

IgPhyML

A phylogenetic inference package for B cell repertoires

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July 2019

Online documentation

IgPhyML documentation has moved online:

<https://changeo.readthedocs.io/en/latest/examples/igphyml.html>

IgPhyML has been integrated with the Change-O repertoire clonal assignment toolkit:

<https://changeo.readthedocs.io>

For Change-O installation:

<https://changeo.readthedocs.io/en/latest/install.html>

For the Immcantation suite more broadly:

<http://immcantation.org>

References

Hoehn, K. B., Vander Heiden, J. A., Zhou, J. Q., Lunter, G., Pybus, O. G., & Kleinstein S. H. (2019) Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. *bioRxiv* 558825; doi: <https://doi.org/10.1101/558825>

Hoehn, K. B., Lunter, G., & Pybus, O. G. (2017). A phylogenetic codon substitution model for antibody lineages. *Genetics*, 206(1), 417-427. doi: <http://dx.doi.org/10.1534/genetics.116.196303>

IgPhyML is based on **codonPhyML**: <https://sourceforge.net/projects/codonphyml>

Gil, M., Zanetti, M.S., Zoller, S., & Anisimova A. (2013) CodonPhyML: fast maximum likelihood phylogeny estimation under codon substitution models. *Mol Biol Evol.* 2013 Jun;30(6):1270-80. doi: 10.1093/molbev/mst034

and **PhyML**: <http://www.atgc-montpellier.fr/phyml>

Guindon, S., Delsuc, F., Dufayard J.F., & Gascuel O. (2009) Estimating maximum likelihood phylogenies with PhyML. *Methods Mol Biol.* 2009;537:113-37. doi: 10.1007/978-1-59745-251-9_6