

# Bootstrapping

Bootstrapping is a method to obtain some more information and certainty about the correctness of a derived [phylogenetic tree](#) or [stemma](#). It involves taking many random samples (usually up to and onward from a 1000 samples) from the original data matrix and constructing stemmata based on those samples. Then for each sample it is determined how often a taxon coincides with the taxa of the stemma computed for the full data set. It is assumed that the higher the number of times a taxon is also derived in the samples the more certain or correct one can be about that taxon's position corresponding to the true stemma. Usually this certainty is indicated as a percentage index on that taxon in the tree visualisation.

## References

- Efron, Bradley, Elizabeth Halloran, and Susan Holmes. 1996. "Bootstrap confidence levels for phylogenetic trees." Corrected version. *Proceedings of the National Academy of Sciences of the United States of America (PNAS)* 93: 13429–13434.
- Skovgaard, Ole. 2004. "Quality of Tree: Bootstrap." Teaching material published on the server of Roskilde Universitet. Accessed 7 October 2015. <http://akira.ruc.dk/~olesk/sekvens/bootstr.htm>.

## In other languages

English term used throughout.

[JZ](#)