

# rearrvisr: an R package to detect, classify, and visualize genome rearrangements

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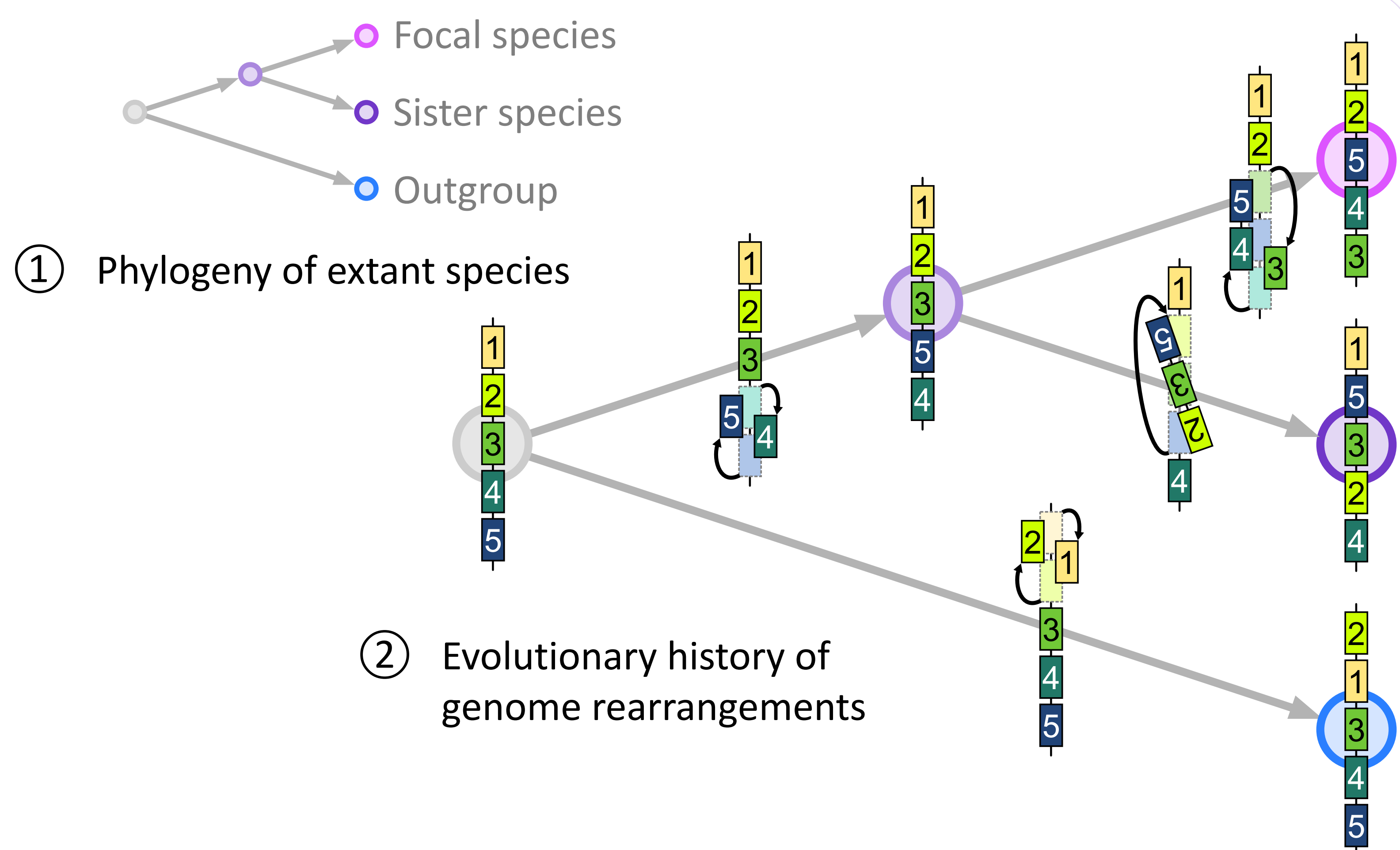
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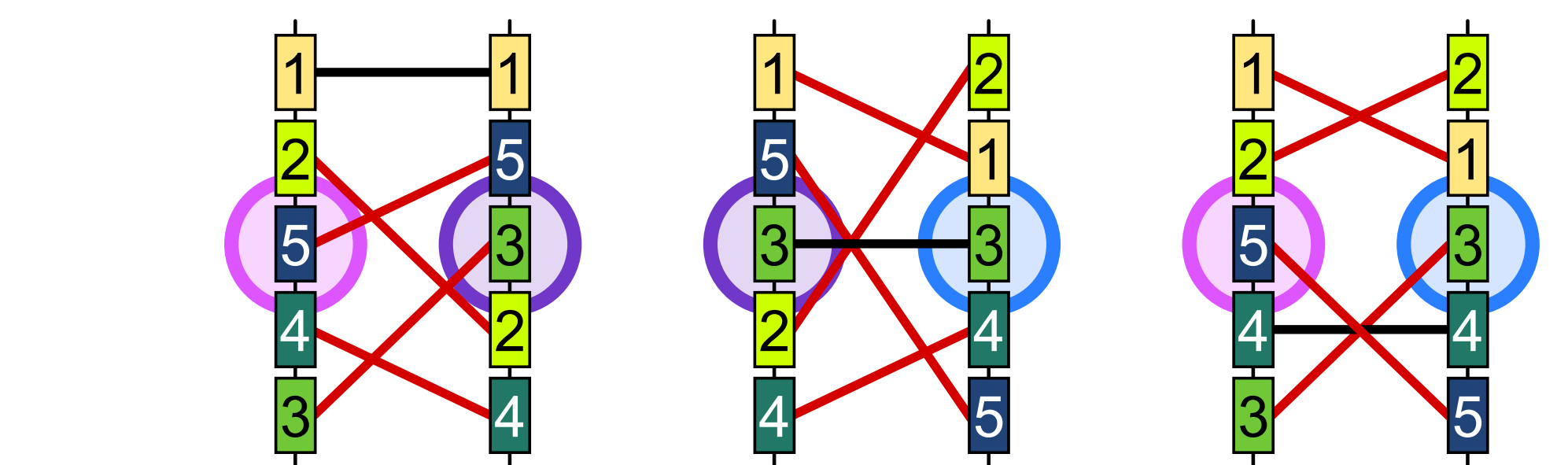


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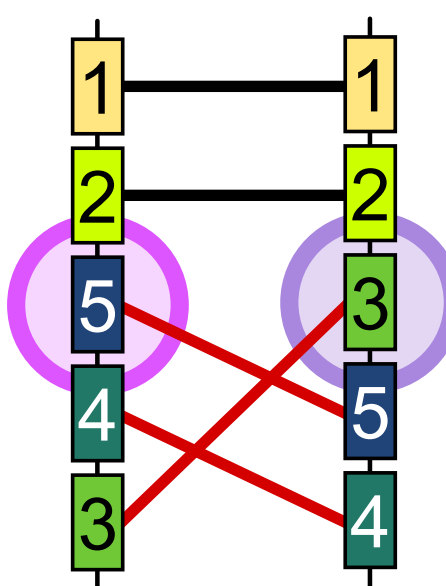
**Abstract:** The detection of genome rearrangements is of direct relevance for understanding genome structural evolution and its potential impacts on gene function and species divergence. However, no method exists that enables an easy localization of rearrangements along a focal genome. We thus developed the R<sup>1</sup> package rearrvisr to detect, classify, and visualize rearrangements. We illustrate the use of our method by applying it to fish genomes.



## ③ Identification of genome rearrangements

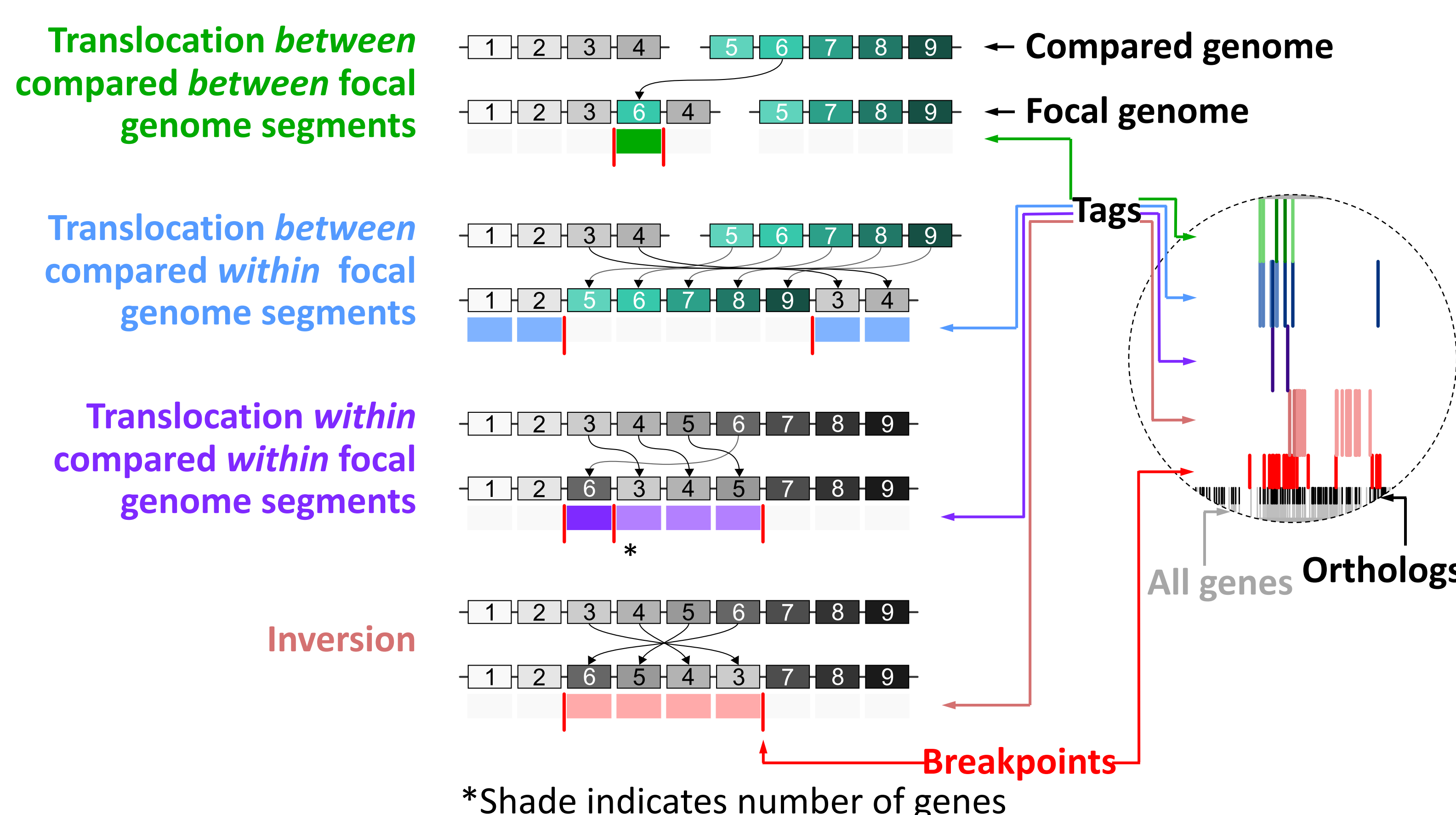


a) Pairwise comparisons among extant genomes can be difficult to interpret (i.e., in which species was gene 5 rearranged?)



b) Comparison to reconstructed ancestral genome reveals lineage-specific rearrangements (i.e., translocation of genes 5 and 4 relative to gene 3 in focal species)

**Method:** Our algorithm can be used to identify lineage-specific rearrangements, given an ancestral genome reconstruction from the software ANGES<sup>2</sup>, and can likewise be applied to compare two extant genomes. Four classes of rearrangements are distinguished.



**Conclusions:** Our method provides a valuable tool to rapidly screen for rearrangements and to determine their genome-wide distribution. It might be used to investigate how structural genomic changes affect phenotypic evolution, or for assembly quality control.

**Availability:** <https://github.com/dorolin/rearrvisr>  
Soon to be available from CRAN as well

**Application:** We reconstructed the genome of the stickleback – tubesnout ancestor with ANGES<sup>2</sup> and identified rearrangements that occurred in each lineage after divergence from their ancestor.

