

## An Open and Modular Phylogenetic Tree Construction Pipeline in R

GGBC Workshop | 17<sup>th</sup> Sept. 2019

## Timetable

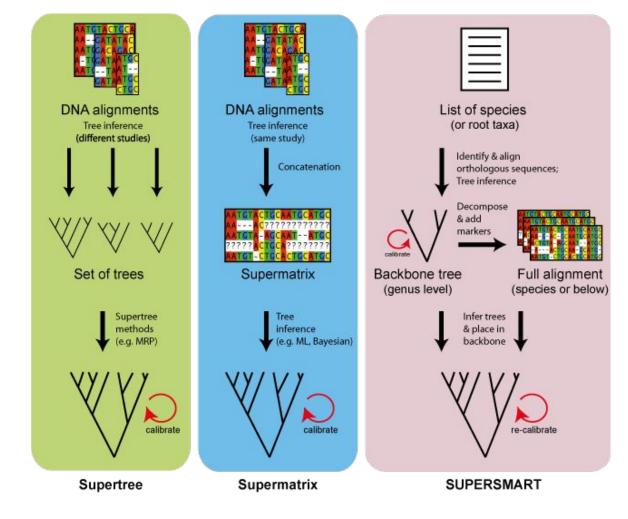
0900 - 0930	Welcome and Introduction to supersmartR
1000 - 1200	<ul> <li>phylotaR Coffee/tea, ~1030</li> <li>outsider</li> <li>Base pipeline</li> </ul>
1200 - 1300	Lunch
1300 - 1700	<ul> <li>Restez Coffee/tea, ~1500</li> <li>Gaius</li> <li>Adapted pipeline</li> </ul>
1700 - 1800	Free-coding session + "advanced" topics

## **SUPERSMART**\*

Pipeline for constructing phylogenetic trees.

Species-level and backbone approach.

Generic, scalable. Maximise data.



<sup>\*</sup> Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages and Relationships of Taxa | Antonelli et al. 2017. Systematic Biology, 66(2),152-166

