The limits of knot detection: alternating links, mutation, and (categorified) quantum invariants

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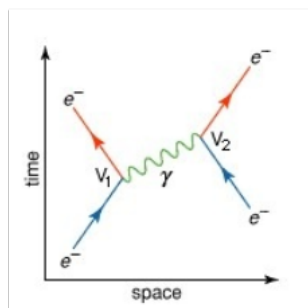
ICERM, October 22, 2025

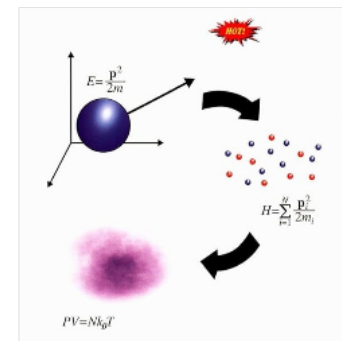# Why quantum (polynomial categorified) invariants matter ?

$$M^{\mathfrak{p}}(\lambda) = U_q(\mathfrak{g}) \otimes_{U_q(\mathfrak{p})} V$$

quantum
field theory

representation
theory

statistical
mechanics

quantum
computation

Quantum
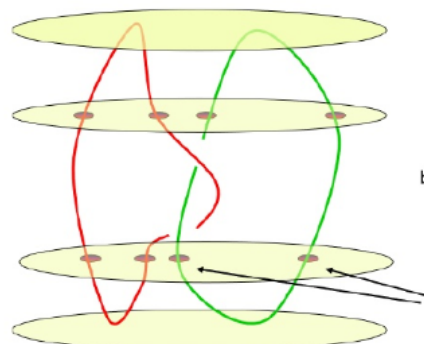invariants

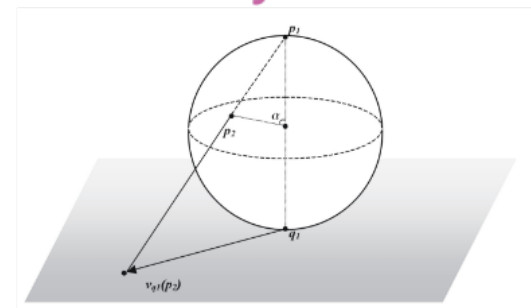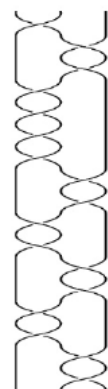Low-Dim. Topology

Geometry

Topological Quantum Computation

Braid Gate

Computation

readout

applying circuits

initialize

Physics

fusion

braiding anyons

create
anyon pairs

2 '23

How effective are these invariants as classifiers?

n	Jones polynomial
3	100
5	100
6	100
7	100
8	100
9	100
10	96.38
11	90.13
12	83.00
13	73.31
14	64.49
15	55.74
16	49.42
17	44.84
18	41.61
19	computing...

Jones polynomial
on prime knots

For each n :
#(polynomials) / #(knots)

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How effective are these invariants as classifiers?

Question

Put all knots in a bag, shake, and draw one.
How likely is a link invariant to single it out?

Khovanov homology detects the unknot (Kronheimer-Mrowka),
the trefoil & the cinquefoil (Baldwin,Sivek), ...

A refinement

→ P1: What is the probability P(n) that an invariant detects a knot among all knots with crossing number up to n?

→ P2: What is the behavior of P(n), as a function of n?

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Main Theorem (A. Lacabanne, D. Tubbenhauer, P.V., V.L. Zhang)

The following invariants detect alternating links with **probability zero**:

①

Polynomials: Jones, Alexander, SL(N), HOMFLYPT, SO(2N+1), SO(2N), SP(2N), Kauffman, G2, colored Jones, colored SL(N) (ext, sym and (N-1,1)), colored HOMFLYPT (ext, sym).

Homological: Khovanov homology over F2, odd Khovanov homology

Other: signature, determinant, (HF) double-branched cover, algebraic concordance, finite type of degree ≤ 10.

②

Most likely (experimental data): Khovanov homology over Z, Khovanov-Rozansky over Z, HOMFLYPT homology over Z, several HFK over F2.

Contents

Theorem

Detection probability

- Choose a random alternating link with up to n crossings.
- Compute invariant -> count number of distinct values.
- Detection probability = distinct / total.
- Measures how often the invariant uniquely identifies a link.

→ N.B. This is a **quantitative failure**, not just existence of counterexamples.

- As we draw more complex links, invariant values repeat more often.
- Growth comparison:

$$\#\text{links} \sim c^n, \quad \#\text{distinct invariant values} \sim a^n, \quad a \ll c.$$

- Hence detection probability $\approx (a/c)^n \to 0.$

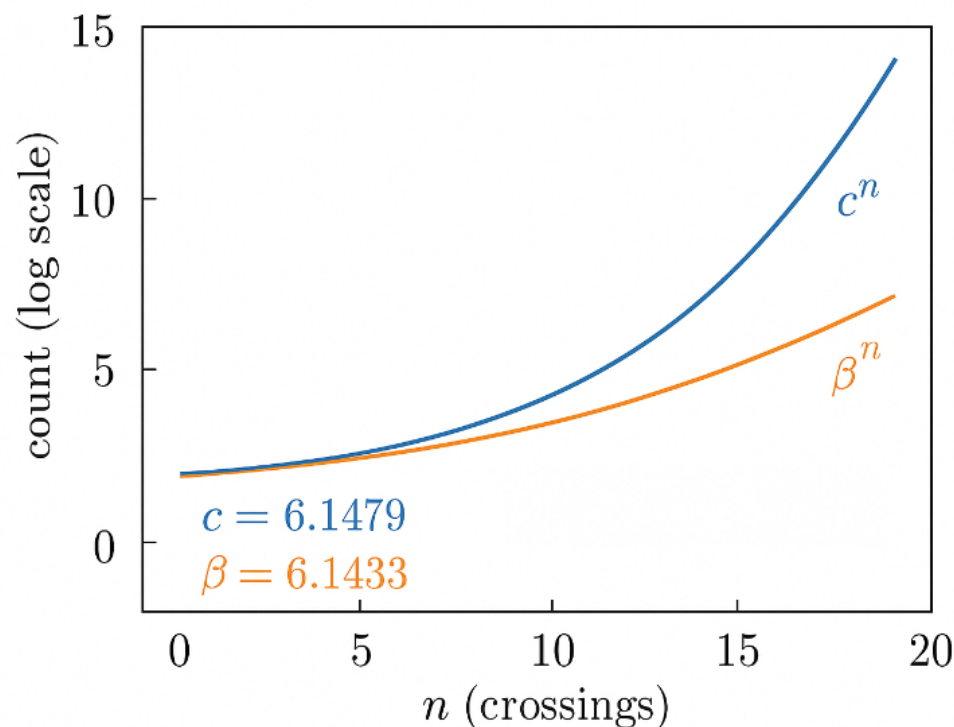8/23

Counting alternating diagrams and mutation classes

■ **Alternating links** can be counted combinatorially (Sundberg-Thistlethwaite '98)
Generation-function analysis gives exponential growth:

$$L_n \sim C\,c^n, \quad c = 6.147902686\ldots$$

■ The number of mutation-invariant classes grows slightly slower:

$$M_n \sim C'\,\beta^n, \quad \beta = 6.143312242\ldots$$

■ N.B. $\beta < c.$

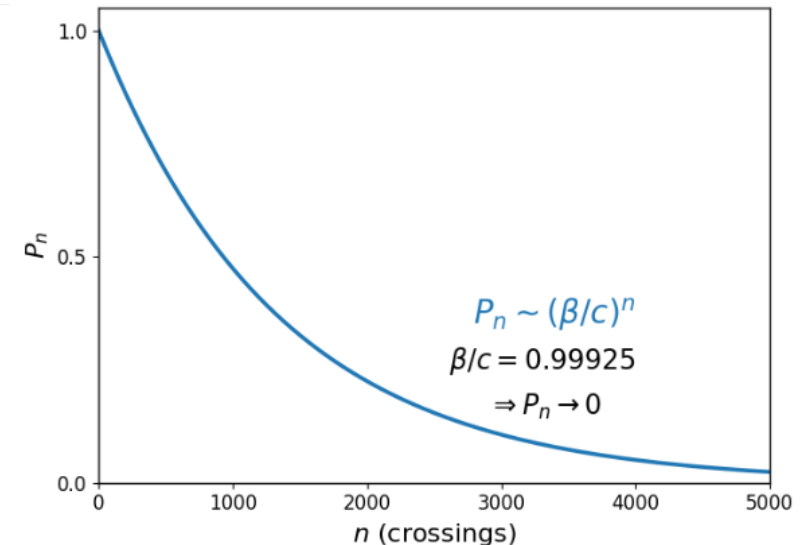# Why mutation-invariant invariants fail to detect links

■ If an invariant I is **invariant under mutation**, then all links in the same mutation class share the same I-value.

■ Therefore, the number of distinct invariant values $\leq$ number of mutation classes:

$$\#\mathrm{Im}(I_n) \leq M_n.$$

■ Detection probability: $P_n = \dfrac{\#\mathrm{Im}(I_n)}{L_n} \leq \dfrac{M_n}{L_n} \sim \left(\dfrac{\beta}{c}\right)^n = (0.99925\ldots)^n \to 0.$

■ So every mutation-invariant polynomial or categorified invariant detects alternating links with probability zero.

■ The **decay is exponential**.

$P_n \sim (\beta/c)^n$
$\beta/c = 0.99925$
$\Rightarrow P_n \to 0$

Mutation-invariant invariants

■ Which invariants ignore mutation:

- Any polynomial quantum invariant that satisfies a skein relation or is multiplicity free is invariant under mutation.

- SL(N) for (N-1,1) : Morton-Cromwell '96 (HOMFLYPT: stabilization).

- Khovanov homology over F2 or odd Khovanov homology: Wehrli '10, Bloom '10.

- Remaining ones: classical result, or Green '13 (double-branched cover related).

Main Theorem (A. Lacabanne, D. Tubbenhauer, P.V., V.L. Zhang)

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② Most likely (experimental data): Khovanov homology over Z, Khovanov-Rozansky over Z, HOMFLYPT homology over Z, several HFK over F2.

Why detection probabilities vanish?

■ Takeaway

Mutation is a **symmetry** invisible to quite a few quantum invariants.

It's exponential abundance among alternating links forces their **detection probabilities to decay to zero**.

Big data and the limits of detection

Computational and experimental results

Setup

- Large-scale computations on knots up to 18 crossings
- Invariants tested:

  - Khovanov homology: **KnotTheory Mathematica package** - the knot atlas
  - Odd Khovanov homology: **KnotJob** program - D. Shüetz
  - Jones polynomial : homemade program
  - HFK homology: **Knot Floer homology calculator** - P. Ozsváth, Z. Szabó
  - Alexander polynomial: **KnotTheory Mathematica package** - the knot atlas
  - SL(3) Khovanov-Rozansky homology: **KnotJob** program - D. Shüetz
  - SL(3) polynomial: **KnotTheory Mathematica package** - the knot atlas
  - HOMFLYPT homology: program by K. Nakagane et S. Taketo
  - HOMFLYPT polynomial: **KnotTheory Mathematica package** - the knot atlas

- Detection probability = proportion of distinct values among prime knots

Resources:

- Katana computational cluster, supporter by UNSW Sydney
- Laboratoire Mathématique Blaise Pascal
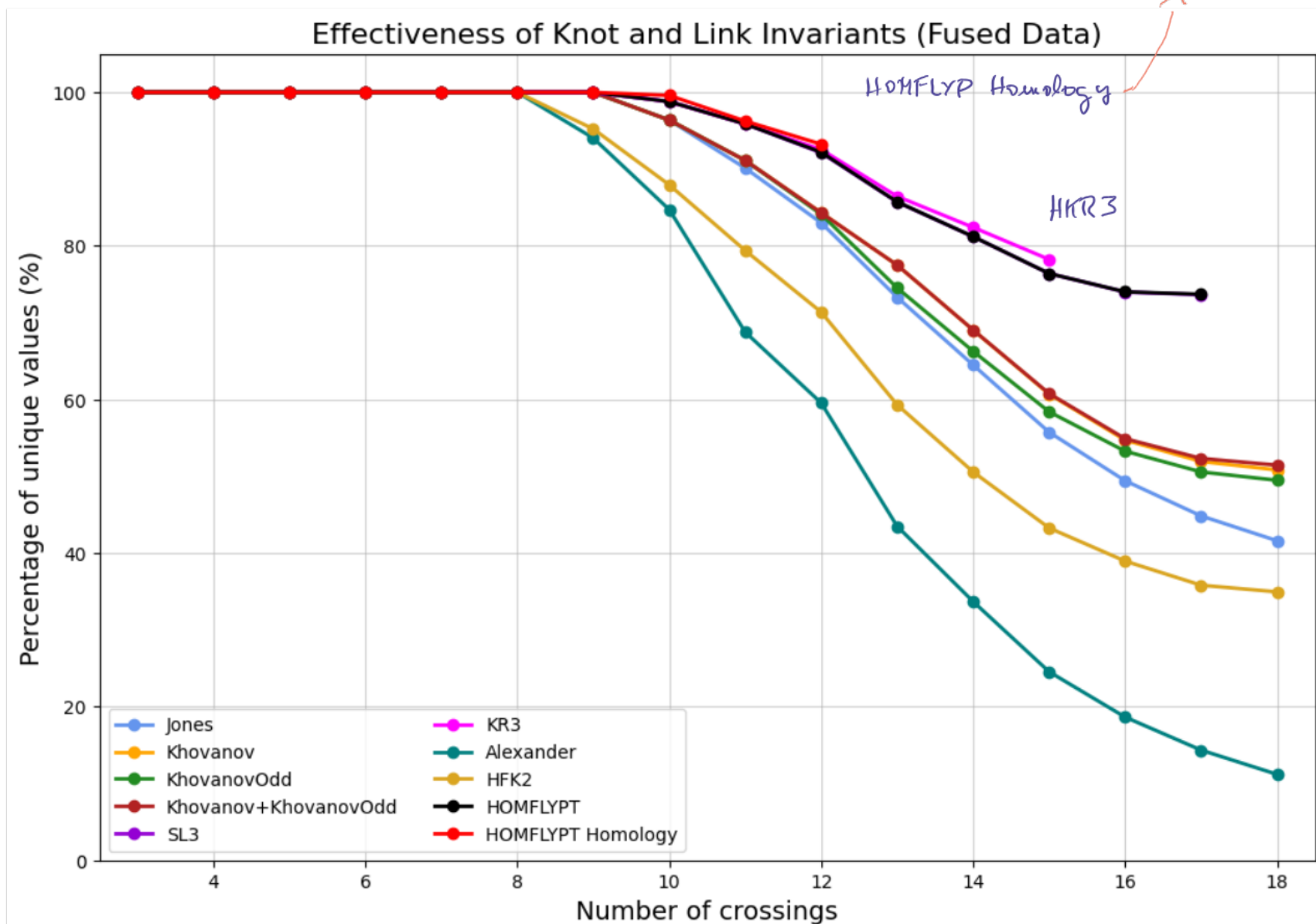
Code-data

Knot tables:

Knotinfo
3-16 Xings

Regina
17-18 Xings

Stoimenow
Braid presentations

15/23

Results

Effectiveness of Knot and Link Invariants (Fused Data)

Annotations on figure:
- Computation still running
- interactive playground
- HOMFLYP Homology
- HKR3
- HOMFLYP polynomial SL(3)
- HKh + HKh Odd
- HKh
- HKh Odd
- Jones
- HFK
- Alexander

Legend:
- Jones
- Khovanov
- KhovanovOdd
- Khovanov+KhovanovOdd
- SL3
- KR3
- Alexander
- HFK2
- HOMFLYPT
- HOMFLYPT Homology

Axis labels: Percentage of unique values (%), Number of crossings

Results

n	Jones	Khovanov	HKhOdd	HKh+HKhOdd	SL3	KR3	Alexander	HFK2	HOMFLYPT	HOMFLYPT Hgy
3	100	100	100	100	100	100	100	100	100	100
4	100	100	100	100	100	100	100	100	100	100
5	100	100	100	100	100	100	100	100	100	100
6	100	100	100	100	100	100	100	100	100	100
7	100	100	100	100	100	100	100	100	100	100
8	100	100	100	100	100	100	100	100	100	100
9	100	100	100	100	100	100	94.04	95.23	100	100
10	96.38	96.38	96.38	96.38	98.79	98.79	84.73	87.95	98.79	99.59
11	90.13	91.13	91.13	91.13	95.88	95.88	68.78	79.4	95.88	96.25
12	83	84.31	84.11	84.31	92.13	92.54	59.55	71.38	92.2	93.24
13	73.31	77.5	74.53	77.5	85.71	86.45	43.49	59.31	85.73	-
14	64.49	69.04	66.28	69.05	81.2	82.41	33.69	50.57	81.21	-
15	55.74	60.69	58.4	60.77	76.4	78.24	24.55	43.27	76.4	-
16	49.42	54.71	53.27	54.9	74	-	18.65	38.96	74.02	-
17	44.84	51.93	50.57	52.33	73.65	-	14.35	35.82	73.7	-
18	41.61	50.83	49.48	51.45	-	-	11.19	34.95	-	-

currently computing n=19

Computing cost
17/18 Xings

In Q3 2025, Restech provided over **18 million core-hours** of compute time through our **Katana Compute Cluster**, and your account was among the most active, with a total of **1,030,265 core-hours** consumed. The estimated/reference value is approximately **$41,211** .
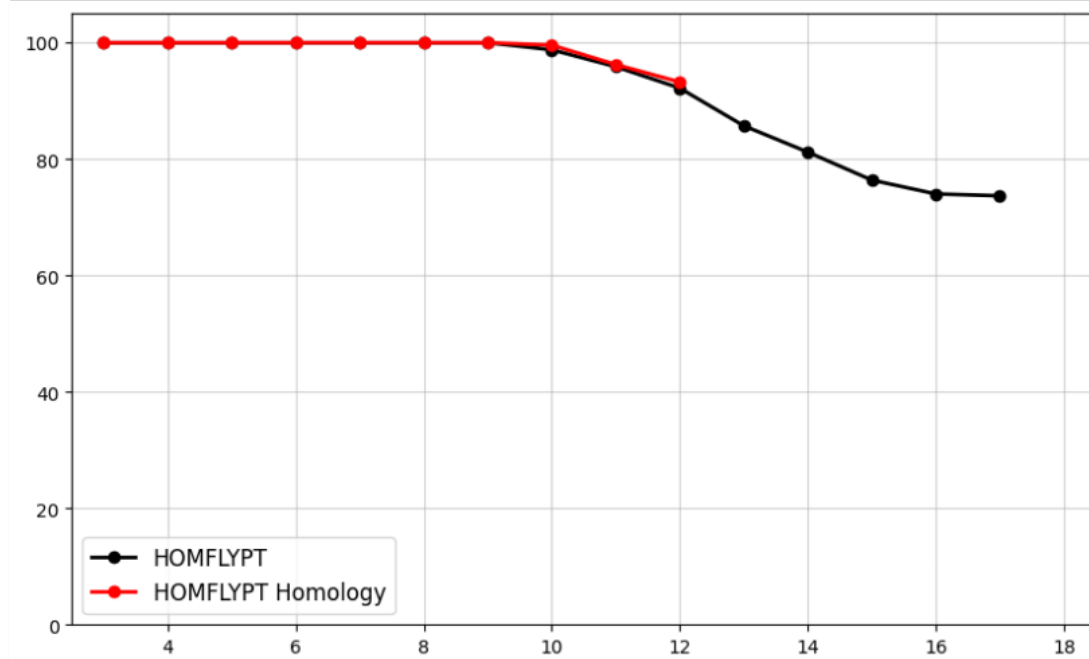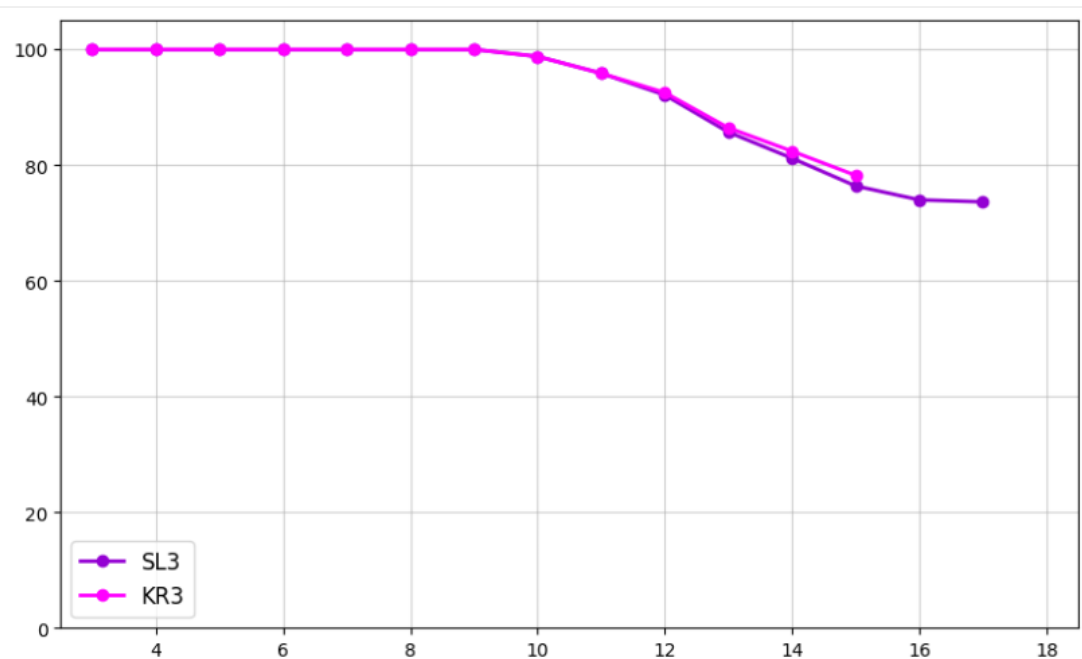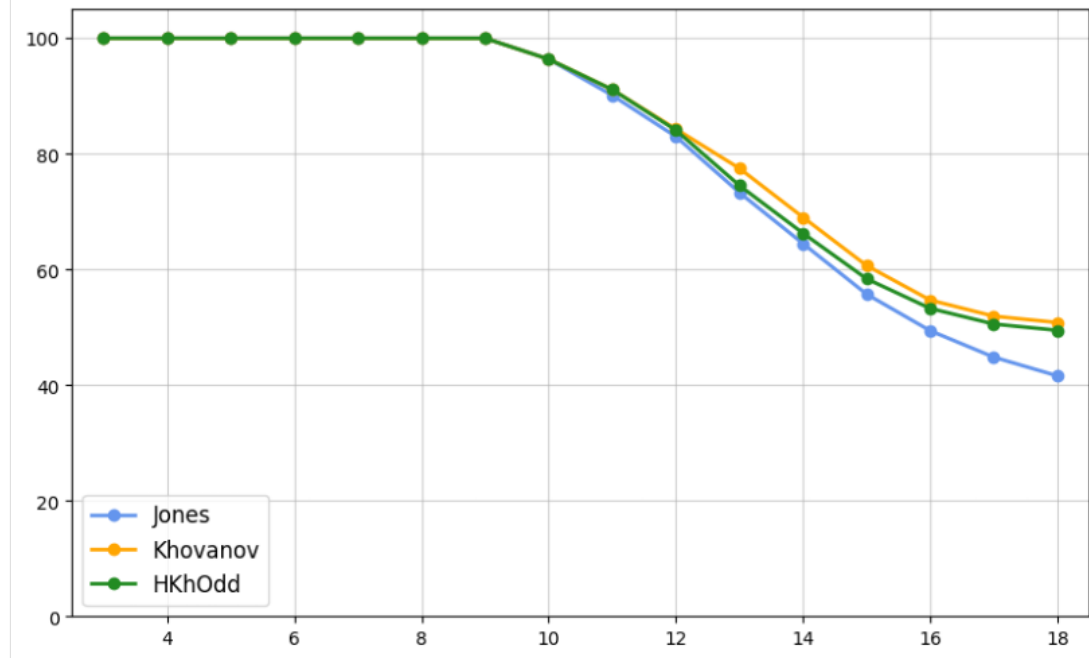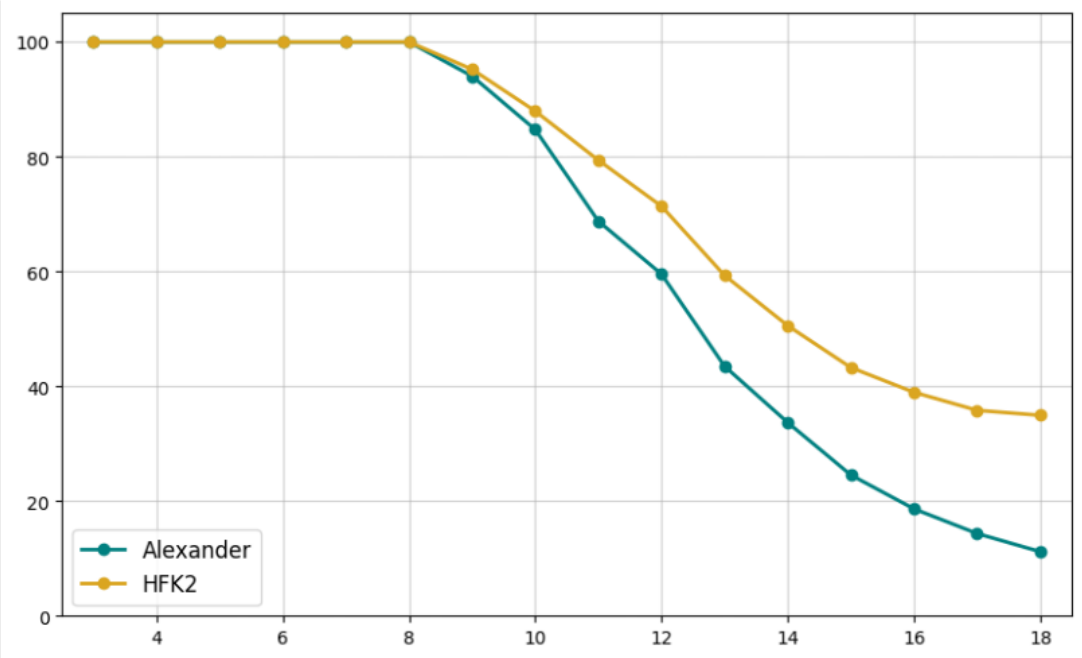
Observations

- **Exponential decay** in detection probability in crossing number

- **Categorified invariants** $\approx$ **polynomial ones** in performance

- Odd Khovanov and HOMFLYPT homologies surprisingly weak

What this results tell us

- **Why this is surprising**
  - Categorification was expected to strengthen detection: more structure, richer gradings.
  - Yet, data and asymptotics show no improvement over polynomial invariants.

- **What it reveals**
  - Mutation invariance acts as a bottleneck: most known invariants collapse on the same class.
  - The set of distinct invariant values grows exponentially slower than the set of links.

- **The message**
  - Most known knot invariants fail as detectors.
  - Categorification refines meaning, not distinguishing power.

 We learned how quantum invariants fail beautifully

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What now?

- Colored invariants with $\sqrt{\otimes}\sqrt{}$ not multiplicity free (e.g. HOMFLYPT polynomial colored with ⧉ detects mutation - Nawata-Ramadevi-Singh '17).

- Consider knots/links up to mutation.

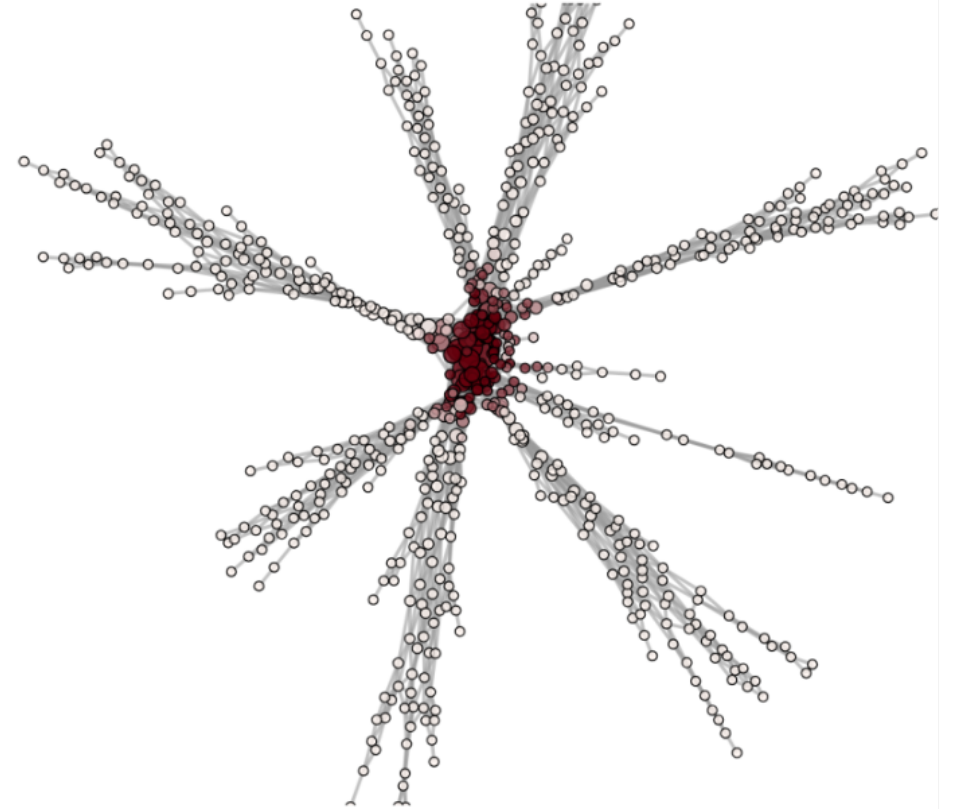- Tools from TDA (ballmaper) to analyze structure of data.

Invariant failure is not weakness - it reveals hidden symmetries in knot space

This is not the end of the story...

TDA - the ballmaper
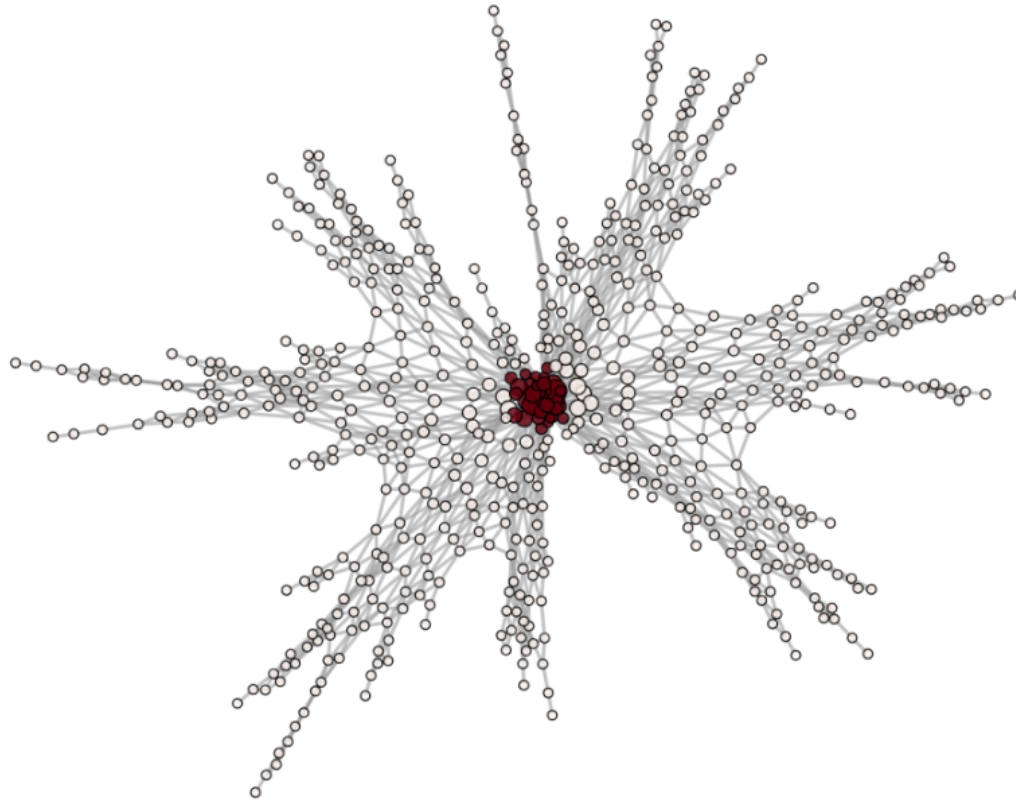
Jones

Khovanov

Thank you !

Slides