Gene trees challenge

@JLSteenwyk

https://jlsteenwyk.com/

Single-copy orthologs are a type of phylogenetic marker

Phylogenomics typically relies on SC-OGs

Many molecular evolution studies *strictly* rely on single-copy orthologs (SC-OGs)

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- Phylogenomics,
- genome-wide surveys of (+) selection
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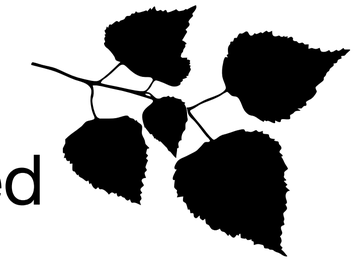
but SC-OGs are hard to find…

The quest for SC-OGs

A dataset of 35 plants

- only one single-copy orthogroup was identified



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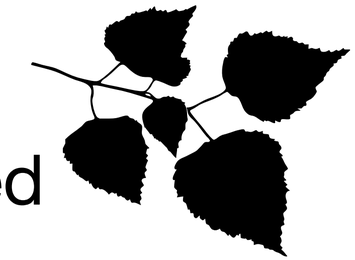

A dataset of 30 turtles, tortoise, birds, crocodile, alligators, and others

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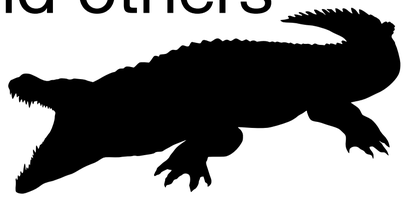

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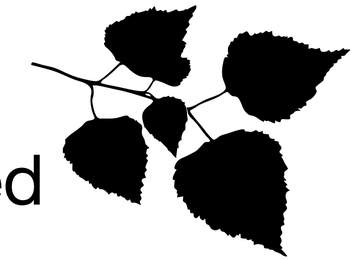

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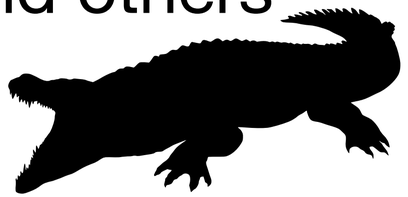

A dataset of 76 arthropods (Thomas et al. (2020), *Genome Biology*)
- Zero single-copy orthogroups with 100% occupancy

Too few phylogenomic markers :(

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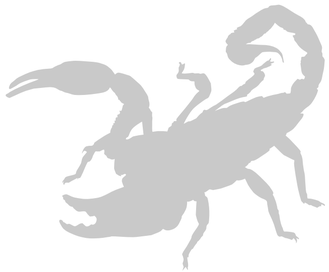
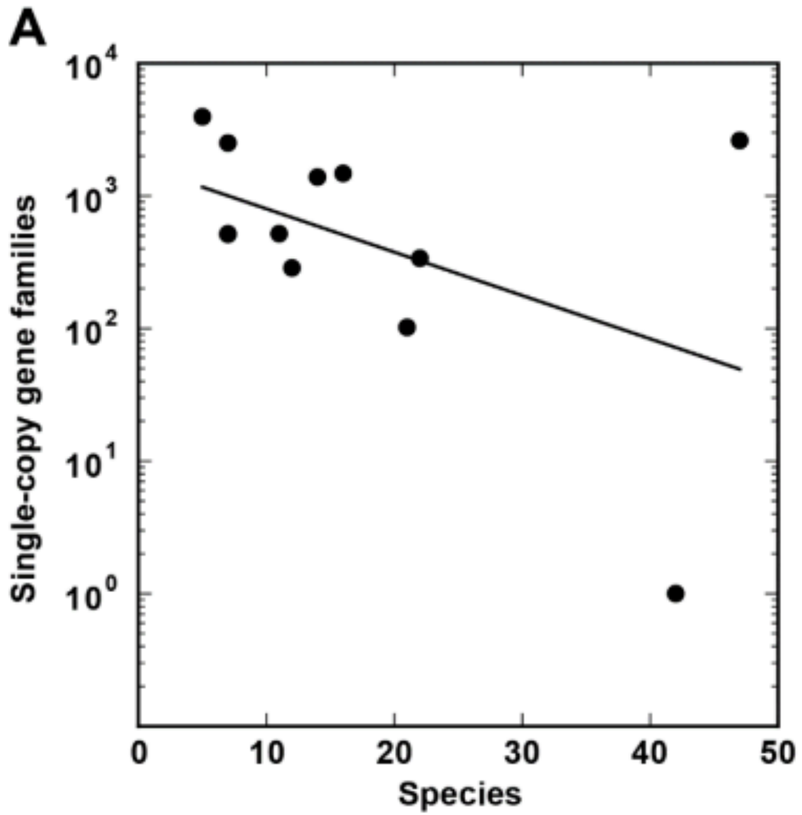


Factors that impact SC-OG identification



The number of single-copy orthologs decreases as the number of species and evolutionary distance among species increases

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Emms, D.M. and Kelly, S. (2018), *bioRxiv*

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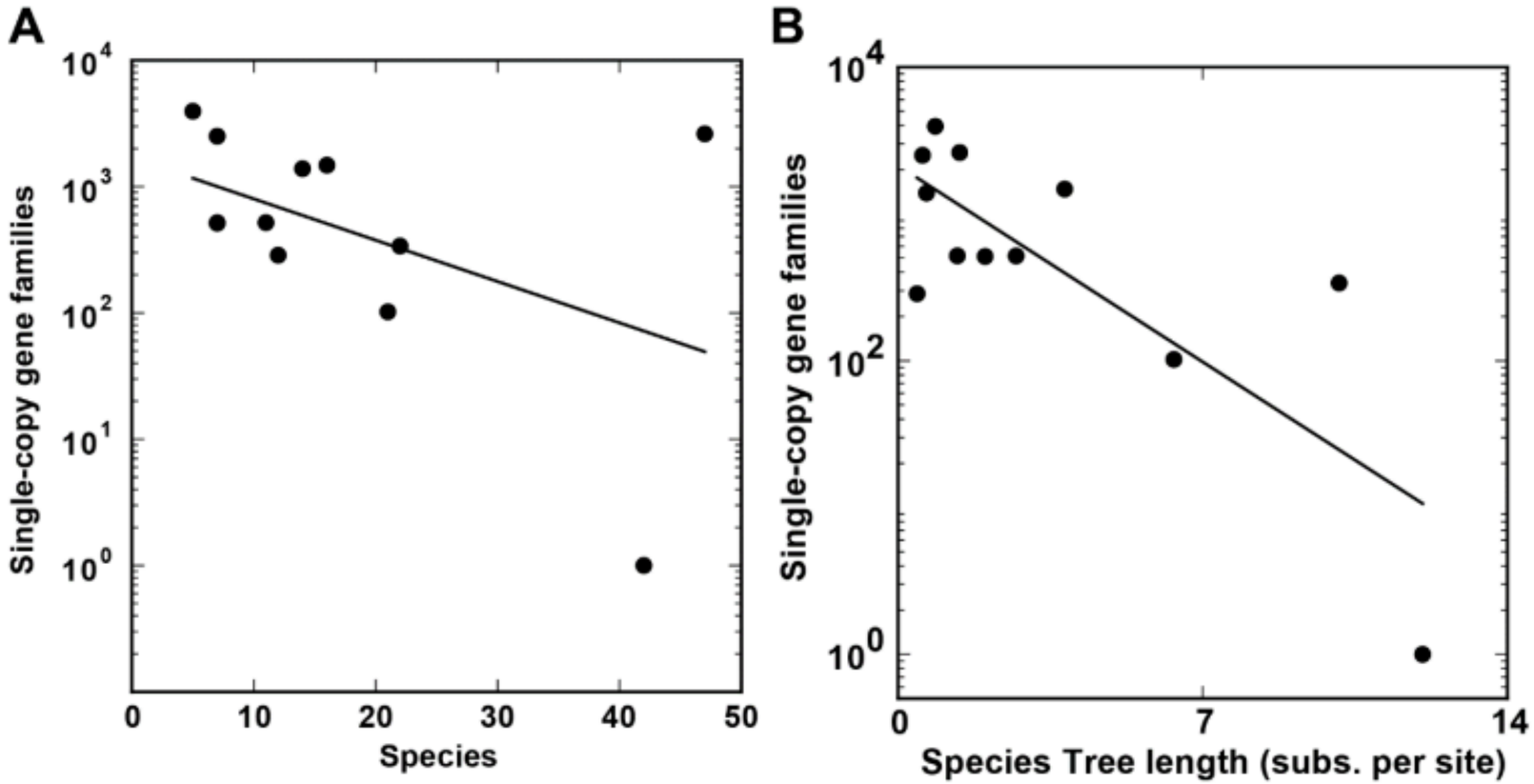

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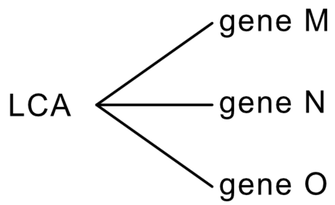
Can other types of orthologs be used for molecular evolution studies?

Factors that impact SC-OG identification

A



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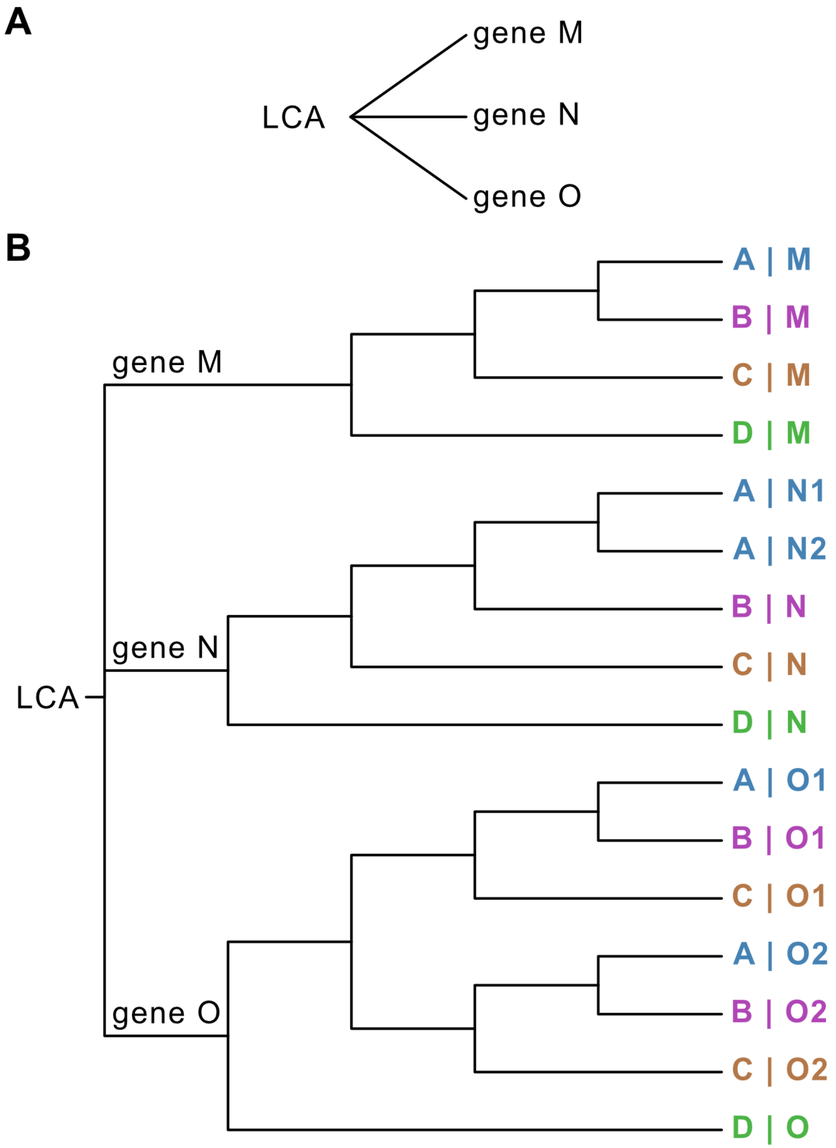

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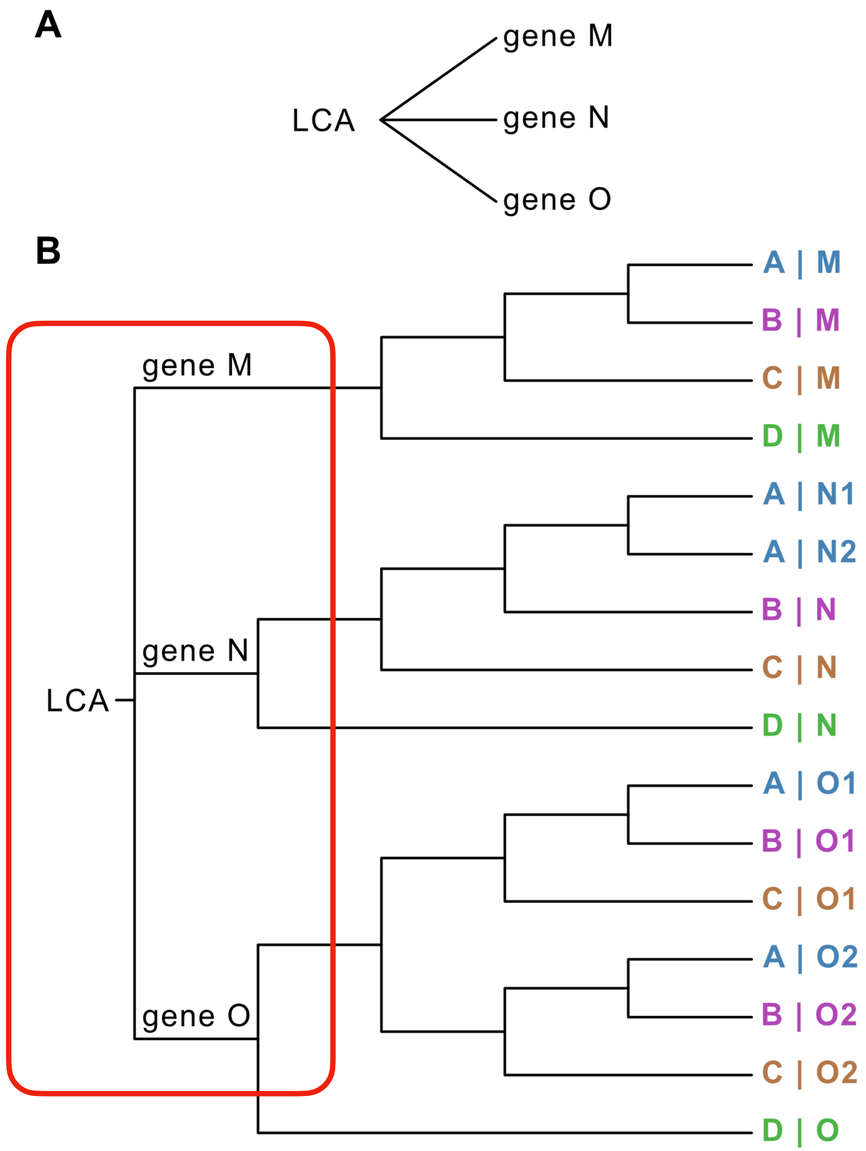

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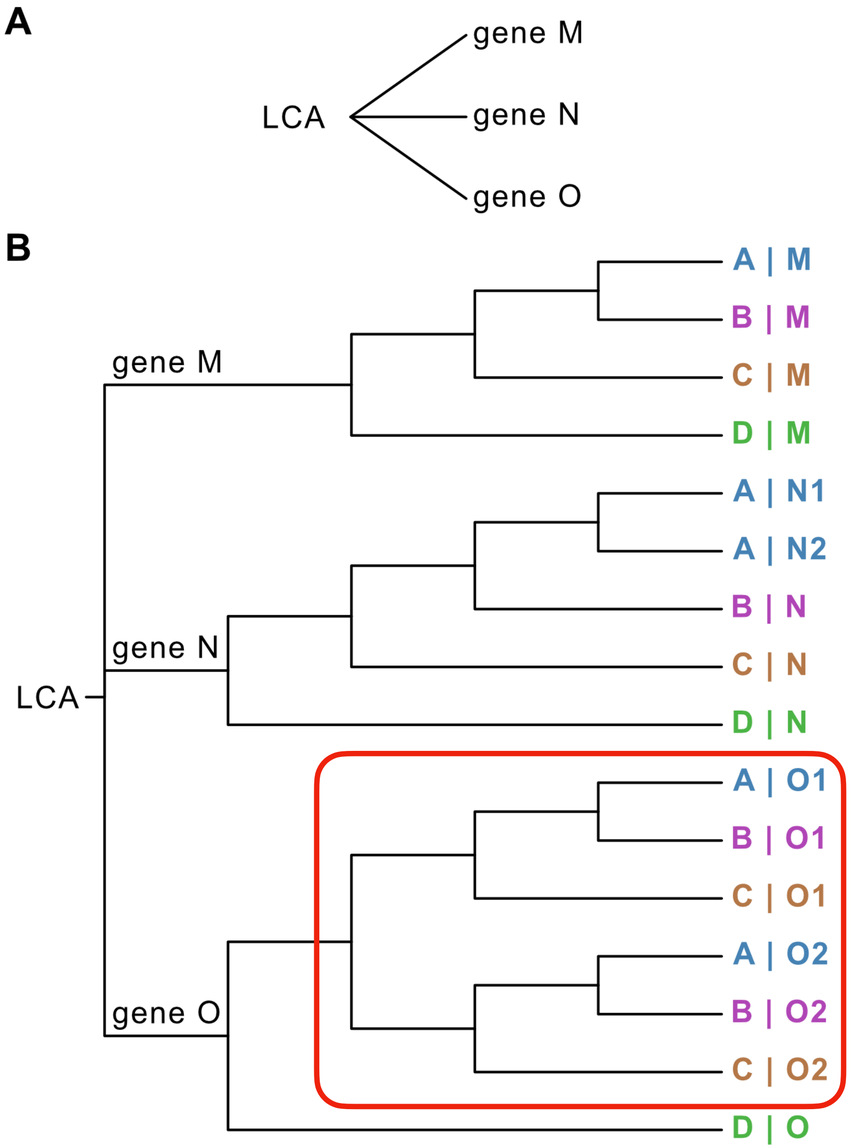

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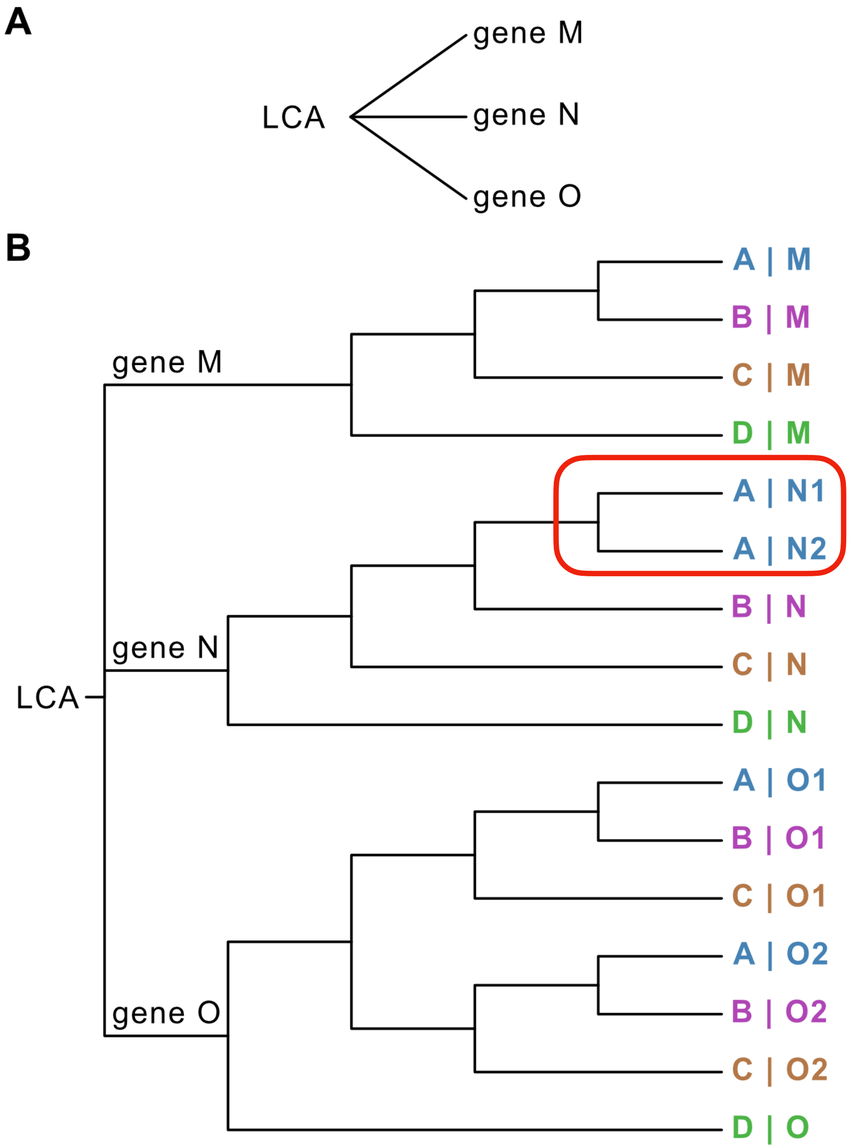
Steenwyk et al. (2022), PLOS Biology

Factors that impact SC-OG identification



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- A | N1 and A | N2 are within species inparalogs

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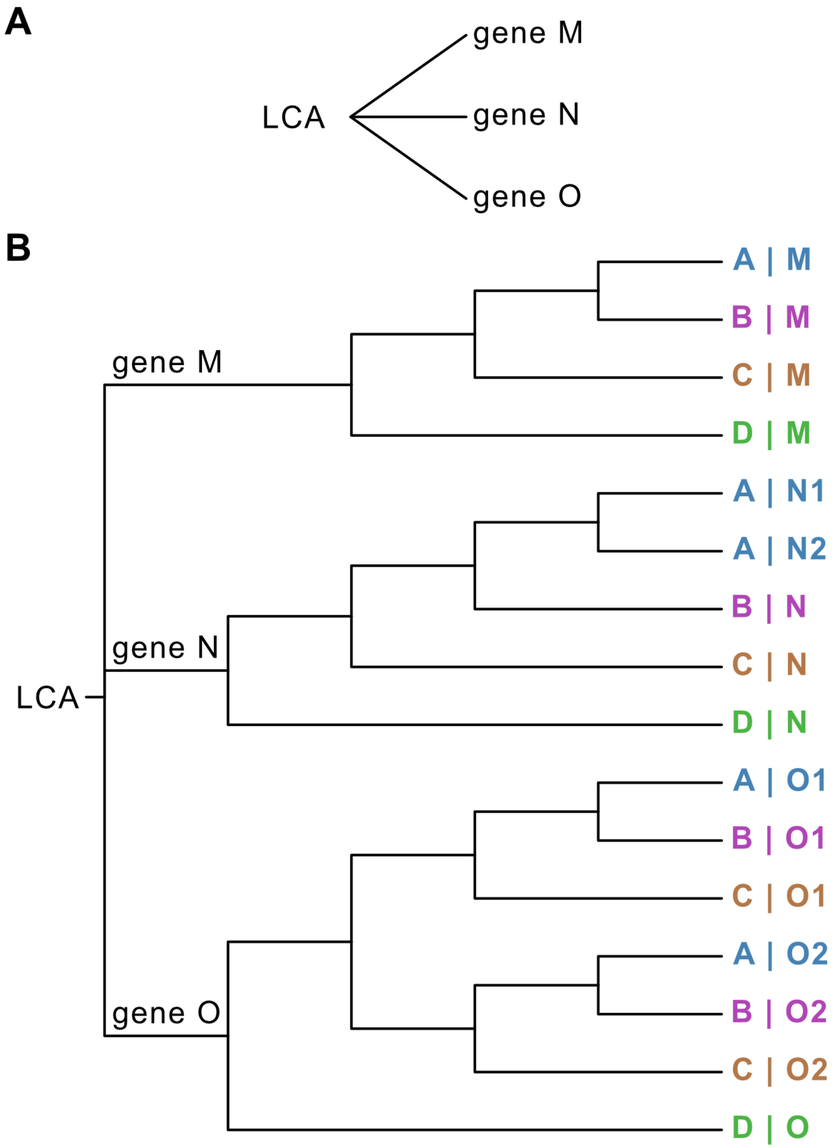

Note, splitting this tree will result in multiple subgroups of single-copy orthologs

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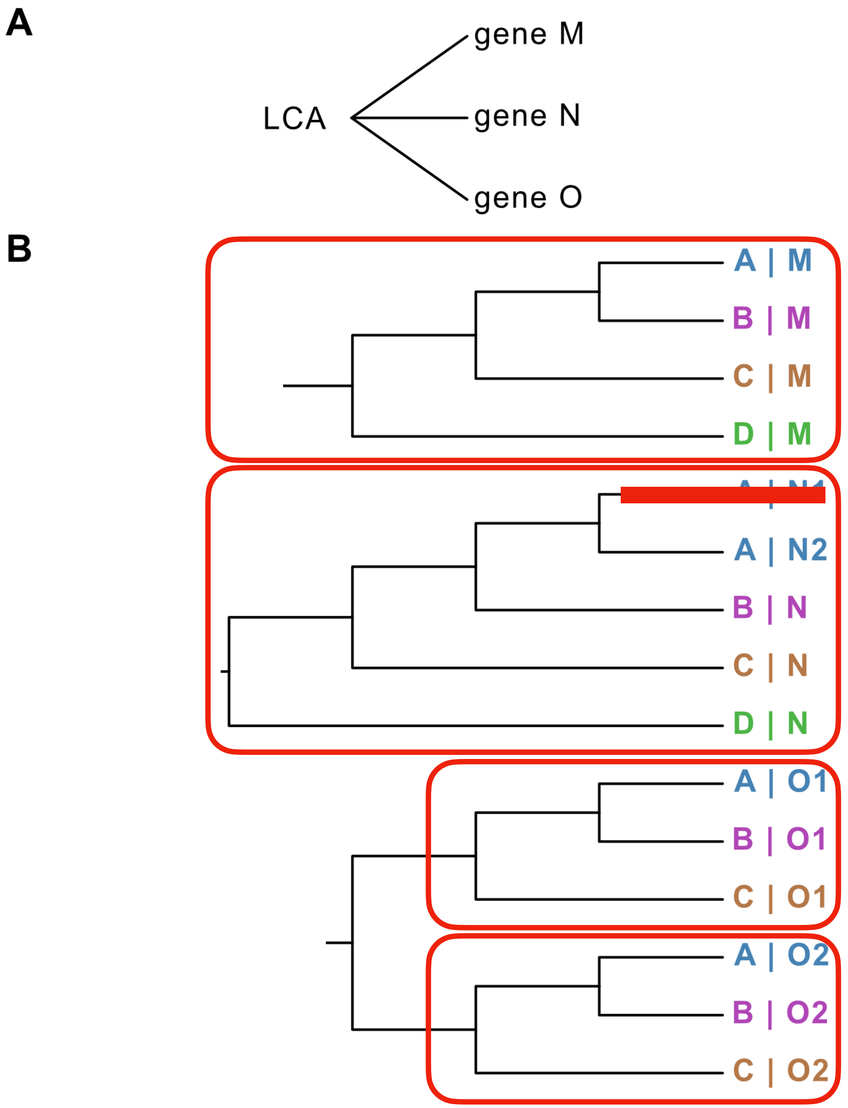

subgroups of single-copy in- and outparalogs from multi-copy orthologous groups of genes

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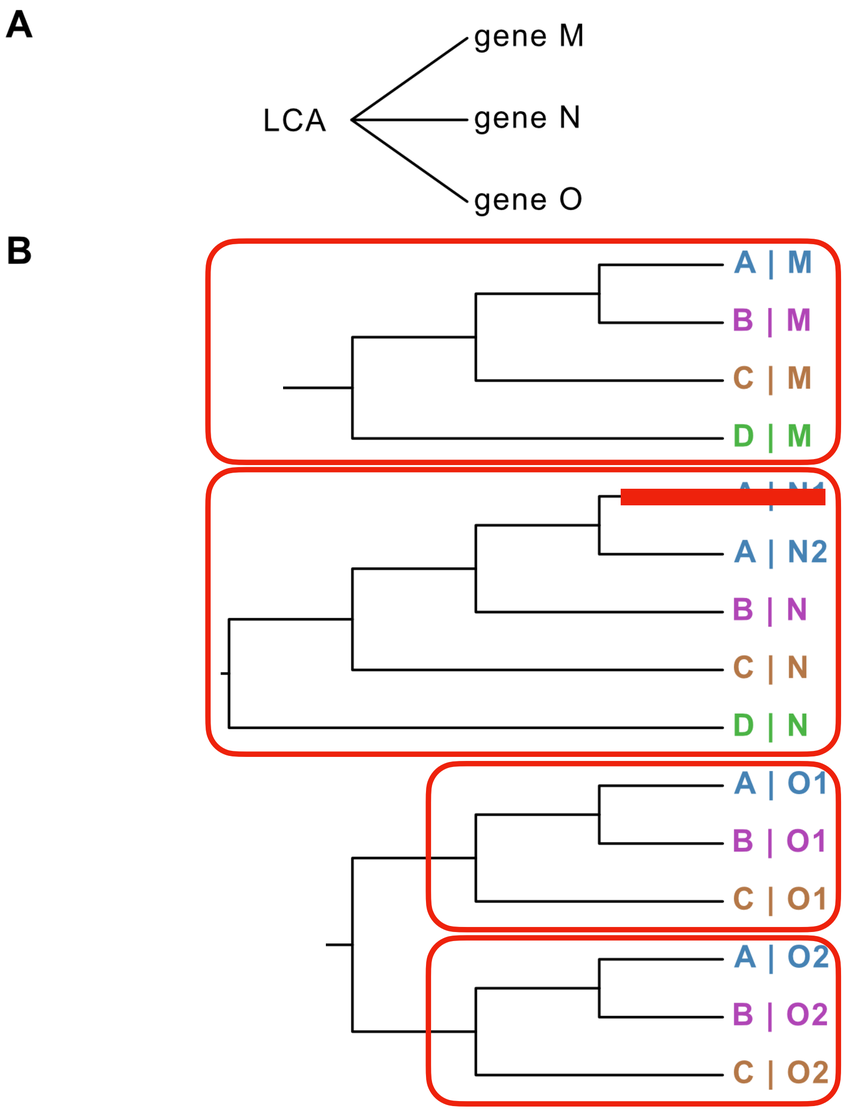

subgroups of single-copy in- and outparalogs from multi-copy orthologous groups of genes

We term these SNAP-OGs because they are orthologs that have undergone a **s**plitti**n**g **a**nd **p**runing procedure

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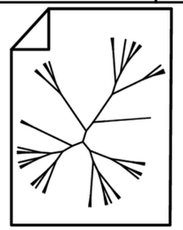
identify single-copy orthologous genes nested within larger gene families

OrthoSNAP methods

A

Gene family sequences with multiple homologs in one or more species

Gene family tree with multiple homologs in one or more species



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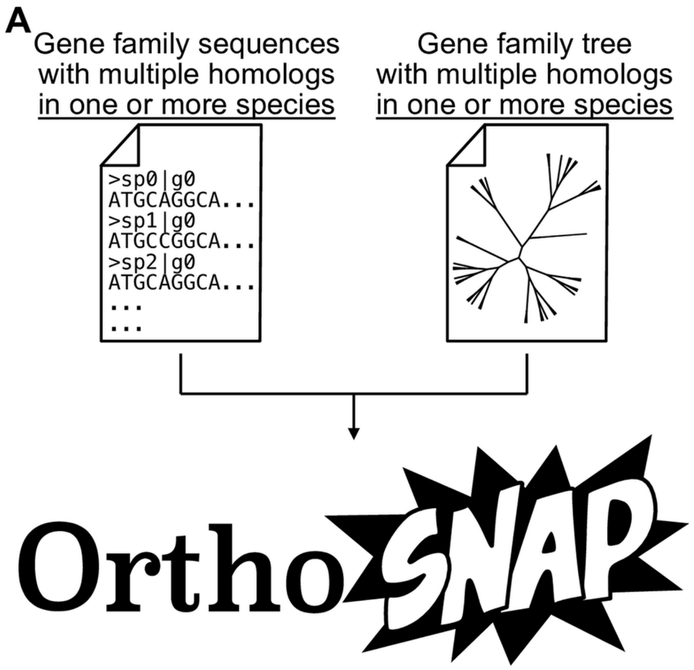
ORTHOlogous group of genes **S**plitti**N**g **A**nd **P**runing

OrthoSNAP methods



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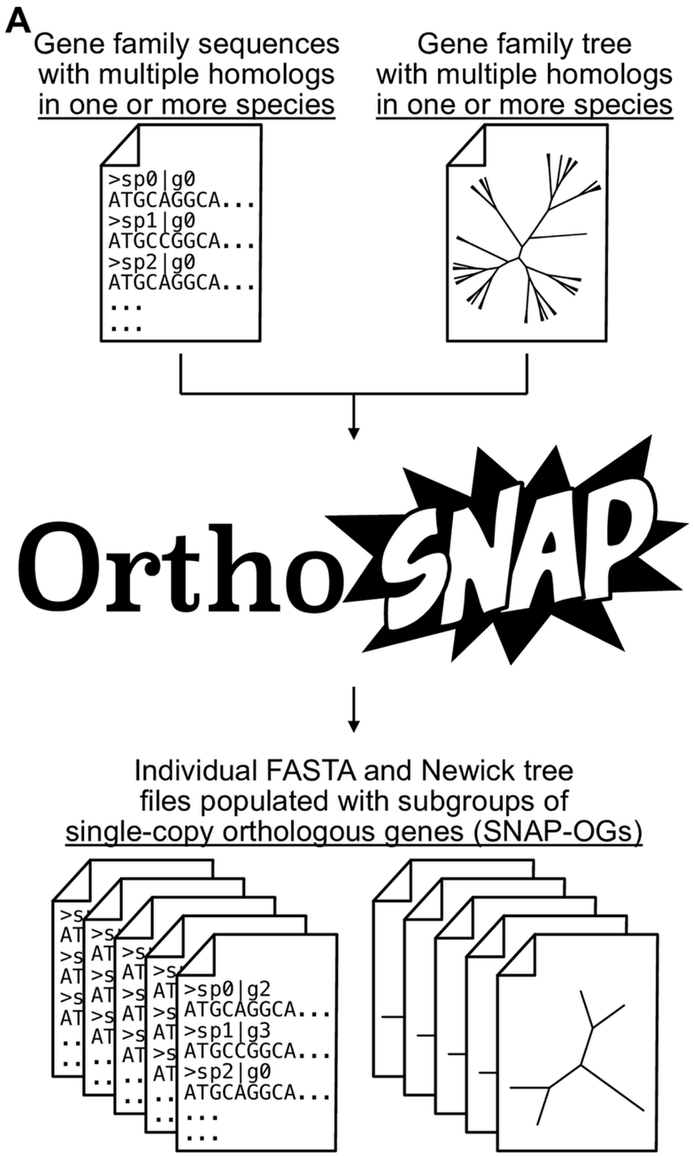

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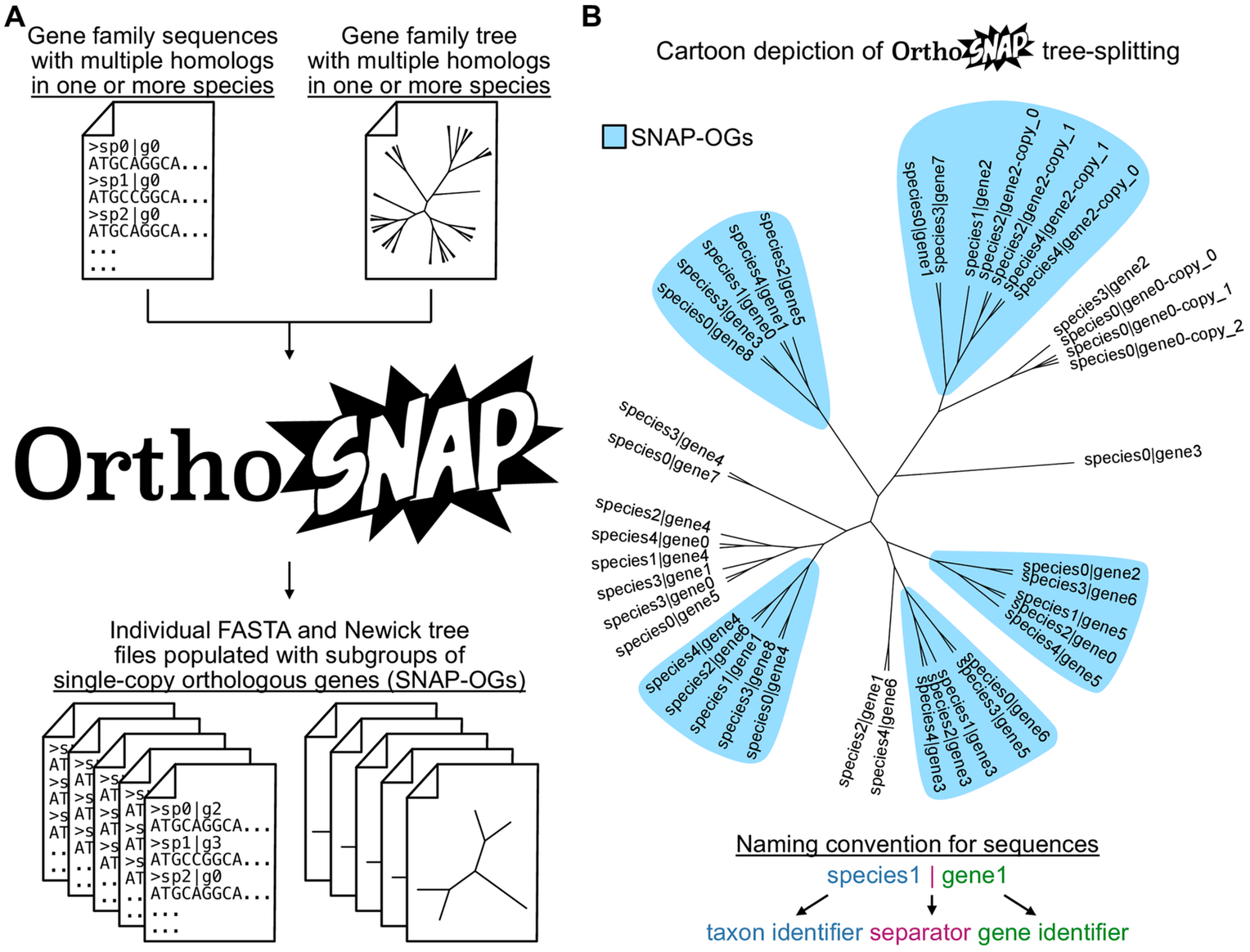

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ORTHOlogous group of genes **S**plitti**N**g **A**nd **P**runing

SNAP-OGs can substantially increase datasets

	SC-OGs	SNAP-OGs	Fold difference
Budding yeast (No WGD)	1,668	1,392	0.83
Budding yeast (WGD)	2,782	1,334	0.48
Filamentous fungi (*Aspergillus* and	4,393	2,035	0.46
Mammals (Eutherians)	321	1,775	5.53
Plants (Complex dup. And	15	653	43.53
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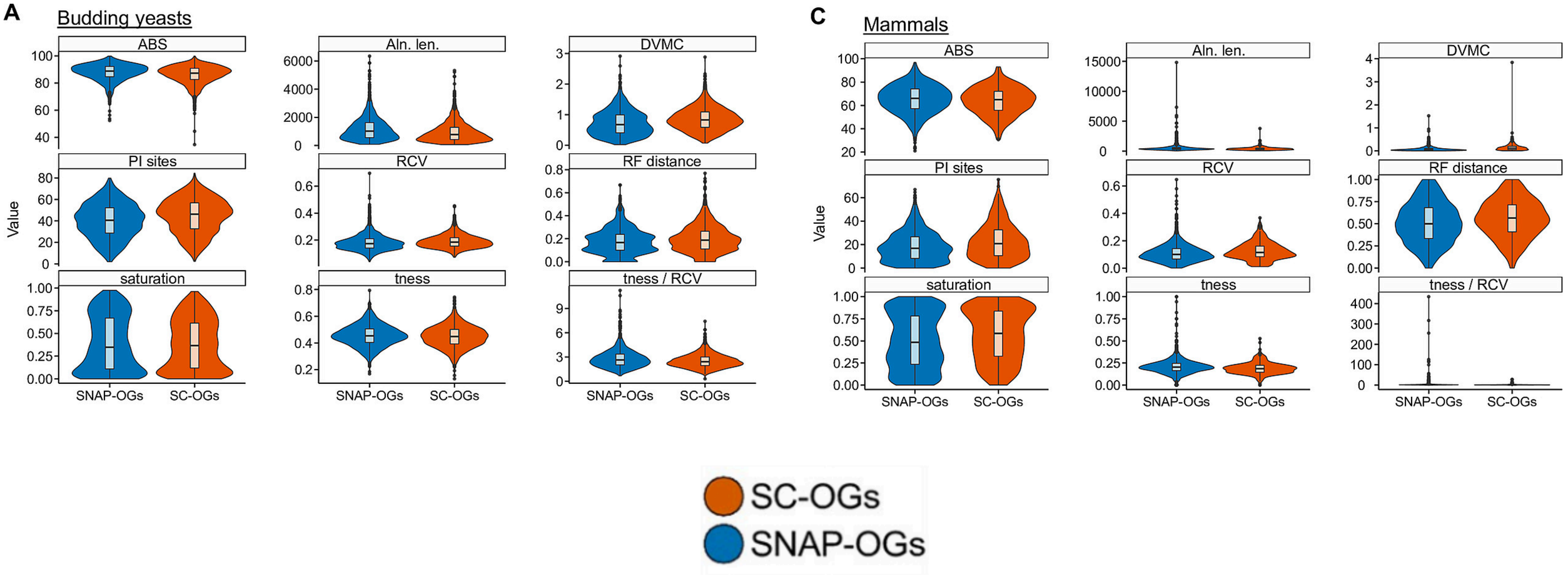
But are SNAP-OGs bad markers?

SNAP- & SC-OGs are statistically indistinguishable



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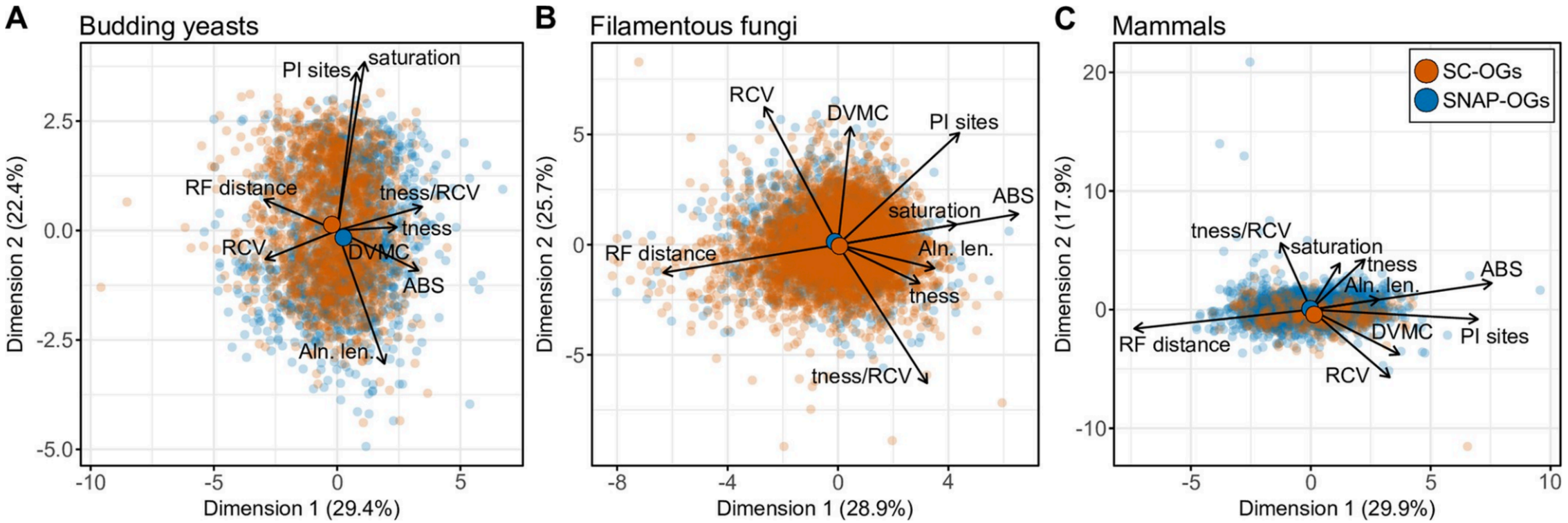

- 3 datasets
- 9 measures of information content
  - Alignment length, RF distance, bootstrap support, etc.

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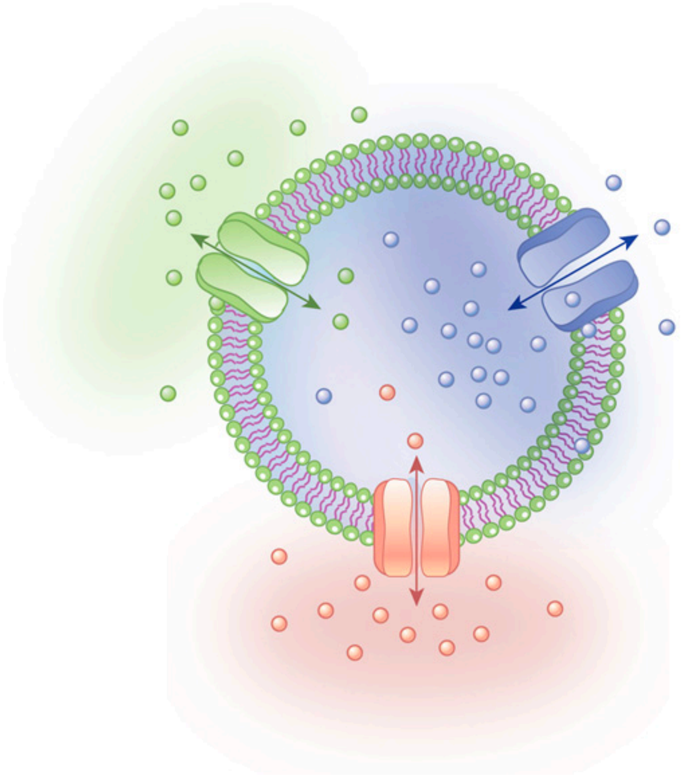
Phylogenomics typically relies on SC-OGs

- High-throughput screens of (+) selection requires SC-OGs

- What types of genes are not typically SC-OGs?
  - Receptors
  - Heat shock proteins
  - Transporters
  - Transcription factors
  - Kinases
  - Etc…

Molecular evolution of *all* types of genes

- 5 SNAP-OGs were identified in OGs of transcription factors
- 5 SNAP-OGs were identified in OGs of MFS transporters
- 4 SNAP-OGs were identified in an OG of kinases



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