Evaluating strategies of phylogenetical analyses by the coherence of their results

Blaise Li

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- Apply various methods.
- Look how coherent the results obtained are when a given method is used on several datasets.
- Choose a posteriori the method that generated the most coherent results.

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- <Insert your favourite strategy item here>

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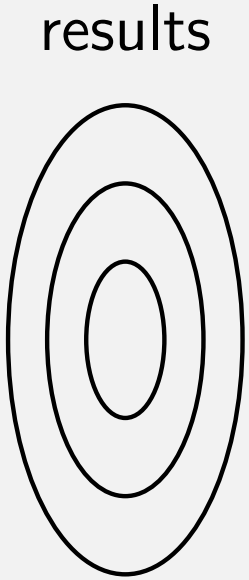

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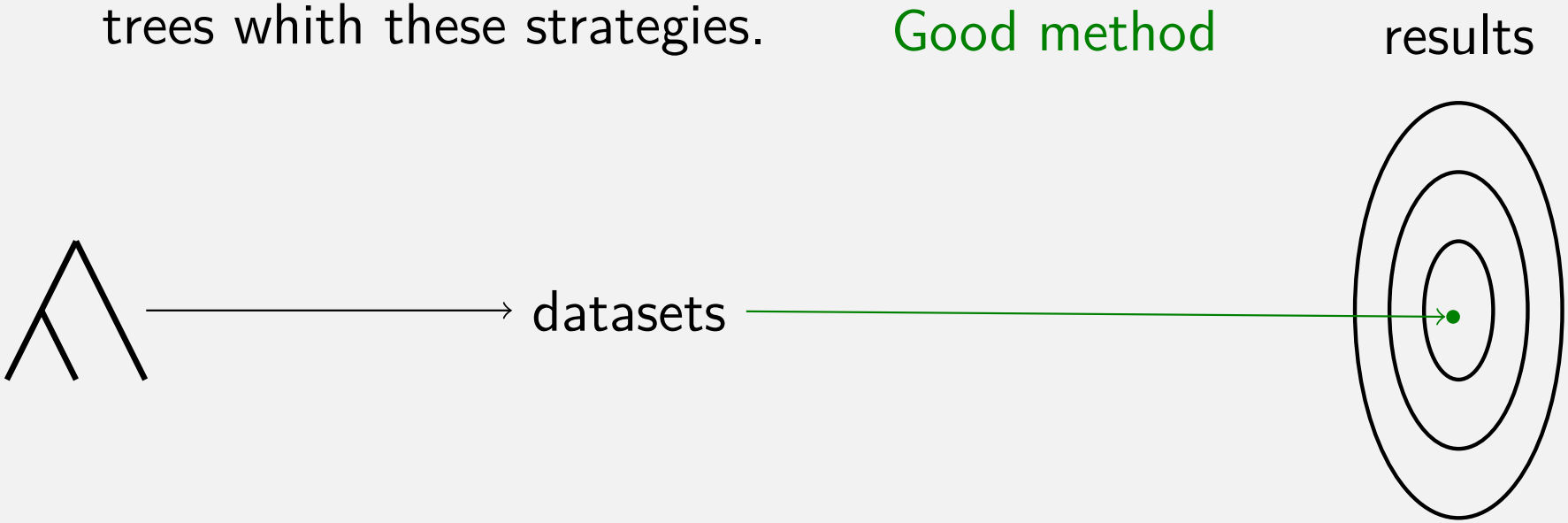

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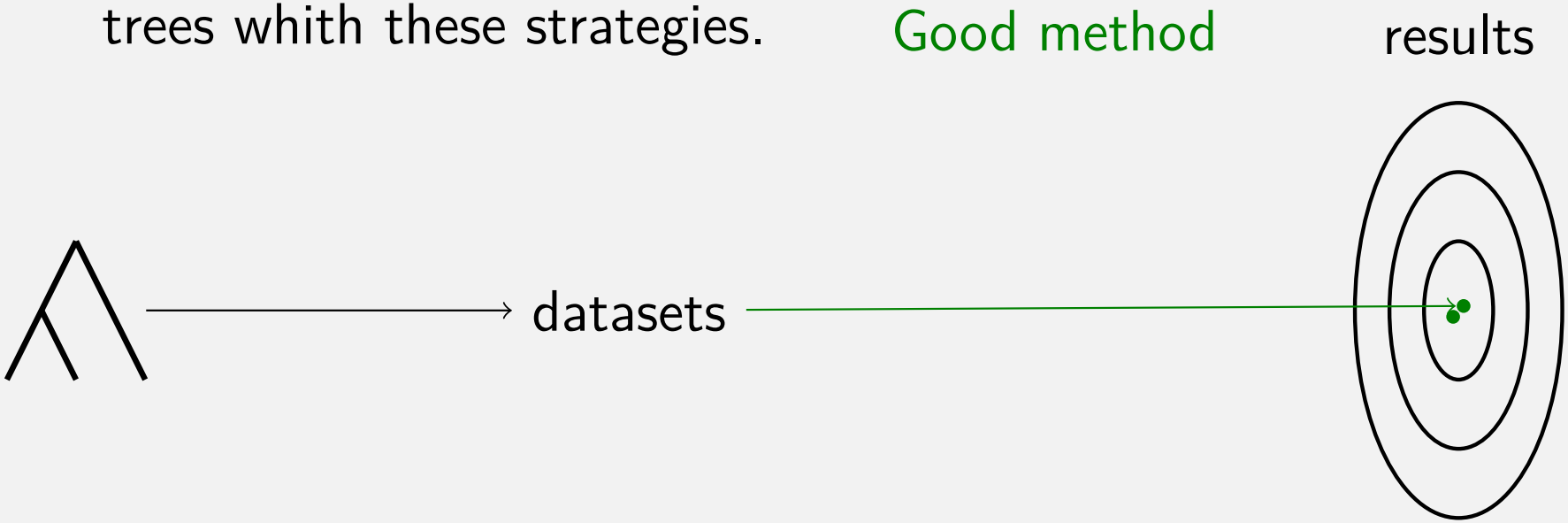

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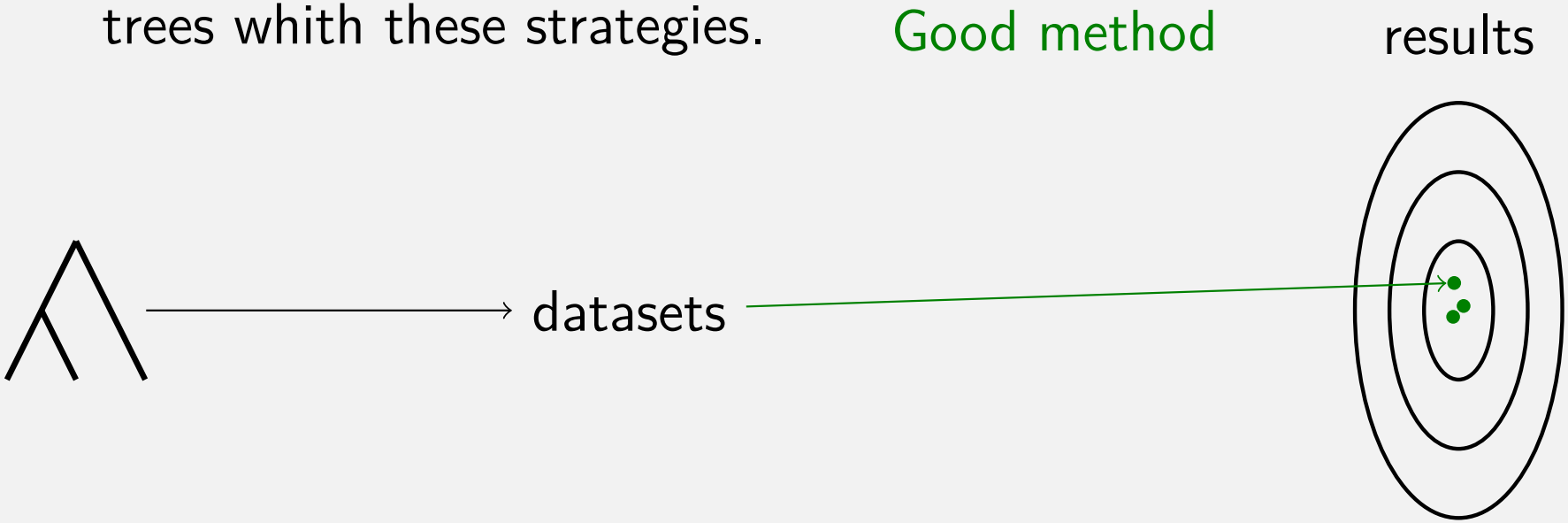

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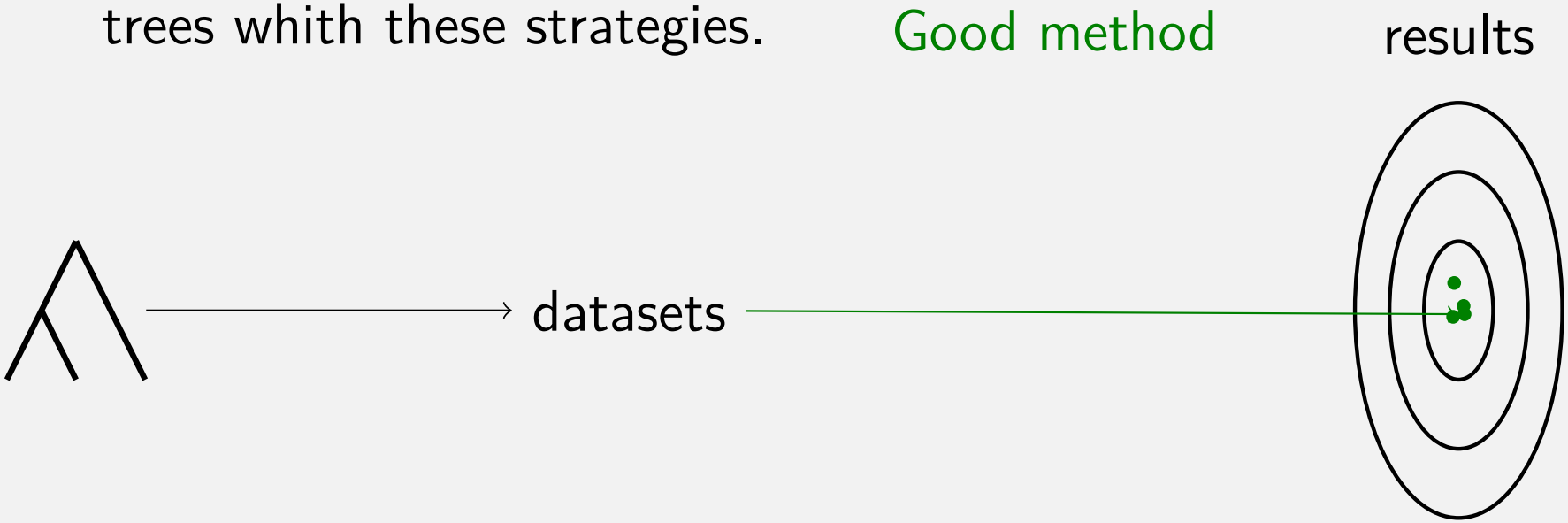

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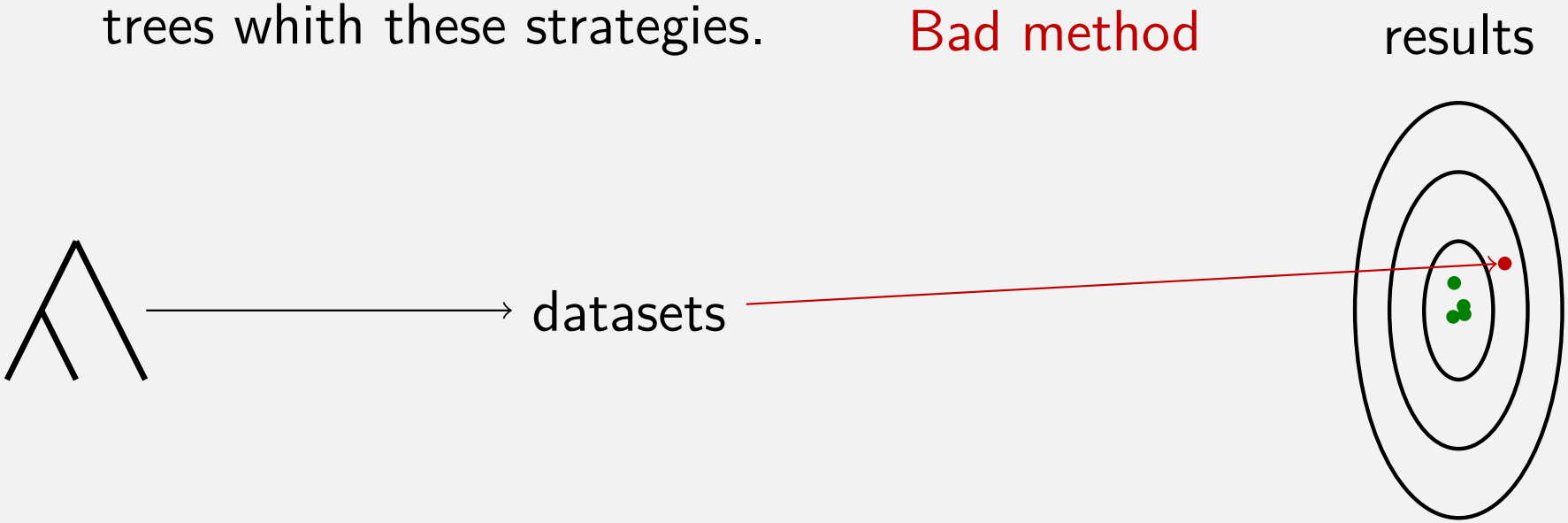

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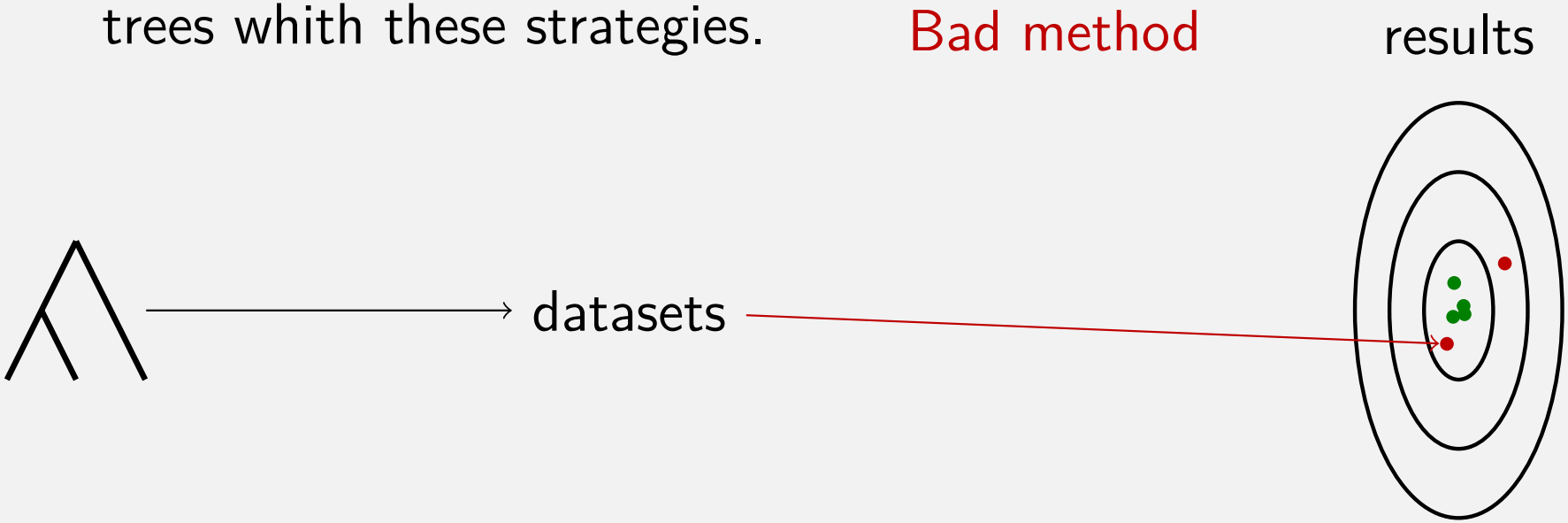

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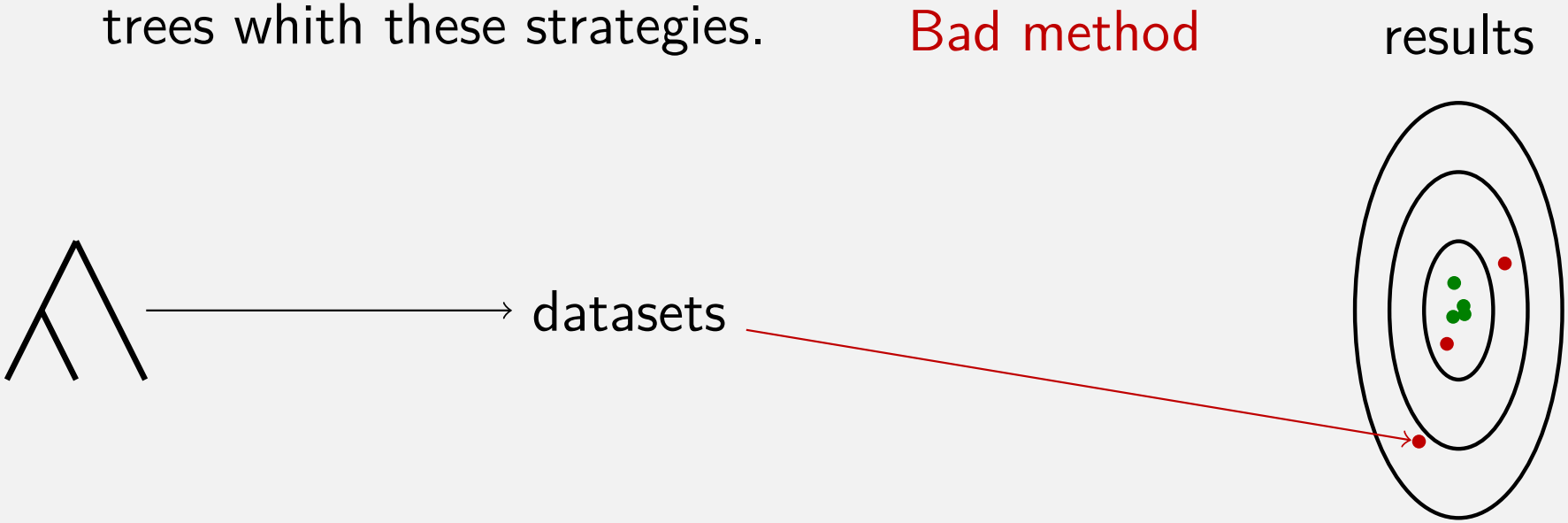

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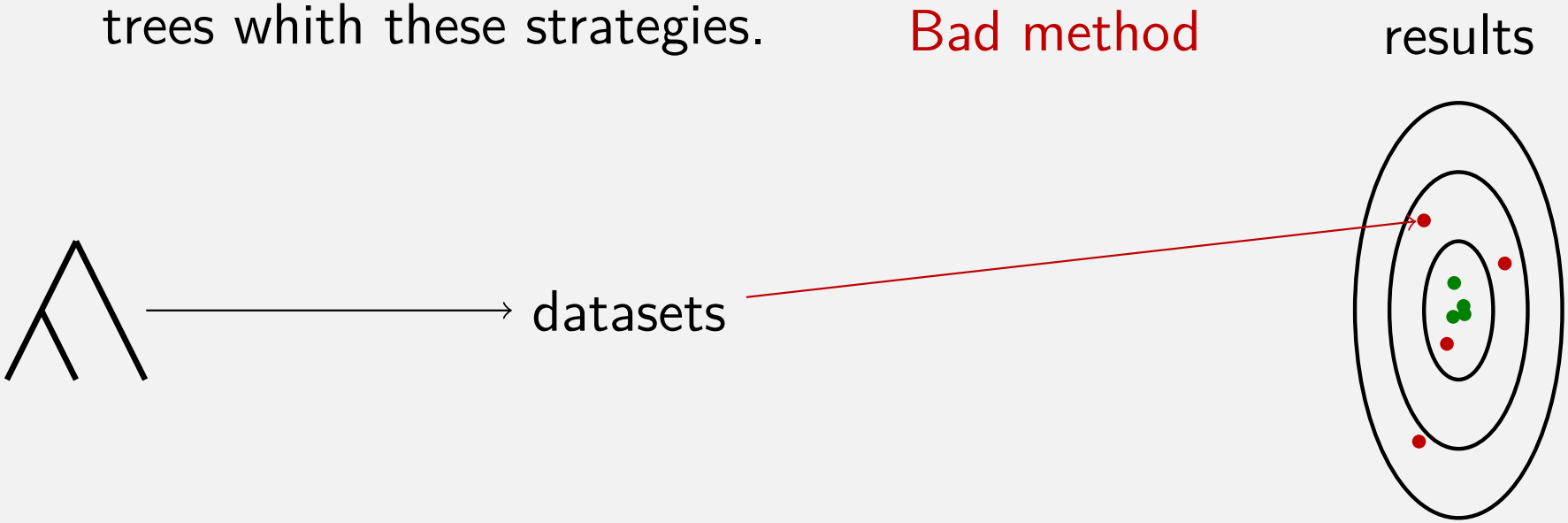

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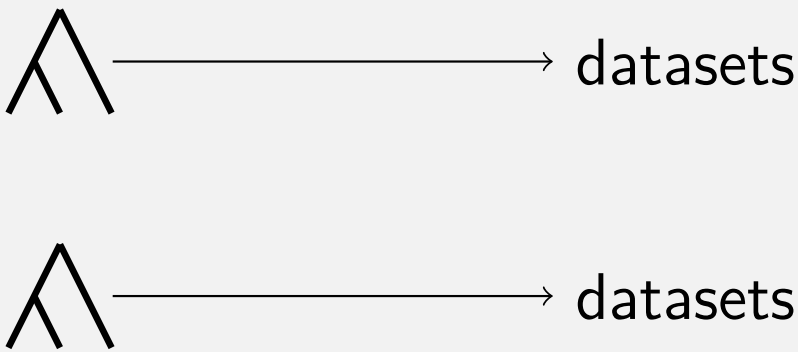

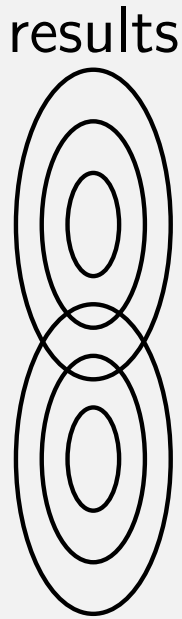

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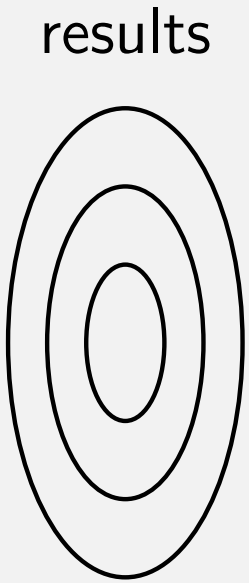

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Due to the internals of `concaterpillar` the analyses of the 4 sets should yield results with some degrees of incoherence, at least for standard maximum likelihood under a $\mathrm{GTR} + \mathrm{I} + \Gamma$ model.

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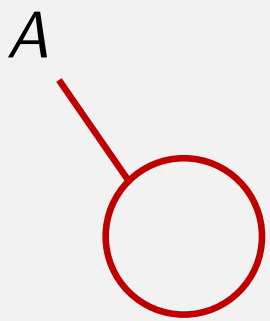
  - distance bootstrap (Jukes-Cantor and LogDet, 200 pseudo-replicates)

Robinson-Foulds distance (a.k.a symmetric difference)



A: bipartitions defined by the branches of one tree

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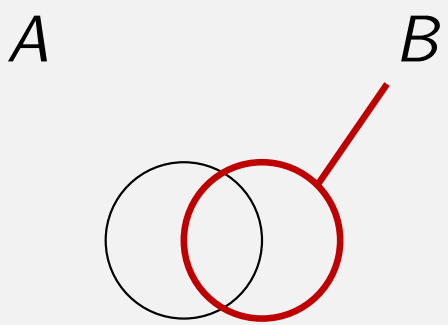

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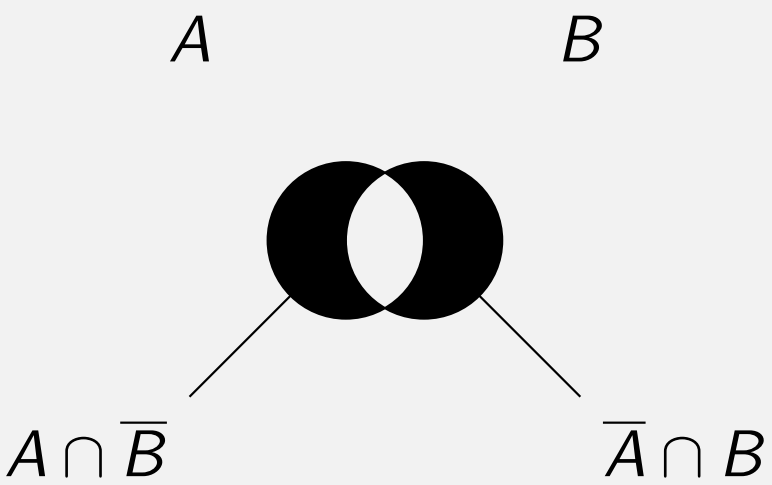
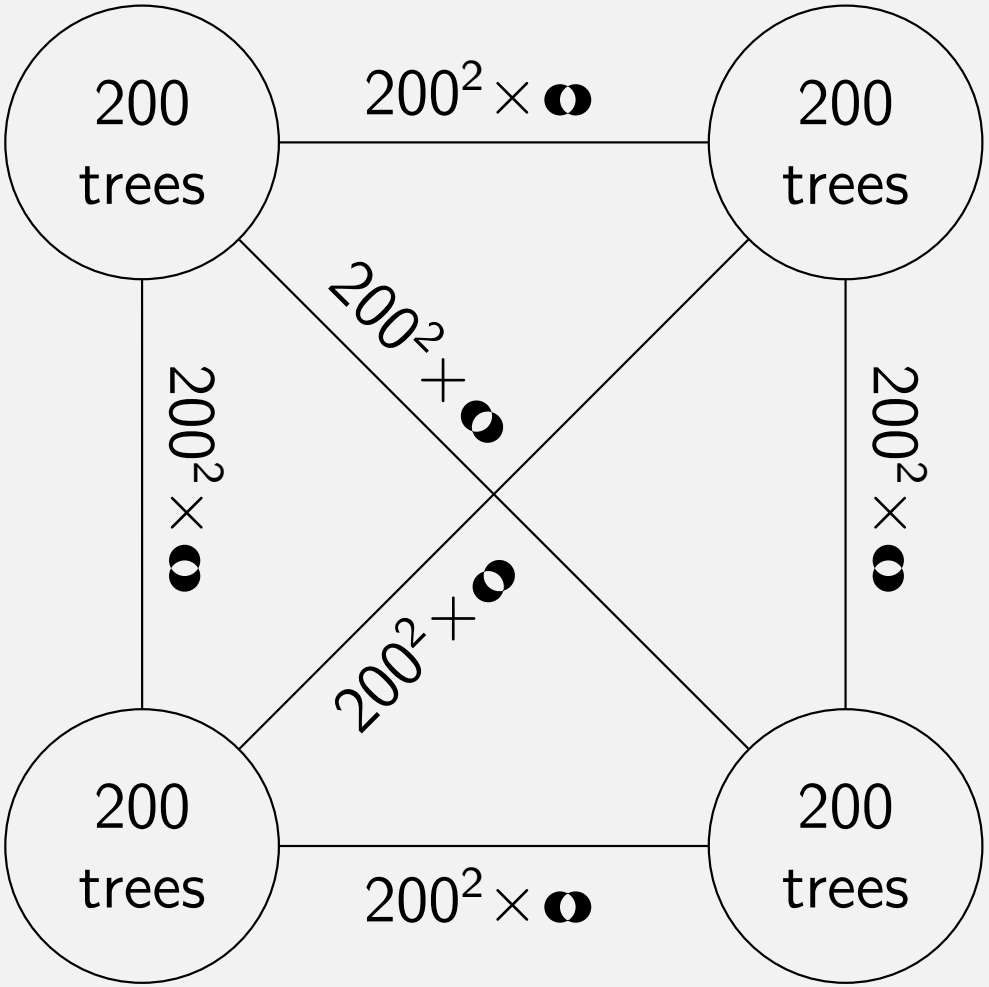


A: bipartitions defined by the branches of one tree
B: bipartitions defined by the branches of the other tree
Distance between the trees:
$RF = |A \cap \overline{B}| + |\overline{A} \cap B|$

Coherence measure



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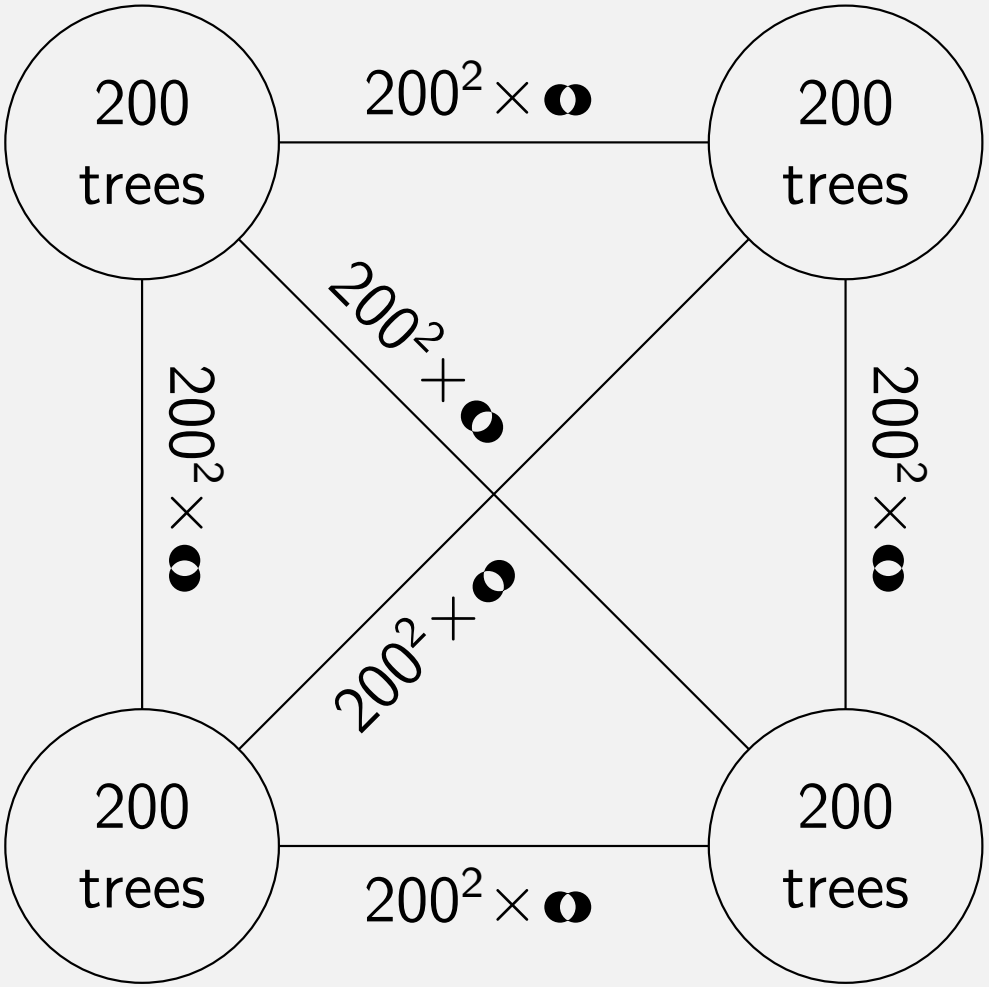

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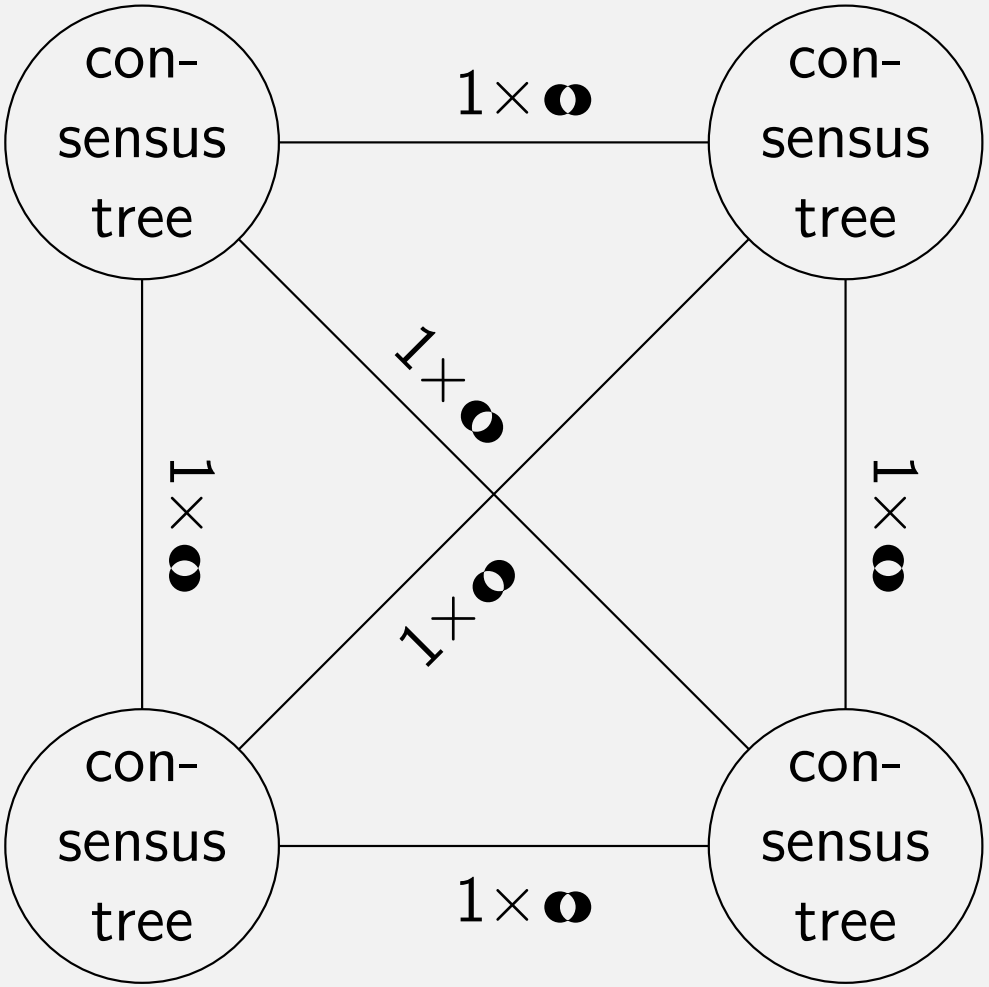

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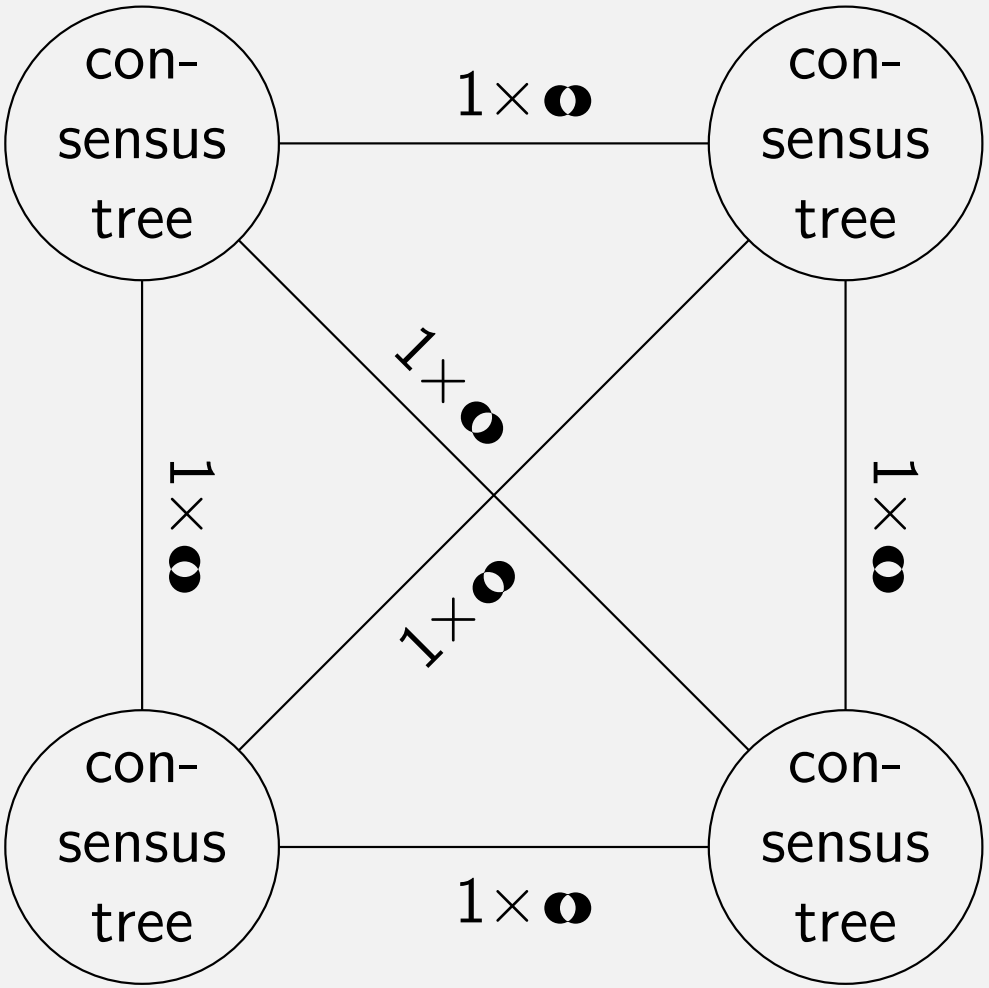

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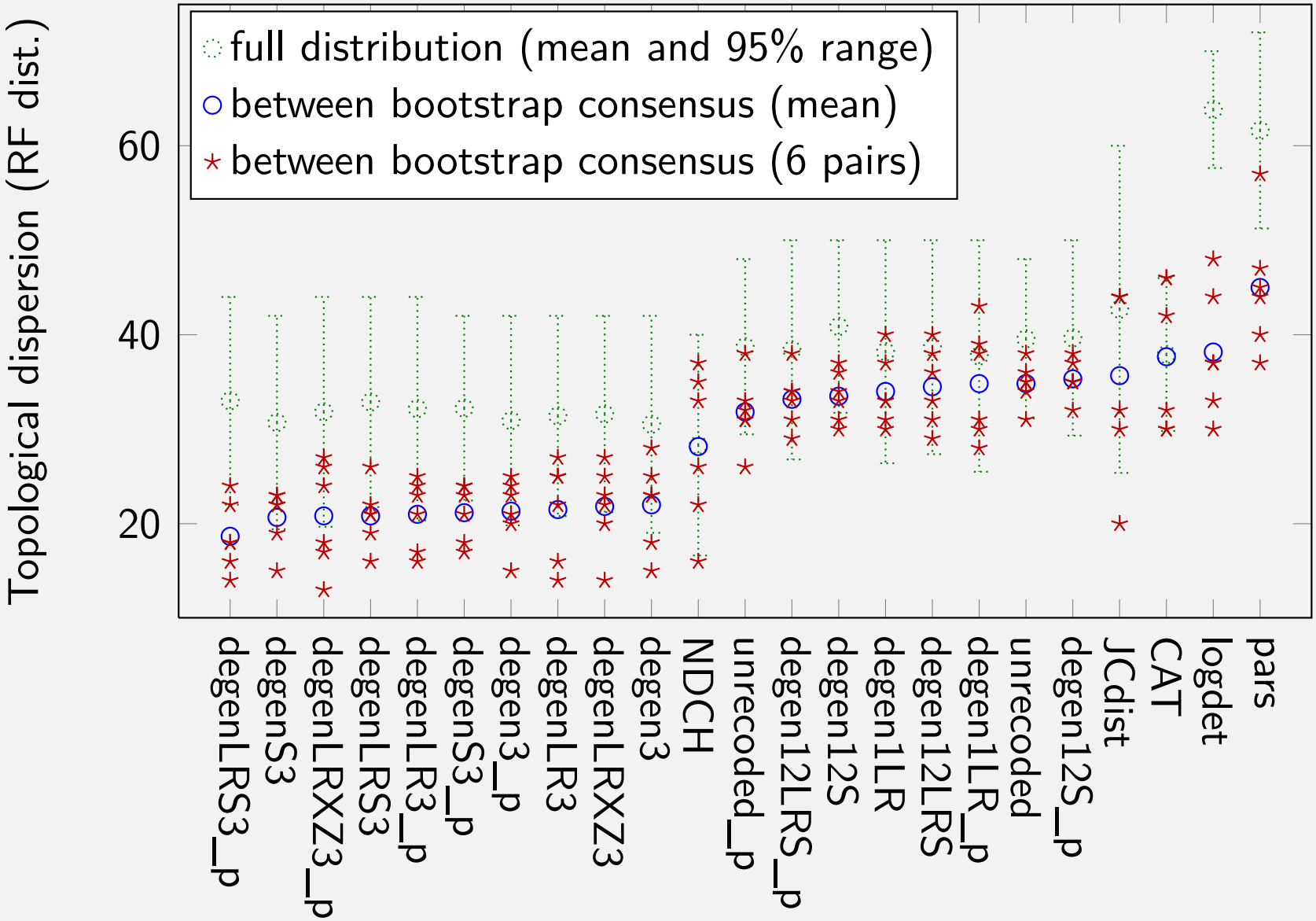
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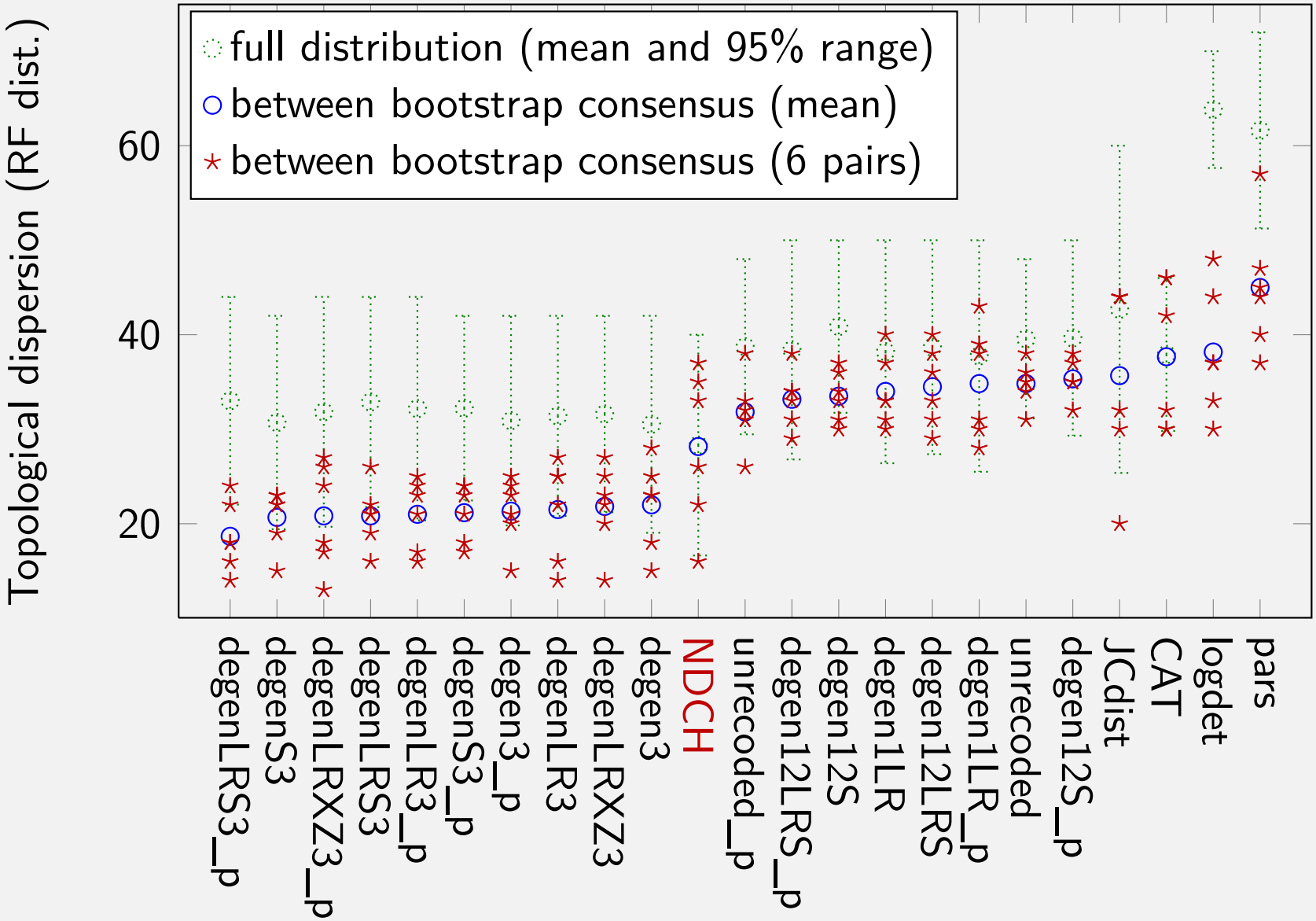
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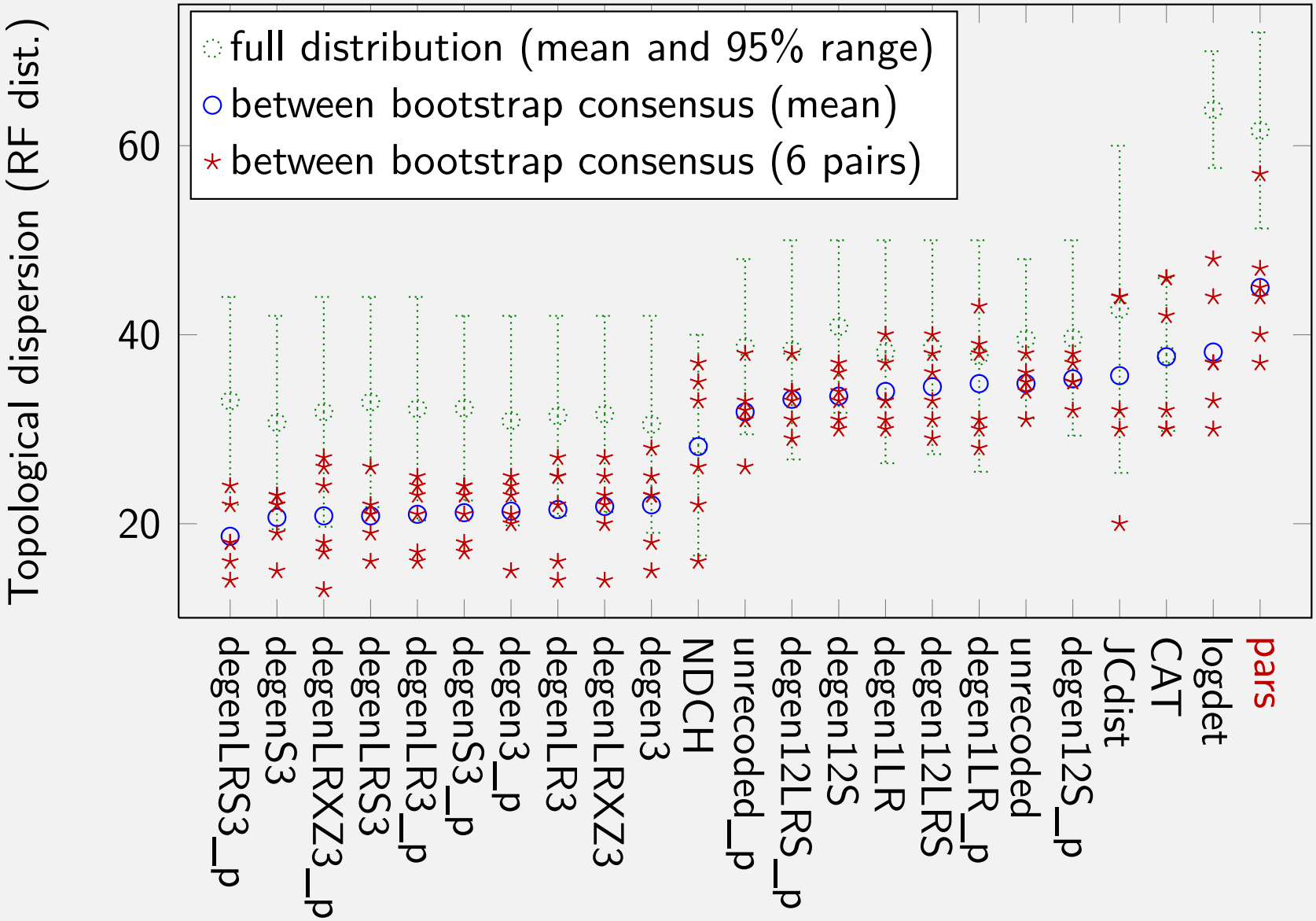
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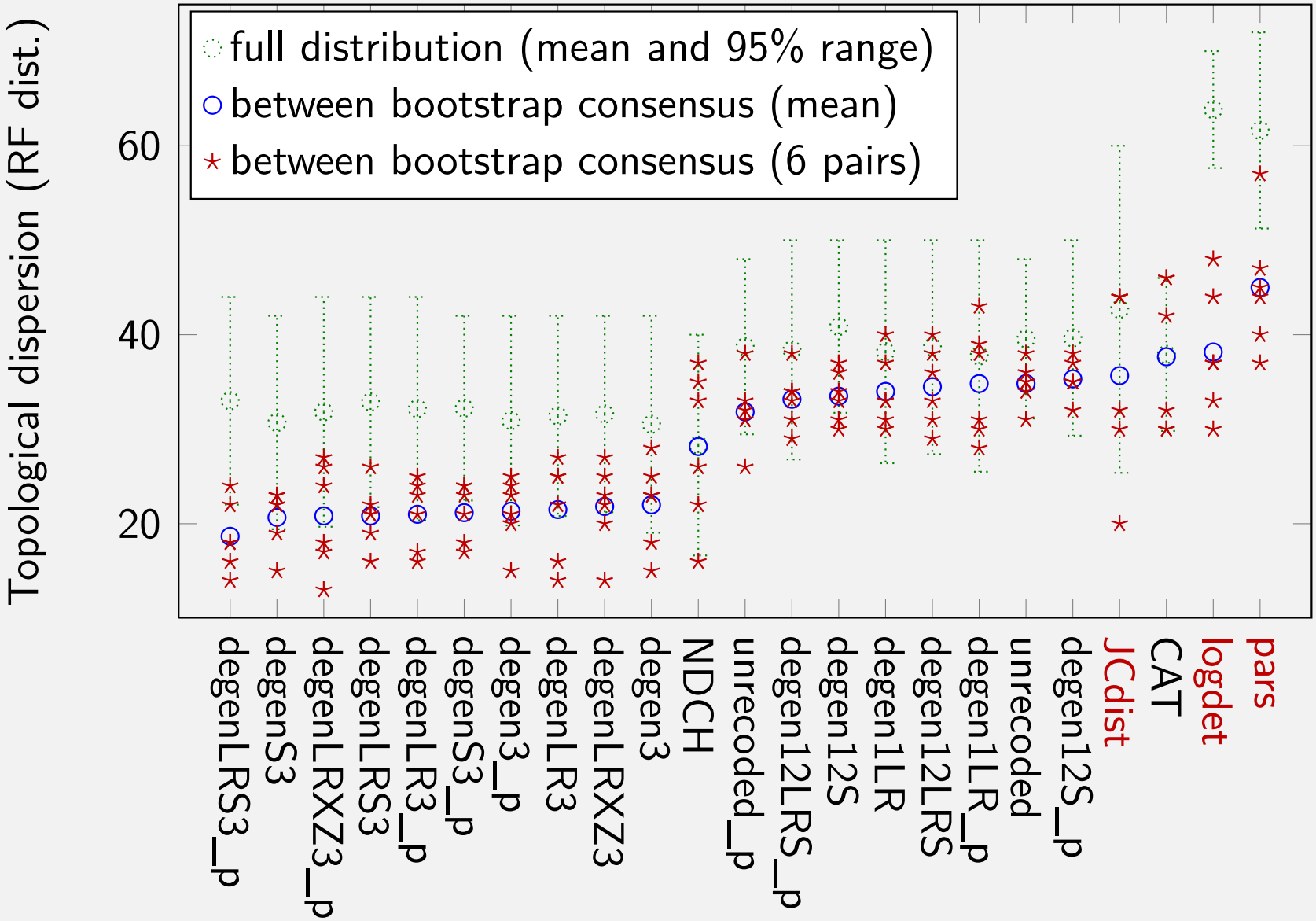
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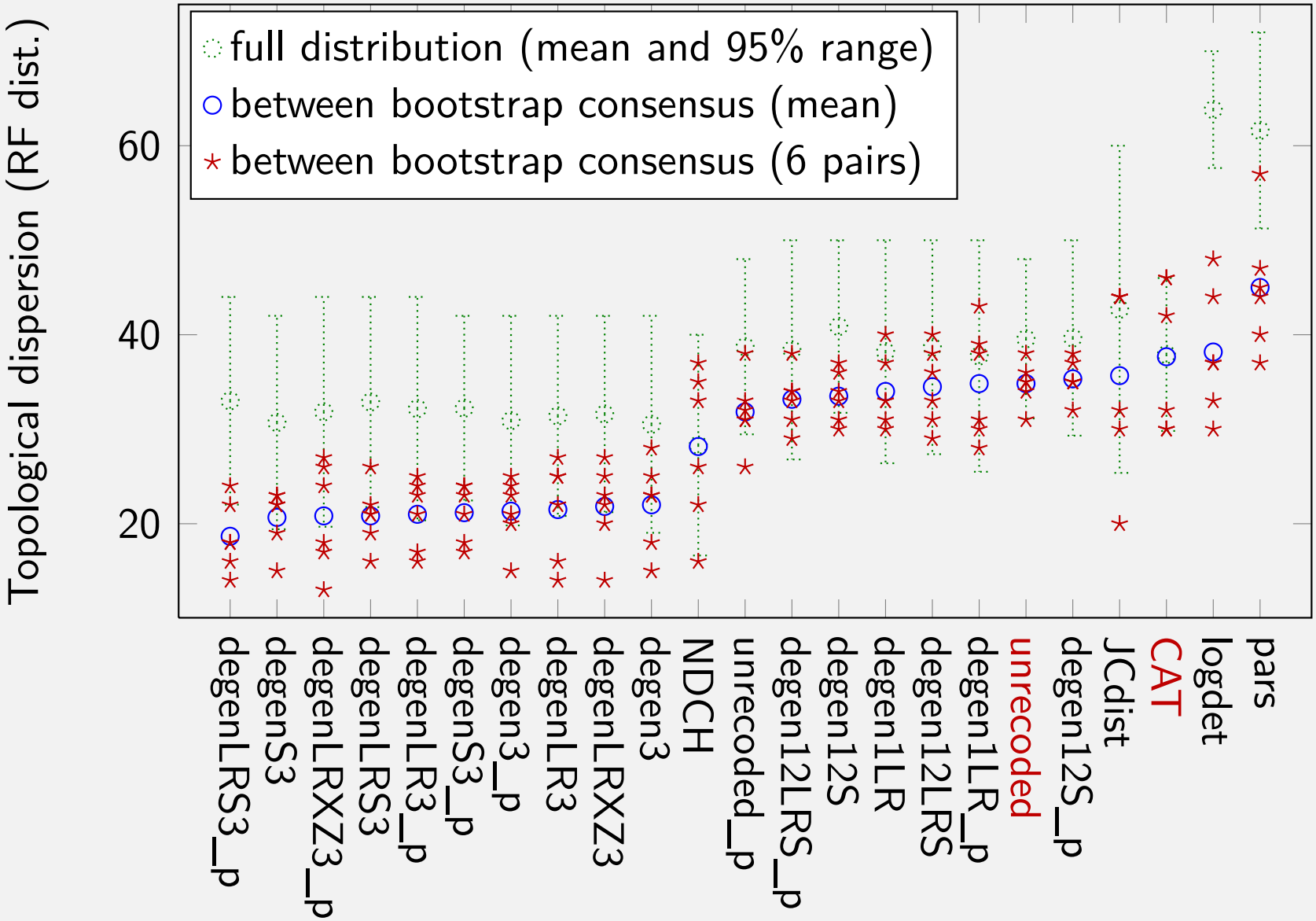
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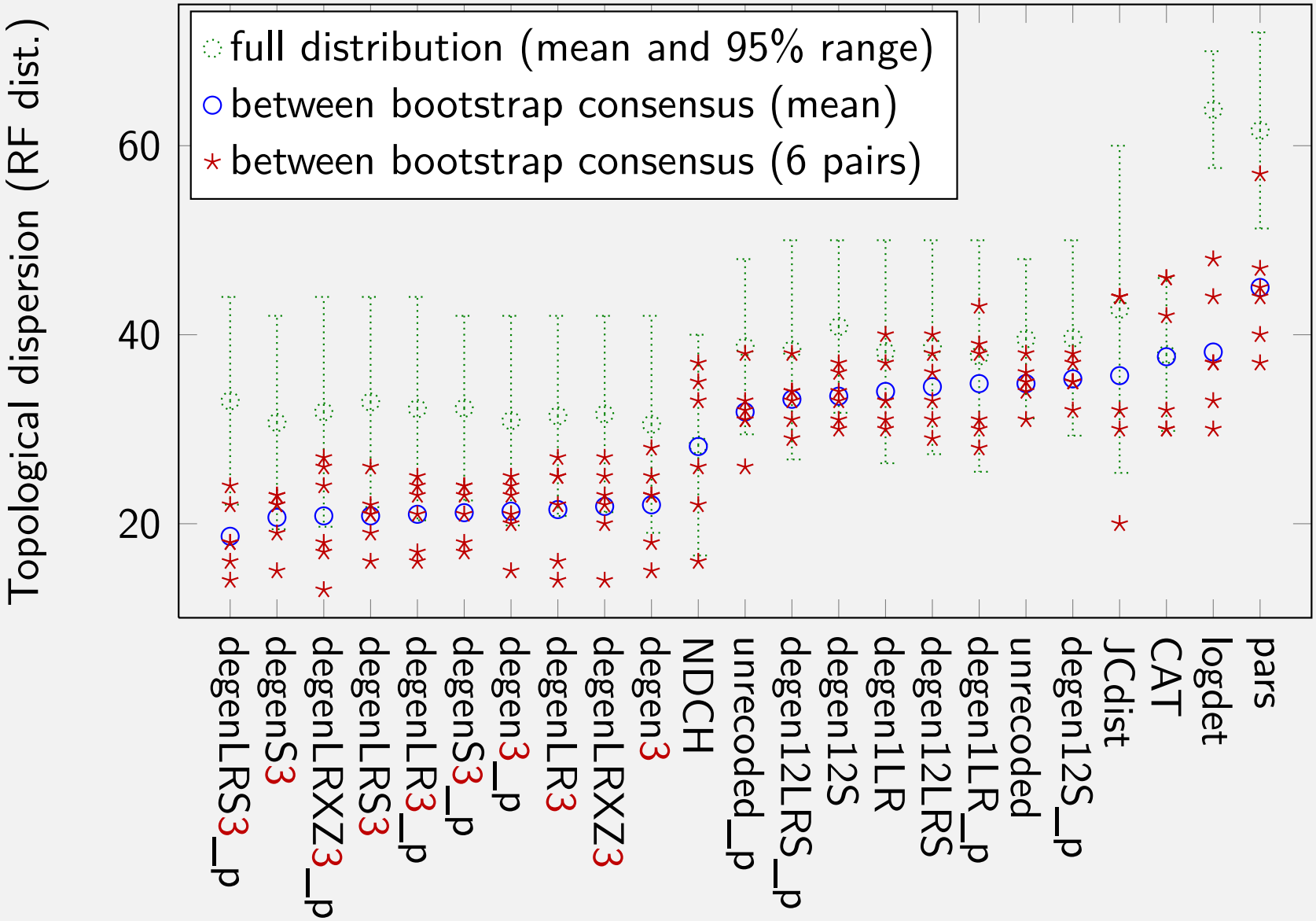
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degenLR3
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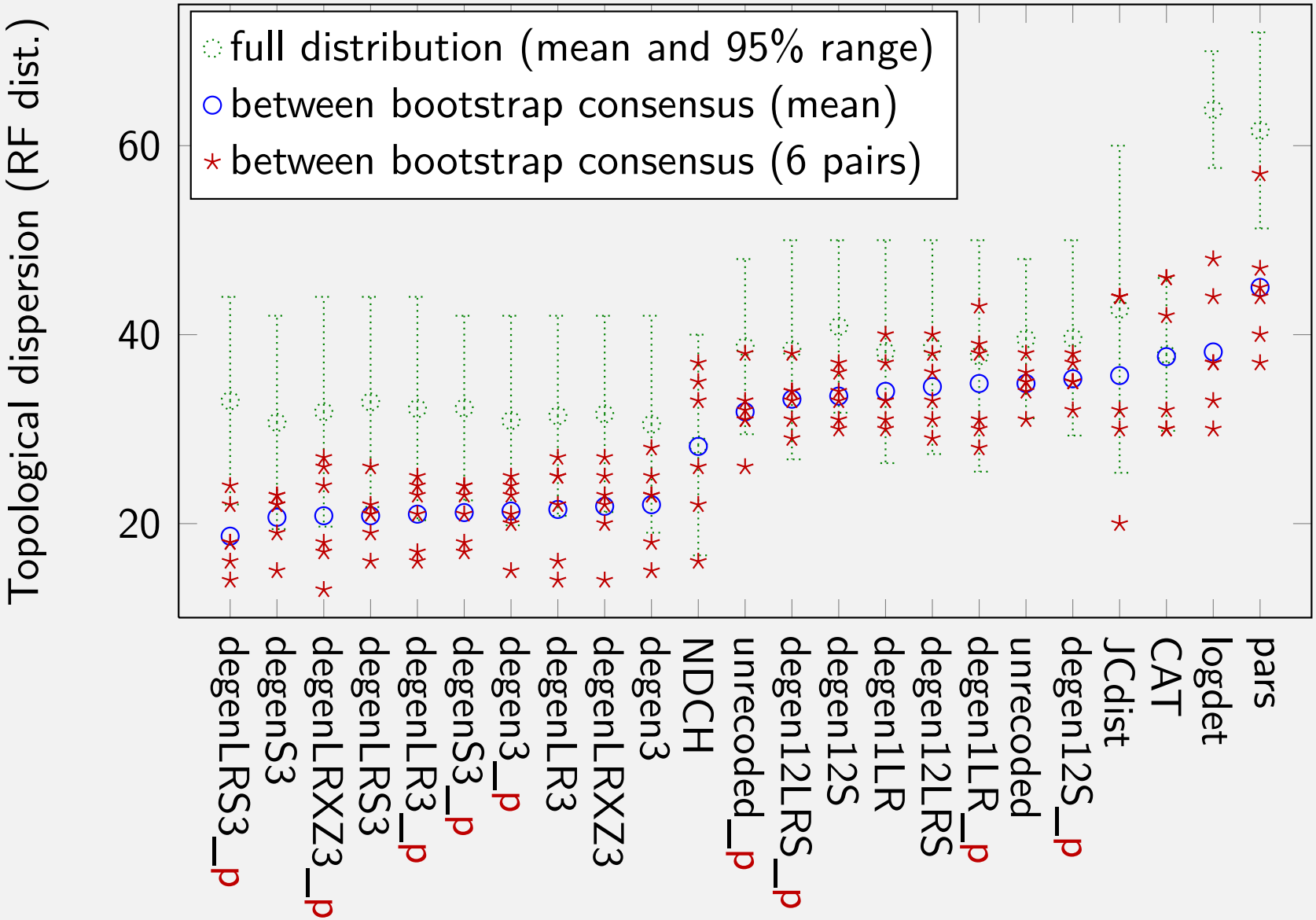
degen3
NDCH
unrecoded_p
degen12LRS_p
degen12S
degen1LR
degen12LRS
degen1LR_p
unrecoded
degen12S_p
JCdist
CAT
logdet
pars

Results


full distribution (mean and 95% range)
between bootstrap consensus (mean)
between bootstrap consensus (6 pairs)
Topological dispersion (RF dist.)
20
40
60
degenLRS3_p
degenS3
degenLRXZ3_p
degenLRS3
degenLR3_p
degenS3_p
degen3_p
degenLR3
degenLRXZ3
degen3
NDCH
unrecoded_p
degen12LRS_p
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- To some extent, coherence seems correlated to phylogenetic accuracy.
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- Could better measures of coherence be designed?
- Including in the pannel a priori poorly performing analysis strategies may help to detect false positives.

Thanks for your attention

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- I'm currently looking for a job, so if you think I can be useful in your lab, feel free to contact me.
- Contact: `blaise.li@normalesup.org`

This work relied heavily on the `Python` programming language.

This presentation was made using the excellent `beamer` and `TikZ/pdf` LaTeX packages.