invariants

Homology theories for knot invariants

- Homology theories are algebraic tools that study topological spaces and their properties by assigning algebraic objects (groups or vector spaces) to capture essential information about the space
- In knot theory, homology theories construct knot invariants which are quantities or algebraic structures that remain unchanged under ambient isotopy (continuous deformations) of the knot
- Homology theories provide a systematic way to associate algebraic invariants to knots
- Examples of homology theories used in knot theory:
 - Khovanov homology
 - Knot Floer homology
 - Heegaard Floer homology

Homology vs polynomial knot invariants

- Polynomial knot invariants (Jones polynomial, HOMFLY-PT polynomial) can be derived from certain homology theories
- Jones polynomial obtained from the Euler characteristic of Khovanov homology
- HOMFLY-PT polynomial obtained from the Euler characteristic of Khovanov-Rozansky homology
- Homology theories provide a categorification (lifting algebraic structures to a higher categorical level) of polynomial invariants
- Homology theories can be seen as a richer and more refined version of polynomial invariants
- The relationship between homology theories and polynomial invariants allows for a deeper understanding of the properties and behavior of knots

Advantages of homology theories

- Homology theories are generally more powerful than polynomial invariants in distinguishing knots by providing more information about the knot than just a polynomial

- Homology groups associated with knots can have a richer algebraic structure (graded modules, bigraded complexes)
- Examples of knots that have the same polynomial invariants but different homology groups:
- Khovanov homology can distinguish certain pairs of knots with the same Jones polynomial
- Knot Floer homology can distinguish certain pairs of knots with the same Alexander polynomial
- Homology theories can provide additional geometric and topological information about knots by detecting certain properties (genus of a knot, existence of certain types of surfaces bounded by the knot)

Chain Complexes and Knot Diagrams

Chain complexes in knot diagrams

- Constructing a chain complex from a knot diagram: 1. Assign an algebraic object (vector space or module) to each crossing in the knot diagram 2. Define a boundary map between these algebraic objects based on the local structure of the knot diagram around each crossing
- Boundary map encodes the relationship between the crossings and adjacent arcs in the knot diagram
- Satisfies the property that the composition of two consecutive boundary maps is zero: $\partial \circ \partial = 0$
- The homology of the chain complex is defined as the quotient of the kernel of the boundary map by its image: $H_*(C) = \ker(\partial)/\text{im}(\partial)$
- The homology groups of the chain complex are knot invariants that remain unchanged under Reidemeister moves and ambient isotopy of the knot
- Different homology theories use different algebraic objects and boundary maps in the construction of the chain complex, determining the specific properties and behavior of the resulting homology theory

12.2 Khovanov homology: definition and construction

Khovanov homology takes knot theory to new heights. It's a powerful tool that builds on the Jones polynomial, creating a chain complex from knot diagrams. This method gives us more info about knots than ever before.

By resolving crossings and using vector spaces, Khovanov homology digs deeper into knot structure. It can tell apart knots that look the same under other methods, making it a game-changer for knot classification.

Khovanov Homology: Definition and Properties

Definition of Khovanov homology

- Associates a bigraded chain complex to a knot diagram
- Homology of this chain complex defines the Khovanov homology
- Categorifies the Jones polynomial by lifting it to a homology theory
- Khovanov homology is a knot invariant that is stronger than the Jones polynomial

Construction of Khovanov chain complex

- Begin with a knot diagram and choose a crossing
- Resolve the crossing in two ways: 1. 0-resolution: replace the crossing with a horizontal smoothing 2. 1-resolution: replace the crossing with a vertical smoothing
- Assign the vector space $V = \mathbb{Z}[0] \oplus \mathbb{Z}[1]$ to each circle in the resolution
- Take the tensor product of the vector spaces for each resolution
- Define maps between the tensor products using cobordisms between the resolutions
- Merging or splitting circles determines the maps
- Signs of the maps are determined by the orientations of the circles

Computation for simple knots

- Unknot:
- Khovanov chain complex has a single $\mathbb{Z}$ in bigrading (0,0)
- Khovanov homology: $H_{i,j}(U) = \mathbb{Z}$ for $(i,j) = (0,0)$, 0 otherwise
- Unlink with n components:
- Khovanov homology: $H_{i,j}(U_n) = \mathbb{Z}^{\binom{n}{j}}$ for $j = i$, 0 otherwise
- Trefoil knot:
- Khovanov homology:
- $H_{i,j}(3_1) = \mathbb{Z}$ for $(i,j) = (0,1), (0,3), (2,5)$
- $H_{i,j}(3_1) = \mathbb{Z}/2\mathbb{Z}$ for $(i,j) = (1,0), (1,2), (1,4)$

Khovanov Homology: Invariance and Relation to the Jones Polynomial

Invariance of Khovanov homology

- Khovanov homology is invariant under Reidemeister moves (I, II, and III)
- Chain homotopy type of the Khovanov chain complex is invariant under Reidemeister moves
- Explicit chain homotopy equivalences can be constructed for each move
- Homology of the Khovanov chain complex is a knot invariant

Khovanov homology vs Jones polynomial

- Jones polynomial can be recovered from Khovanov homology via the graded Euler characteristic:
$$J(L)(q) = \chi_q(C(L)) = \sum_{i,j} (-1)^j q^j \text{rank}(H_{i,j}(L))$$
- Khovanov homology is a categorification of the Jones polynomial
- Provides a stronger invariant with more information than the Jones polynomial

- Khovanov homology can distinguish knots with the same Jones polynomial
- Knots 5_1 and 10_{132} have the same Jones polynomial but different Khovanov homologies

12.3 Applications and recent developments in categorification

Categorification in knot theory takes familiar concepts and lifts them to a higher level. It's like upgrading from a 2D map to a 3D model, revealing hidden details and connections. This process has led to powerful new tools like Khovanov homology.

Khovanov homology, a supercharged version of the Jones polynomial, has found uses beyond knot theory. It's helping solve problems in topology, physics, and even string theory. This shows how a simple idea can have far-reaching impacts across different fields.

Categorification and Its Applications in Knot Theory

Concept of categorification in knot theory

- Categorification process replaces set-theoretic concepts with category-theoretic analogues
- Lifts algebraic structures to a higher categorical level (groups to groupoids, vector spaces to categories)
- Provides richer and more refined invariants captures additional information and structure
- In knot theory, categorification has led to the development of powerful knot invariants
- Khovanov homology categorifies the Jones polynomial
- Assigns a bigraded abelian group to each knot or link (graded by homological and quantum degrees)
- Captures more information than the Jones polynomial alone detects finer properties of knots
- Categorified invariants often have better properties and reveal deeper connections uncover hidden structures and relationships

Applications of Khovanov homology

- Khovanov homology has found applications in various areas of low-dimensional topology
- Provides a lower bound for the slice genus of knots (minimum genus of a surface bounded by the knot in 4-dimensional ball)
- Detects the unknotting number of certain knots (minimum number of crossings that need to be changed to obtain the unknot)
- Gives a new proof of the Milnor conjecture on the slice genus of torus knots (slice genus equals the genus for torus knots)
- In physics, Khovanov homology has connections to various theories
- Related to the BPS states in string theory and M-theory (states that preserve a fraction of supersymmetry)
- Plays a role in the study of gauge theories and supersymmetry (symmetry between bosons and fermions)

- Provides a link between knot theory and quantum field theory (mathematical framework for describing subatomic particles)

Khovanov homology vs Floer homology

- Khovanov homology is related to various Floer homology theories
- Shares similarities with Heegaard Floer homology, a powerful tool in 3-manifold topology
- Both theories assign homological invariants to knots and links (Khovanov homology for links, Heegaard Floer homology for 3-manifolds)
- There are spectral sequences connecting Khovanov homology and Heegaard Floer homology (algebraic tools for relating homology theories)
- Has connections to instanton Floer homology and symplectic Floer homology
- These theories also provide invariants for knots and 3-manifolds (instanton Floer homology uses gauge theory, symplectic Floer homology uses symplectic geometry)
- The relationships between these theories are an active area of research exploring connections and analogies

Categorification of knot invariants

- Researchers have been working on categorifying other knot polynomials and invariants
- Categorification of the HOMFLY-PT polynomial
- Leads to a triply-graded homology theory for knots and links (graded by homological, quantum, and a third grading)
- Provides a unifying framework for various knot homologies (encompasses Khovanov homology and other theories as special cases)
- Categorification of the Kauffman polynomial and the Kauffman bracket
- Results in new homological invariants with interesting properties (detects certain properties of knots and links)
- Relates to the representation theory of quantum groups (algebraic structures used in quantum topology)
- Categorification of the Alexander polynomial and the knot Floer homology
- Gives rise to a categorified version of the Alexander polynomial (polynomial invariant related to the fundamental group of the knot complement)
- Connects with the study of knot concordance and slice knots (knots that bound a disk in the 4-dimensional ball)

Unit 13 – Three–Manifolds and Knot Complements

13.1 Introduction to 3-manifolds and their relationship to knots

Three-dimensional manifolds, or 3-manifolds, are spaces that look like our everyday 3D world up close. They're the playground for knots, those loopy curves we study in knot theory. Understanding 3-manifolds helps us grasp how knots behave in different spaces.

Knots can be embedded in various 3-manifolds, not just the usual 3D space we're used to. This affects how knots interact with their surroundings. The relationship between knots and 3-manifolds reveals deep insights about both, shaping our understanding of topology.

Introduction to 3-Manifolds

Basics of 3-manifolds

- A 3-manifold is a topological space that locally resembles Euclidean 3-space ($\mathbb{R}^3$) meaning every point has a neighborhood homeomorphic to an open subset of $\mathbb{R}^3$
- 3-manifolds are three-dimensional spaces without boundaries that can be thought of as generalizations of surfaces to higher dimensions
- Examples of 3-manifolds include $\mathbb{R}^3$ (Euclidean 3-space), S^3 (3-sphere), and $S^1 \times S^2$ (product of a circle and a 2-sphere)
- 3-manifolds can be orientable or non-orientable
- Orientable 3-manifolds have a consistent choice of orientation (handedness) throughout the space like a sphere or torus
- Non-orientable 3-manifolds, such as the 3-dimensional real projective space ($\mathbb{RP}^3$), do not have a consistent orientation and contain Möbius band-like structures

Knot embedding in 3-manifolds

- A knot is a closed, non-self-intersecting curve in a 3-manifold defined mathematically as an embedding of the circle (S^1) into the 3-manifold
- Knots can be embedded in various 3-manifolds, such as $\mathbb{R}^3$ (the most common setting for studying knots), S^3 (obtained by compactifying $\mathbb{R}^3$ with a point at infinity), and other 3-manifolds like lens spaces or Seifert-fibered spaces
- The embedding of a knot in a 3-manifold is called a knot type or knot class, and knots are considered equivalent if there exists an ambient isotopy between them within the 3-manifold

Relationship between Knots and 3-Manifolds

Knots and 3-manifolds relationship

- The complement of a knot in a 3-manifold is the 3-manifold obtained by removing the knot and its interior, for example, the knot complement of a knot K in S^3 is $S^3 \setminus K$

- The knot complement is a 3-manifold with boundary, where the boundary is a torus ($S^1 \times S^1$), and it encodes important information about the knot, such as its fundamental group (knot group), Alexander polynomial, and Jones polynomial
- Surgery on a knot in a 3-manifold produces a new 3-manifold through a process called Dehn surgery, which involves removing a tubular neighborhood of the knot and gluing in a solid torus with different surgery coefficients resulting in different 3-manifolds

Topology of knot-containing 3-manifolds

- The genus of a knot is the minimum genus of any orientable surface bounded by the knot in the 3-manifold and serves as a measure of the knot's complexity related to the topology of the 3-manifold
- The Thurston-Bennequin number and the rotation number are invariants of Legendrian knots in contact 3-manifolds that provide information about the contact structure and the knot's embedding
- The JSJ decomposition (Jaco-Shalen-Johannson decomposition) decomposes a 3-manifold into simpler pieces along incompressible tori, which can be used to study the structure of 3-manifolds containing knots
- The geometrization theorem, proved by Perelman, states that every closed, orientable 3-manifold can be decomposed into geometric pieces, and the geometry of these pieces is related to the properties of knots embedded in the 3-manifold

13.2 Knot complements and their topological properties

Knot complements are the spaces left when we remove a knot from a 3-sphere. They're crucial for understanding knots, as two knots are the same if their complements can be continuously deformed into each other.

The fundamental group of a knot complement is a key tool for studying knots. We can compute it using the Wirtinger presentation, which involves assigning generators to arcs and writing relations at crossings in the knot diagram.

Knot Complements

Knot complement definition and role

- Knot complement represents the 3-dimensional space remaining after removing a tubular neighborhood of the knot from the 3-sphere (S^3)
- Denoted as $S^3 \setminus N(K)$, where $N(K)$ is an open neighborhood surrounding the knot K
- Knot complements enable studying knots by examining the topology of the space around the knot
- Two knots are equivalent if and only if their complements are homeomorphic (can be continuously deformed into each other)
- Properties of the knot complement, such as its fundamental group and homology groups, help distinguish knots and derive knot invariants (quantities that remain unchanged under knot deformations)

Fundamental group of knot complement

- Fundamental group of a knot complement, denoted as $\pi_1(S^3 \setminus K)$, serves as a powerful tool for studying knots

- To compute the fundamental group, use the Wirtinger presentation: 1. Choose an orientation for the knot and a base point above the knot diagram 2. Assign a generator to each arc in the diagram, following the orientation 3. At each crossing, write a relation in terms of the generators
- For an over-crossing with generators a , b , and c , the relation is $a = c^{-1}bc$
- Fundamental group is the free group generated by the arc generators, modulo the crossing relations (relations obtained from the crossings)

Knot complements vs knot invariants

- Fundamental group of a knot complement serves as a knot invariant
- If two knots have different fundamental groups, they are distinct (not equivalent)
- Peripheral subgroup of the fundamental group encodes information about the knot
- Generated by the meridian (curve that bounds a disk intersecting the knot once) and longitude (curve that runs parallel to the knot) of the knot
- Peripheral subgroup can be used to compute the Alexander polynomial (polynomial invariant associated with the knot) and other invariants
- JSJ decomposition of a knot complement reveals information about the knot's structure
- Decomposes the complement into simple pieces, such as Seifert-fibered spaces (3-manifolds admitting a circle action) and hyperbolic components (3-manifolds with a hyperbolic geometry)

Topological analysis of knot complements

- Apply algebraic topology tools to compute homology and cohomology groups of knot complements
- These groups provide information about the knot's genus (minimal genus of a surface bounded by the knot), fibering properties (whether the knot complement fibers over the circle), and more
- Apply the Poincaré duality theorem to relate the homology and cohomology groups of the knot complement
- Investigate the geometric structures on knot complements
- Many knot complements admit hyperbolic structures, which can be studied using hyperbolic geometry (geometry of spaces with constant negative curvature)
- Hyperbolic volume and other geometric invariants of the complement help distinguish knots
- Utilize 3-manifold theory to study the topology of knot complements
- Techniques such as Dehn surgery (modifying a 3-manifold by removing a solid torus and gluing it back differently) and studying incompressible surfaces (surfaces that cannot be simplified by compressing along a disk) provide insights into the structure of knot complements

13.3 Dehn surgery and its applications in knot theory

Dehn surgery is a powerful technique in knot theory that creates new 3-manifolds by modifying existing ones. It involves removing a solid torus around a knot and reattaching it differently, using specific coefficients to determine the new structure.

This process is crucial for understanding how knots relate to 3-manifolds. By performing Dehn surgery on knot complements, we can generate various 3-manifolds and study how knot invariants change, providing insights into topology and knot theory relationships.

Dehn Surgery and Knot Theory

Concept of Dehn surgery

- Dehn surgery creates new 3-manifolds from existing ones by removing a solid torus neighborhood of a knot or link and gluing a new solid torus back in with a specific homeomorphism of the boundary
- Closely connected to knot theory as knot complements, the 3-manifolds obtained by removing a tubular neighborhood of a knot, serve as the starting point for Dehn surgery
- Different surgeries on the same knot complement can produce different 3-manifolds (lens spaces, Seifert-fibered spaces)
- Dehn surgery coefficients (p, q) specify the homeomorphism used to glue the solid torus, where the meridian of the new solid torus is mapped to a curve that winds p times meridionally and q times longitudinally around the knot

Dehn surgery on knot complements

- Performing Dehn surgery on a knot complement involves: 1. Removing a tubular neighborhood of the knot, creating a knot complement with a torus boundary 2. Choosing surgery coefficients (p, q) to specify the gluing homeomorphism 3. Gluing a solid torus to the knot complement using the specified homeomorphism
- The resulting 3-manifold depends on the choice of surgery coefficients, with different choices of (p, q) yielding different 3-manifolds, even for the same knot complement (trefoil knot, figure-eight knot)
- Lens spaces can be obtained by performing Dehn surgery on the unknot, with surgery coefficients of the form $(p, 1)$ yielding lens spaces $L(p, 1)$

Effects on knot invariants

- Dehn surgery affects various knot invariants:
- Knot genus, the minimal genus of any Seifert surface for the knot
- Knot signature, a numerical invariant derived from the knot's Seifert matrix
- Knot Floer homology, a powerful knot invariant that categorifies the Alexander polynomial
- The effects of Dehn surgery on these invariants provide insights into the structure of the resulting 3-manifolds, such as using the knot Floer homology of a knot to compute the Heegaard Floer homology of surgeries on that knot

Applications in topology

- Dehn surgery is a versatile tool for studying knots and 3-manifolds, allowing the construction of 3-manifolds with specific properties and establishing relationships between different knots and 3-manifolds
- The cyclic surgery theorem states that non-trivial knots have only finitely many cyclic surgeries, which are those that produce 3-manifolds with cyclic fundamental groups, limiting the possible Dehn surgeries

on a given knot

- Dehn surgery can be used to study the behavior of knot invariants under various operations, such as studying how knot signature changes under Dehn surgery to provide information about the resulting 3-manifolds

Unit 14 – Knot Theory in Biology and Chemistry

14.1 DNA topology and knotting in molecular biology

DNA topology is a fascinating field that explores how DNA twists, coils, and knots in 3D space. It's not just about the double helix – supercoiling, linking numbers, and writhing all play crucial roles in how our genetic material functions.

Knots and links in DNA aren't just tangles – they're important players in replication and gene expression. Topoisomerases, nature's molecular unknotters, help manage these structures. Understanding DNA topology is key to grasping how our genes work at a fundamental level.

DNA Topology and Knotting

Topological properties of DNA

- DNA topology involves the three-dimensional arrangement and intertwining of DNA strands
- Supercoiling occurs when DNA is twisted beyond its natural helical state
- Positive supercoiling results from overtwisting the double helix (more compact structure)
- Negative supercoiling arises from undertwisting the double helix (more relaxed structure)
- Linking number (Lk) is a topological invariant quantifying the number of times one DNA strand crosses over the other
- $Lk = Tw + Wr$ describes the relationship between linking number, twisting number (Tw), and writhing number (Wr)
- Tw measures the helical twist of the DNA (rotation of base pairs around the axis)
- Wr measures the coiling or writhing of the DNA axis itself (supercoiling)
- Topological properties of DNA play crucial roles in biological processes
- Supercoiling facilitates efficient DNA packaging into compact structures (chromosomes, nucleoids)
- Topological state of DNA influences interactions with proteins (transcription factors) and regulates gene expression

Knots and links in DNA processes

- DNA knots form during replication and recombination events when DNA strands become entangled
- Knots can impede the progression of DNA replication and transcription machinery
- Topoisomerases are enzymes that regulate DNA topology by introducing temporary breaks in the DNA backbone
- Type I topoisomerases introduce single-strand breaks to relax supercoils or unknot DNA
- Type II topoisomerases introduce double-strand breaks to resolve knots and tangles

- DNA catenanes (links) occur when two circular DNA molecules become interlocked during replication
- Catenanes are commonly observed in the replication of circular DNA (plasmids, mitochondrial DNA)
- Topoisomerases are essential for resolving catenanes and ensuring proper segregation of daughter DNA molecules

Effects of DNA supercoiling

- Positive supercoiling has a stabilizing effect on the DNA double helix
- Overtwisted DNA is more compact and resistant to denaturation
- Excessive positive supercoiling can hinder DNA unwinding and access to genetic information
- Negative supercoiling promotes DNA unwinding and strand separation
- Undertwisted DNA facilitates the formation of alternative DNA structures
- Cruciform structures form at inverted repeat sequences and resemble a cross-shaped configuration
- Z-DNA adopts a left-handed helical conformation and is favored by alternating purine-pyrimidine sequences
- Triple-helical DNA can form when a third strand binds to the major groove of the double helix
- DNA supercoiling influences gene expression by modulating the binding of transcription factors and RNA polymerase
- Local changes in supercoiling can fine-tune the expression of specific genes (supercoiling-sensitive promoters)

Techniques for studying DNA topology

- Gel electrophoresis separates DNA molecules based on size and topology
- Agarose gel electrophoresis is suitable for larger DNA molecules (kilobases to megabases)
- Distinguishes between relaxed, linear, and supercoiled DNA based on their migration patterns
- Polyacrylamide gel electrophoresis (PAGE) is used for smaller DNA molecules and higher resolution analysis
- Resolves different topoisomers with varying linking numbers (topological isomers)
- Electron microscopy provides direct visualization of DNA molecules at high magnification
- Scanning electron microscopy (SEM) reveals the surface topology and overall structure of DNA
- Transmission electron microscopy (TEM) allows imaging of the internal structure and organization of DNA
- Requires sample staining (heavy metal salts) or shadowing (metal coating) to enhance contrast
- Atomic force microscopy (AFM) enables high-resolution imaging of DNA molecules
- Provides three-dimensional information about DNA structure and topology
- Can visualize DNA-protein complexes and dynamic processes (conformational changes)

14.2 Knots in proteins and other biomolecules

Knots in proteins are fascinating structural features that can enhance stability and function. From simple trefoil knots to complex figure-eight knots and slipknots, these topological elements form during or after protein synthesis, often with chaperone assistance.

Understanding protein knots has practical applications in biotechnology and drug design. Scientists use various methods to detect and study these structures, including X-ray crystallography, NMR spectroscopy, and computational algorithms based on mathematical knot theory.

Knots in Proteins

Types of protein knots

- Trefoil knot (31)
 - Simplest nontrivial knot type found in proteins
 - Discovered in proteins such as carbonic anhydrase and acetohydroxy acid isomeroreductase
 - Enhances thermal stability and resistance to chemical denaturation compared to unknotted proteins
- Figure-eight knot (41)
 - More complex knot type than trefoil knot
 - Identified in proteins like ketol-acid reductoisomerase and S-adenosylmethionine synthetase
 - Increases protein stability and resistance to proteolytic degradation by creating a more compact structure
- Slipknot
 - Formed when a loop of the protein backbone passes through another loop, creating a knotted topology
 - Found in proteins such as thymidine kinase and alkaline phosphatase
 - May facilitate protein folding by providing a framework for the formation of the native structure and enhance stability by reducing conformational flexibility

Mechanisms of knot formation

- Cotranslational knotting
 - Knots form during protein synthesis on the ribosome as the nascent polypeptide chain is being synthesized
 - Nascent polypeptide chain threads through loops as it emerges from the ribosome exit tunnel
 - Knotting may be influenced by the rate of translation and the presence of chaperone proteins
- Posttranslational knotting
 - Knots form after protein synthesis is complete, requiring the assistance of chaperone proteins
 - Involves the threading of one protein terminus (N- or C-terminus) through a loop formed by another part of the protein

- Chaperones may help to stabilize intermediate states and guide the threading process
- Slipknotting
 - Occurs when a protein loop is threaded by another part of the protein chain, creating a slipknot topology
 - May involve the formation of intermediate structures such as lassos or twisted loops
 - Slipknotting can occur spontaneously or with the assistance of chaperone proteins

Applications and Detection of Knots in Proteins

Applications of knot theory

- Designing knotted proteins with enhanced stability
- Introducing knots into proteins to improve their thermal and chemical stability for biotechnological applications
- Potential applications in the development of more robust enzymes for industrial processes (biocatalysis, bioremediation)
- Targeting knotted regions in proteins for drug design
- Knotted regions may represent unique structural features for selective drug binding and modulation of protein function
- Designing small molecules that specifically interact with knotted regions to inhibit or activate protein activity
- Studying the role of knots in protein misfolding and aggregation
- Understanding how knots contribute to the formation of protein aggregates in neurodegenerative diseases (Alzheimer's, Parkinson's)
- Developing strategies to prevent or reverse knotting-induced protein misfolding and aggregation

Methods for knot detection

- X-ray crystallography
 - Provides high-resolution 3D structures of proteins at atomic level
 - Allows direct visualization of knotted regions in the protein backbone
 - Requires the growth of high-quality protein crystals, which can be challenging for some proteins
- Nuclear Magnetic Resonance (NMR) spectroscopy
 - Provides information on the local structure and dynamics of proteins in solution
 - Can detect the presence of knots by analyzing the patterns of long-range nuclear Overhauser effect (NOE) contacts
 - Suitable for studying proteins that are difficult to crystallize or have flexible regions
- Computational methods
 - Algorithms for detecting and classifying knots in protein structures based on mathematical knot theory

- Topological analysis of protein backbone using polynomial invariants (Alexander polynomial) and Gauss linking number
- Molecular dynamics simulations to study the formation, stability, and dynamics of knots in proteins

14.3 Chemical topology and molecular knots

Chemical topology explores how molecules connect and arrange in space, focusing on knots and links. This field helps us understand complex structures and predict their behavior, going beyond just chemical makeup.

Scientists create molecular knots through self-assembly, using techniques like metal-directed assembly and hydrogen bonding. They then use tools like NMR and X-ray crystallography to figure out the knots' shapes and features.

Introduction to Chemical Topology and Molecular Knots

Concept of chemical topology

- Studies properties and behavior of molecules based on connectivity and spatial arrangement rather than specific chemical composition
- Focuses on topological properties of molecules such as knottedness, linking, and braiding
- Provides framework for understanding and classifying complex molecular structures like knots
- Allows researchers to analyze knottedness of molecules and predict their properties and behavior

Synthesis of molecular knots

- Involves self-assembly of molecular components through non-covalent interactions (metal-directed self-assembly, hydrogen bonding, π - π stacking)
- Requires careful design of molecular components and control of self-assembly process to create knotted and linked structures
- Characterization techniques determine topology and structural features
- NMR spectroscopy provides information about connectivity and spatial arrangement of atoms
- X-ray crystallography reveals three-dimensional structure including knotted topology
- Mass spectrometry confirms molecular weight and composition of knotted or linked structure

Applications and Challenges in Molecular Knot Research

Applications in materials and catalysis

- Unique topological properties and structural complexity enable various applications
- Materials science: create polymeric materials with enhanced mechanical strength, elasticity, and toughness
- Knotted topology prevents polymer chains from slipping past each other
- Catalysis: act as selective and efficient catalysts for chemical reactions

- Knotted structure creates confined spaces and specific binding sites for substrates enhancing catalytic activity and selectivity
- Molecular machines: components for construction of nanoscale devices and motors
- Controlled movement and manipulation of knots harnesses mechanical work at nanoscale

Challenges in molecular knot design

- Precise control over self-assembly process to ensure formation of desired knotted topology
- Small changes in molecular components or reaction conditions can lead to undesired topologies or byproducts
- Optimization of synthesis conditions requires extensive trial and error experimentation
- Scalability of synthesis process for practical applications
- Many syntheses rely on low-yielding, multi-step reactions difficult to scale up for large-scale production
- Developing efficient and scalable synthesis methods remains active research area
- Characterizing and studying properties of knots can be challenging due to complex topologies
- Some analytical techniques may not provide sufficient resolution or sensitivity to fully characterize knotted structure
- Computational modeling and simulation of knots can be computationally expensive and time-consuming

Unit 15 – Knot Theory in Physics and Quantum Fields

15.1 Knots in statistical mechanics and polymer physics

Knots in polymers and biological systems are more than just tangles. They influence properties like elasticity, viscosity, and flow in polymers. In DNA and proteins, knots affect stability, function, and even evolution.

Knot theory provides tools to understand these complex structures. Invariants like crossing numbers and polynomials help classify knots, while statistical mechanics reveals how knots impact energy and entropy in molecular systems.

Knot Theory in Polymer Physics

Role of knots in polymer entanglement

- Polymer chains become intertwined and form knots (trefoil knot, figure-eight knot) which affects mechanical properties
- Elasticity reduced due to restricted chain motion
- Viscosity increased as knots impede flow
- Knot complexity influences the degree of entanglement
- Higher complexity knots (cinquefoil knot) lead to more restricted polymer motion compared to simpler knots (unknot)
- Knots introduce topological constraints on polymer chains
- Limit the conformational freedom of the polymer resulting in fewer available configurations
- Knotted polymers exhibit unique rheological behavior
- Increased viscosity and reduced flow compared to unknotted polymers
- Non-Newtonian flow characteristics (shear thinning, shear thickening) more pronounced in knotted systems

Knot invariants for polymer structures

- Knot invariants are mathematical quantities that remain unchanged under continuous deformations of the knot
- Crossing number provides a measure of knot complexity
- Minimum number of crossings in any projection of the knot (trefoil knot has crossing number 3)
- Alexander polynomial encodes information about the knot's structure and symmetries
- Computed from a knot diagram and distinguishes different knot types (unknot has Alexander polynomial 1)
- Jones polynomial distinguishes between different knots and their mirror images

- Powerful invariant that can detect chirality (left-handed vs right-handed trefoil knots have different Jones polynomials)
- Knot invariants help assess the stability of knotted polymer structures
- More complex knots (figure-eight knot) tend to be more stable and resistant to untying compared to simpler knots (unknot)

Statistical mechanics of knotted polymers

- Configuration space is the set of all possible spatial arrangements of a knotted polymer
- Constrained by the topological invariant of the knot leading to a reduced configuration space compared to unknotted polymers
- Partition function determines the equilibrium properties of the knotted polymer system
- Sum over all possible configurations weighted by their Boltzmann factors $Z = \sum_i e^{-E_i/kT}$
- Free energy depends on the knot type and complexity
- More complex knots have higher free energy and lower entropy due to reduced configuration space
- Probability distribution describes the likelihood of finding the polymer in a particular configuration
- Influenced by the knot type and external conditions (temperature, solvent)
- Boltzmann distribution $P_i = \frac{e^{-E_i/kT}}{Z}$ favors lower energy configurations

Knot Theory in Biological Systems

Knot theory in biological macromolecules

- DNA knotting occurs naturally in circular DNA molecules (plasmids, mitochondrial DNA)
- Can be induced by enzymes (topoisomerases) or physical processes (replication, recombination)
- Knot spectrum provides insights into the mechanisms of knot formation and removal
- Distribution of different knot types in a population of DNA molecules (trefoil knots, figure-eight knots)
- Topoisomerases are enzymes that regulate the topology of DNA
- Type I topoisomerases (topoisomerase I) change the linking number by ± 1 through single-strand breaks
- Type II topoisomerases (topoisomerase II) change the linking number by ± 2 through double-strand breaks
- Knotted structures can form during the folding process of some proteins (carbonic anhydrase)
- May affect protein stability, function, and degradation
- Knots can be conserved across different species suggesting evolutionary significance
- Some viral capsids exhibit knotted topologies (bacteriophage P4)
- Knot type may influence the assembly and stability of the capsid
- Could provide targets for antiviral therapies

15.2 Topological quantum field theories and knot invariants

Topological Quantum Field Theories (TQFTs) bridge knot theory and quantum physics. They assign algebraic objects to manifolds and operations to cobordisms, providing a framework for calculating knot invariants like the Jones polynomial using the Chern-Simons TQFT.

TQFTs reveal deep connections between knots and quantum entanglement. Knots represent entangled states, with invariants quantifying entanglement. This link to quantum physics opens doors to applications in topological quantum computation and understanding quantum materials.

Topological Quantum Field Theories (TQFTs)

Principles of TQFTs and knot theory

- TQFTs are quantum field theories sensitive only to the topology of spacetime, independent of the choice of metric or geometry and invariant under smooth deformations (diffeomorphisms)
- Assign algebraic objects (vector spaces, categories) to manifolds and algebraic operations (linear maps, functors) to cobordisms between manifolds
- Provide a framework for constructing knot invariants by assigning algebraic objects to 3-dimensional manifolds and knots embedded within them

Calculation of knot invariants

- Calculate the Jones polynomial using the Chern-Simons TQFT, a 3-dimensional theory based on a gauge group ($SU(2)$, $SU(N)$)
- Represent the knot as a Wilson loop in the Chern-Simons path integral
- Evaluate the path integral using perturbative or non-perturbative methods (Feynman diagrams, exact solutions)
- The resulting value is the Jones polynomial, a Laurent polynomial in the variable q
- Other TQFTs (Witten-Reshetikhin-Turaev TQFT) can also calculate knot invariants (HOMFLY polynomial, Kauffman polynomial)

Physical Interpretation and Applications

Physical meaning of knot invariants

- In Chern-Simons theory, the Jones polynomial relates to the expectation value of the Wilson loop operator, a gauge-invariant observable measuring the holonomy of the gauge field along a closed loop
- Knot invariants encode information about the linking and braiding of knots, revealing properties of the underlying quantum field theory (phase structure, symmetries, excitations)
- Physical interpretation depends on the specific TQFT and its relation to physical systems (condensed matter systems, quantum gravity models)

Knots in quantum entanglement

- Knots and links represent entangled quantum states, with entanglement structure encoded in the topology

- Knot invariants (Jones polynomial) quantify the entanglement of these states
- Topological quantum computation utilizes properties of topological phases of matter (anyons) to perform quantum computations
- Anyons are quasiparticles with non-trivial braiding statistics, described by knot and link diagrams
- Braiding anyons implements quantum gates, with computations topologically protected against local perturbations
- TQFTs provide a mathematical framework for describing topological phases of matter and their excitations
- Algebraic objects assigned to manifolds and knots encode information about anyonic excitations and their braiding properties
- Studying the connection between knots, TQFTs, and topological quantum computation leads to insights into quantum entanglement and fault-tolerant quantum computing architectures

15.3 Knots in string theory and other areas of theoretical physics

String theory explores the idea of particles as tiny vibrating strings, which can form knots. These knots relate to the topology of extra dimensions and higher-dimensional theories like M-theory. Knots in string theory open up new ways to understand the fundamental structure of the universe.

Knot theory also helps classify exotic spacetime topologies in general relativity and string theory. It provides a framework for studying wormholes and time loops, using knot invariants to distinguish between different spacetime structures. This connection is crucial for developing a complete theory of quantum gravity.

Knots in String Theory and Theoretical Physics

Knots in string theory

- String theory posits fundamental particles composed of tiny, vibrating strings can be open or closed, forming loops
- Closed loops can be knotted, leading to the study of knots in string theory
- Knots in string theory related to topology of extra dimensions (tori, manifolds)
- Higher-dimensional generalizations of string theory (M-theory) involve knotted structures
- M-theory includes two-dimensional membranes can form knotted configurations
- Active area of research studies knots in higher-dimensional theories

Knot theory and spacetime topologies

- Exotic spacetime topologies are non-trivial topological structures arising in general relativity and string theory (wormholes, time loops)
- Knot theory provides mathematical framework for classifying and studying exotic spacetime topologies
- Different types of knots correspond to different topological properties of spacetime
- Jones polynomial and other knot invariants distinguish between spacetime topologies

- Understanding relationship between knot theory and exotic spacetime topologies crucial for developing complete theory of quantum gravity unifying general relativity and quantum mechanics, accounting for possible exotic spacetime structures

Applications in quantum gravity

- Quantum gravity describes gravity at quantum scale, where effects of quantum mechanics and general relativity become important
- Loop quantum gravity uses mathematics of knot theory
- Space represented by network of loops (spin network) can be knotted
- Properties of knots determine geometry of space at quantum level
- Knot invariants (Jones polynomial) play crucial role in loop quantum gravity
- Calculate amplitudes of different quantum states of gravitational field
- Values depend on knotting of spin network, linking topology of space to dynamics of quantum gravity

Connections to theoretical physics

- Knot theory has applications in various areas of theoretical physics beyond string theory and quantum gravity
- Condensed matter physics uses knot theory to study topology of quantum systems
- Quantum systems (superconductors, superfluids) exhibit topological properties described by knot theory
- Knotting of vortices affects physical properties and phase transitions
- Topological insulators are materials insulating in interior but conduct electricity on surface
- Surface states protected by topological properties described using knot theory
- Knotting of electronic wavefunctions in surface states determines robustness and transport properties
- Cross-disciplinary research combining knot theory with other fields advances understanding of fundamental physical phenomena