

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

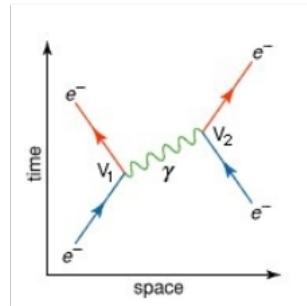
Pedro Vaz, Université catholique de Louvain

ICERM, October 22, 2025



slides

Why (classical, quantum, categorified) knot invariants matter ?



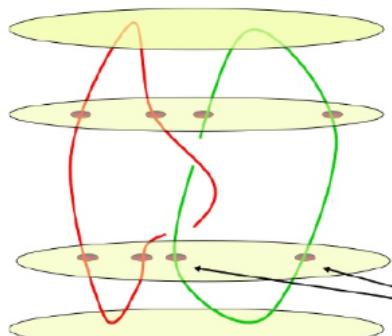
quantum
field theory

quantum
computation

Topological Quantum Computation

Computation

readout

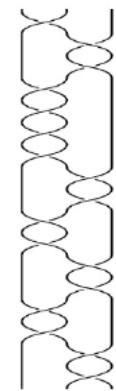


Physics

fusion

braiding anyons
create anyon pairs

Braid Gate

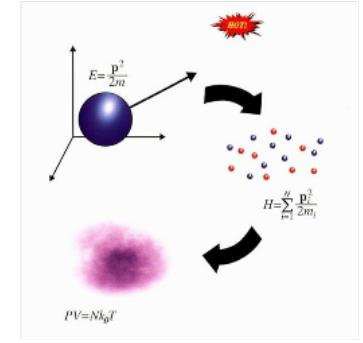


knot
invariants

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

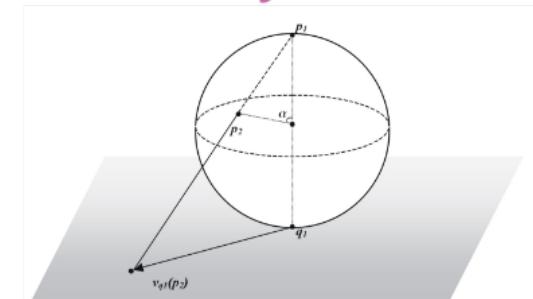
representation
theory

statistical
mechanics



Low-Dim. Topology

Geometry



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 function of n ?

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).

② **Homological:** Khovanov homology over F_2 , odd Khovanov homology

③ **Other:** signature, determinant, (HF) double-branched cover, algebraic concordance, finite type of degree ≤ 10 .

④ **Most likely (experimental data):** Khovanov homology over Z , Khovanov-Rozansky over Z , HOMFLYPT homology over Z , several HFK over F_2 .

Contents



Main Theorem



Experimental
data



Theorem

Detection probability

- Choose a random alternating link with up to n crossings.
- Compute invariant \rightarrow 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:
 $\# \text{links} \sim c^n, \quad \# \text{distinct invariant values} \sim \alpha^n, \quad \alpha \ll c.$
- Hence detection probability $\approx (\alpha/c)^n \rightarrow 0.$

Counting alternating diagrams and mutation classes

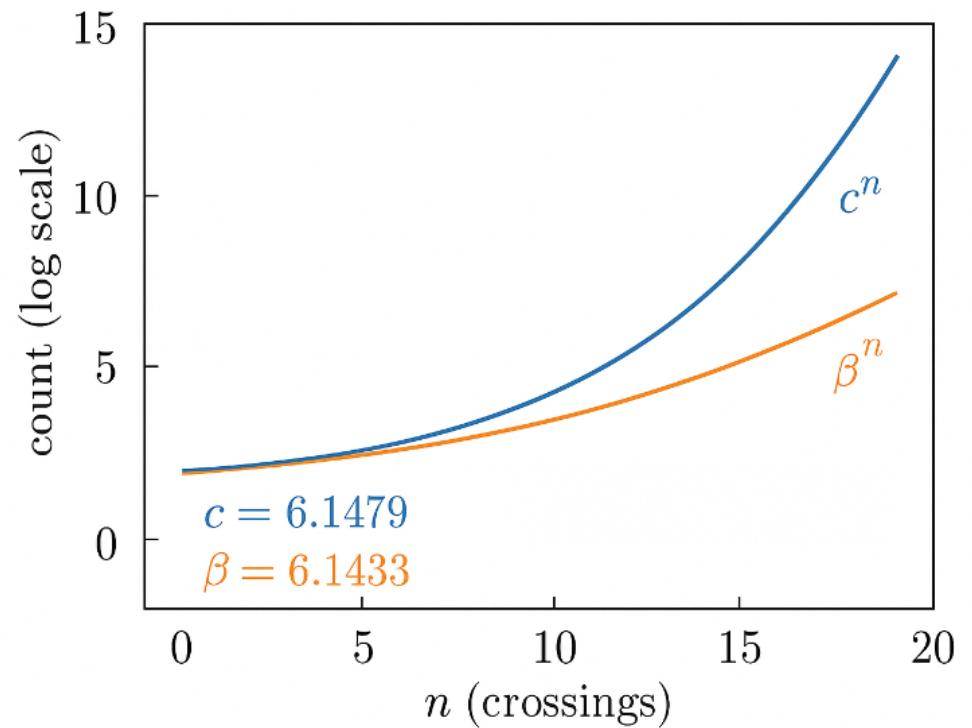
- Alternating links can be counted combinatorially (Sundberg-Thistlethwaite '98)
Generation-function analysis gives exponential growth:

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

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

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

- N.B. $\beta < c$.



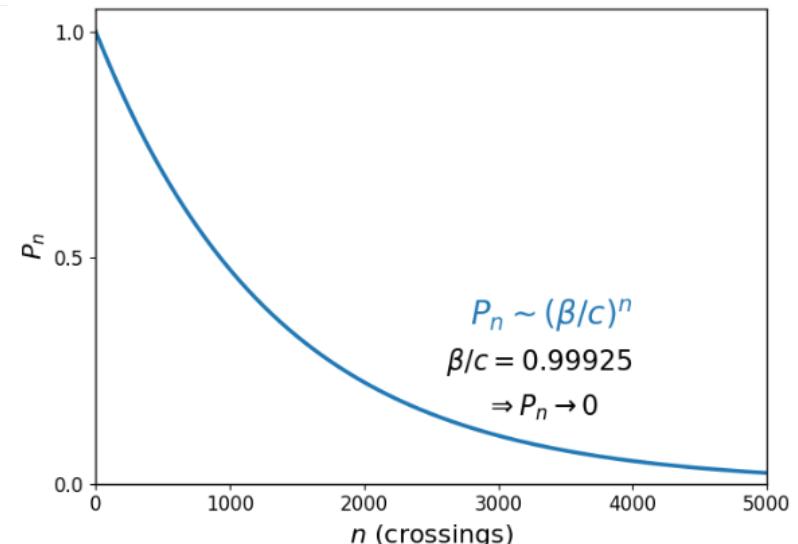
Why mutation-invariant invariants fail to detect links

- If an invariant Q is **invariant under mutation**, then all links in the same mutation class share the same Q -value.
- Therefore, the number of distinct invariant values \leq number of mutation classes:

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

- Detection probability: $P_n = \frac{\#\text{Im}(I_n)}{L_n} \leq \frac{M_n}{L_n} \sim \left(\frac{\beta}{c}\right)^n = (0.99925 \dots)^n \rightarrow 0.$

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



Mutation-invariant invariants

■ Which invariants ignore oriented mutation:

- Any polynomial quantum invariant that satisfies a skein relation or is multiplicity free is invariant under (general) mutation.
- $SL(N)$ for $(N-1,1)$: Morton-Cromwell '96 (HOMFLYPT: stabilization).
- Khovanov homology over F_2 or odd Khovanov homology: Wehrli '10, Bloom '10.
- Remaining ones: classical result, or Green '13 (double-branched cover related).

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



code-data

- 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

Knot tables:



Knotinfo

3-16 Xings



Regina

17-18 Xings



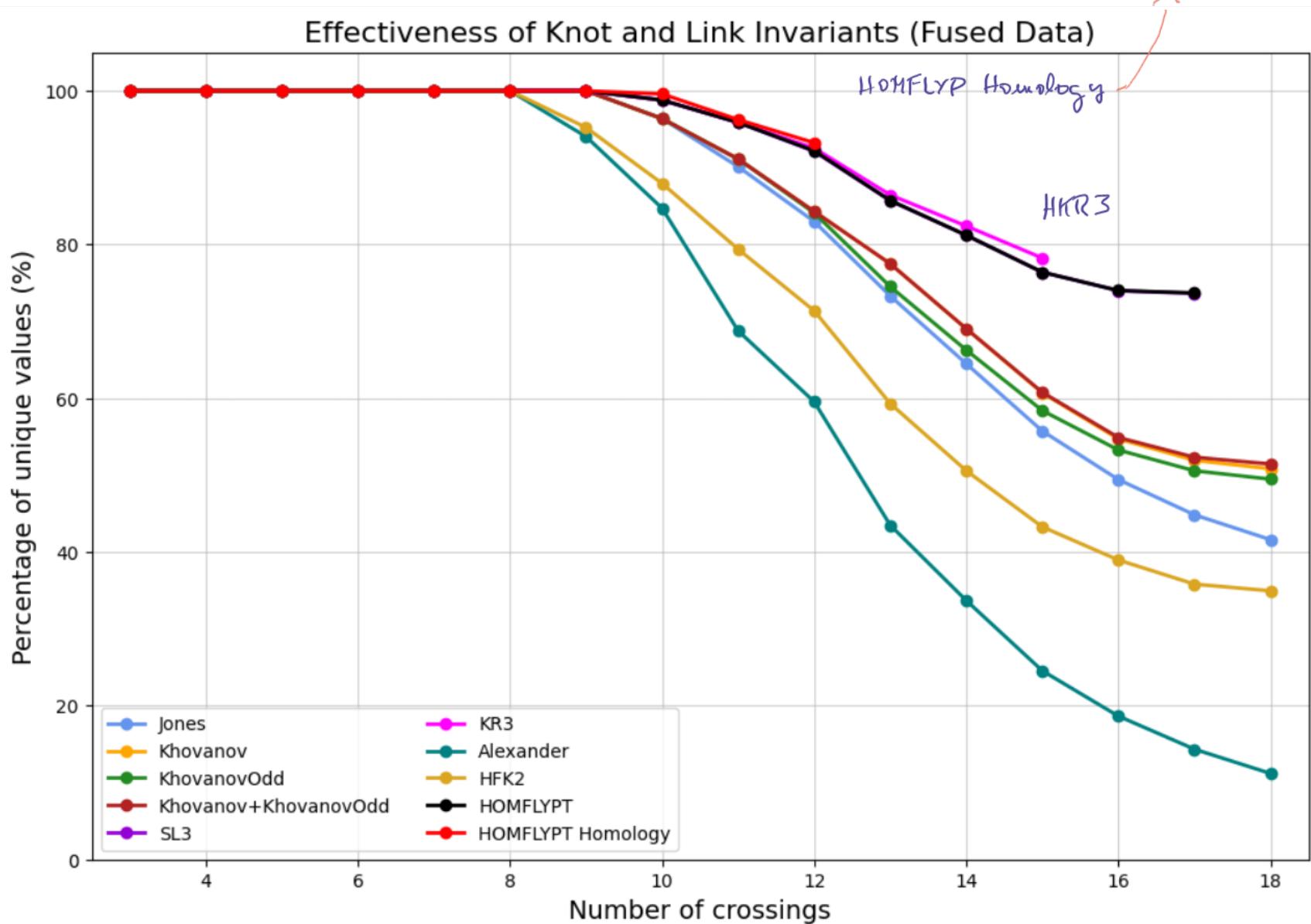
Stoimenow

Braid presentations

Resources:

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

Results



Computation still running
(~ 88 %)



interactive
playground

HOMFLYP polynomial
SL(3)

HKh + HKh Ddd
HKh
HKh Ddd

Jones

HFK

Alexander

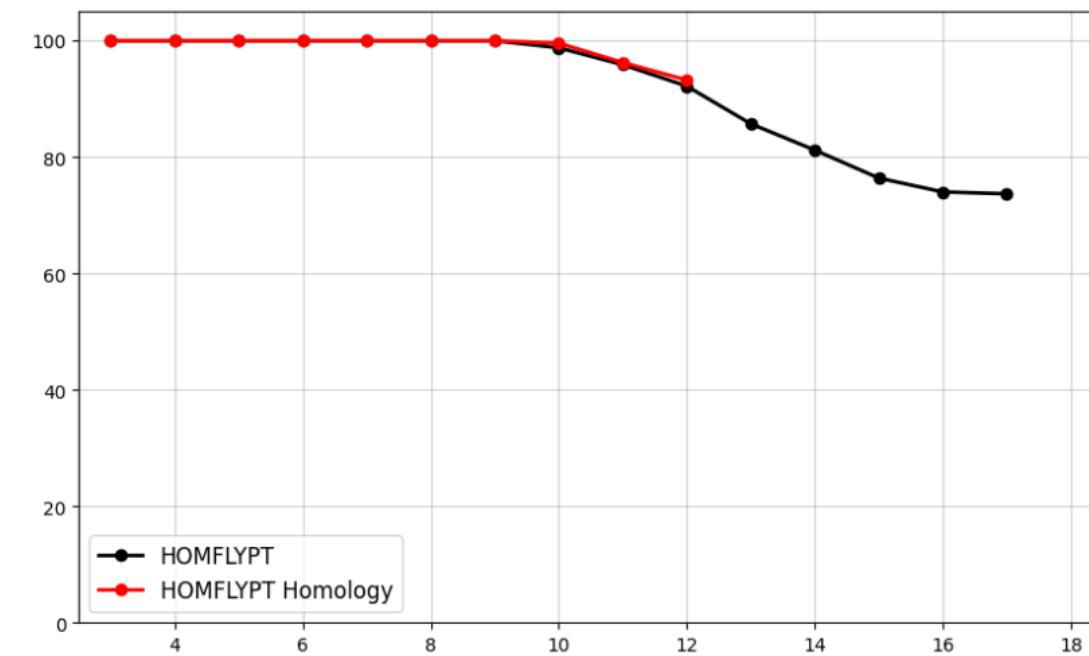
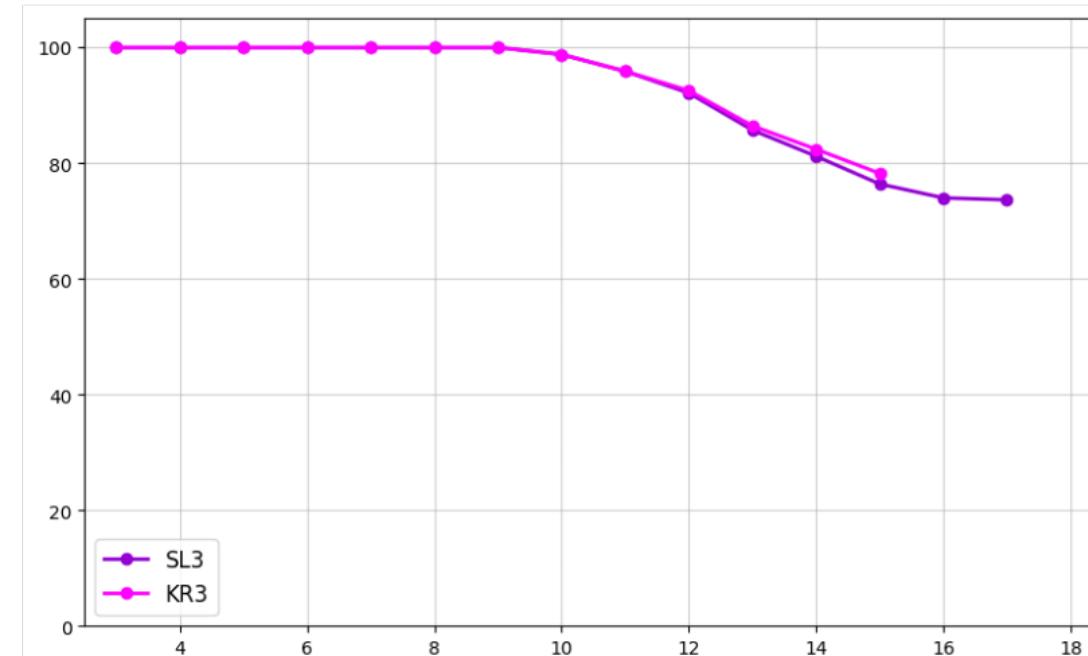
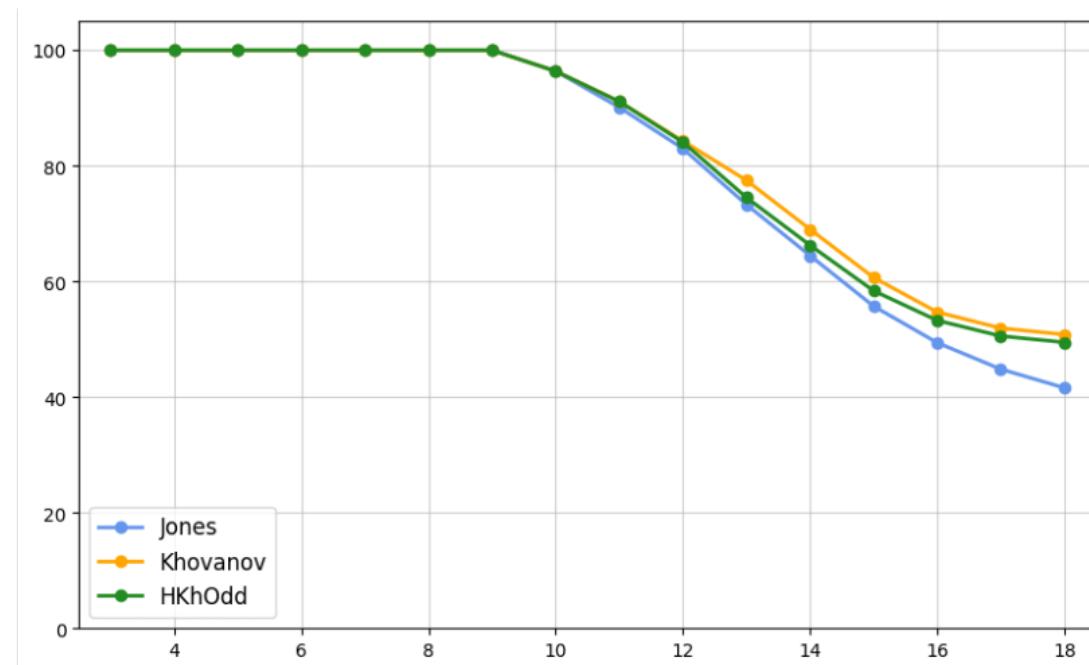
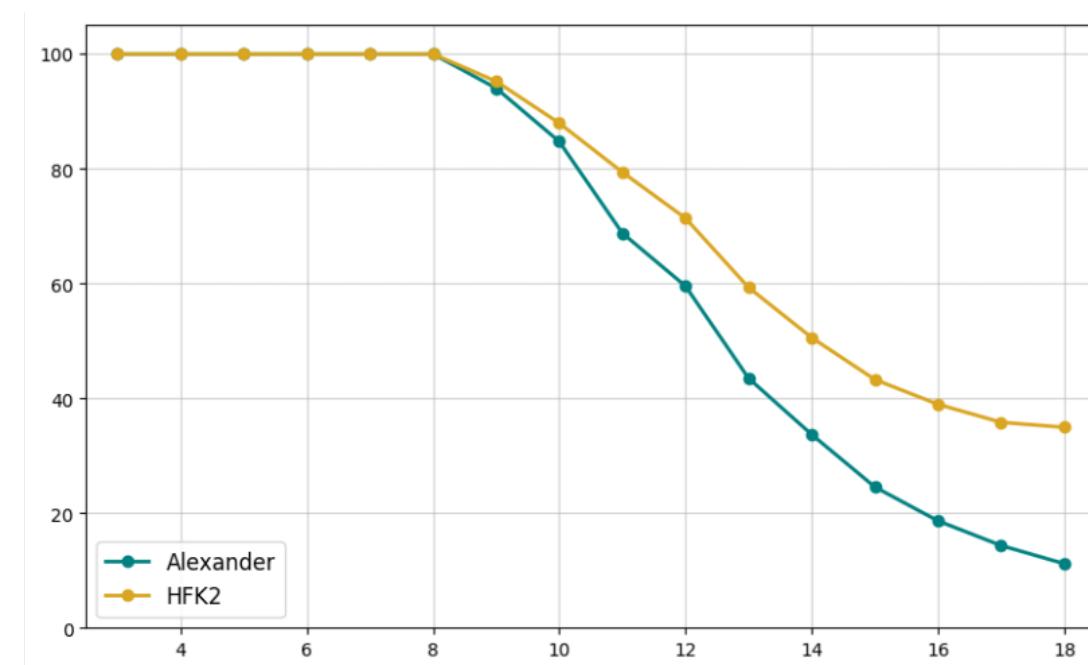
Results

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	93.3
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

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.

Thank you !



Slides