

Survey of Fast Methods for large-scale tree estimation



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Introduction



- Final paper will look at different methods that can be used for large-scale tree estimation
- Will focus on how papers evaluated methods
 - Were they compared to other methods?
 - What datasets were used?
 - What other criteria went into the evaluation?

Methods



- **Qtree**
 - Randomized quartet based algorithm
- **Local-Sensitivity Hashing**
 - Implementation is based on three ideas
 - Used on trees with short branch length
- **GPU-UPGMA**
 - UPGMA ported onto GPU by using CUDA

Methods Continued



- **FastTree-2**
 - Improves on FastTree by adding minimum evolution subtree-pruning-regrafting (SPR) and maximum likelihood nearest neighbor interchanges (NNI)
- **NINJA**
 - Speeds up neighbor joining

Works Cited



- Brown, Daniel G., and Jakub Truszkowski. "Fast reconstruction of phylogenetic trees using locality-sensitive hashing." (2012): n. pag. *Cornell University Library*. Web. <<http://arxiv.org/abs/1111.0379>>.
- Brown, Daniel G., Jakub Truszkowski, and Yanqi Hao. "Towards a practical $O(n \log n)$ phylogeny algorithm." (2012): n. pag. *BioMed Central*. Web. <<https://almob.biomedcentral.com/articles/10.1186/1748-7188-7-32>>.
- Price, Morgan N., Paramvir S. Dehal, and Adam P. Arkin. "FastTree 2 – Approximately Maximum-Likelihood Trees for Large Alignments." *PLOS* (2010): n. pag. Web.. <<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0009490>>.
- Wheeler T.J. (2009) Large-Scale Neighbor-Joining with NINJA. In: Salzberg S.L., Warnow T. (eds) Algorithms in Bioinformatics. WABI 2009. Lecture Notes in Computer Science, vol 5724. Springer, Berlin, Heidelberg