

INCEPTION softwares list

PastML

<https://pastml.pasteur.fr/>

Ishikawa SA, Zhukova A, Iwasaki W, Gascuel O. A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. *Mol Biol Evol* 2019. 10.1093/molbev/msz131.

NGPhylogeny

<https://ngphylogeny.fr/>

Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F *et al.* NGPhylogeny.fr: new generation phylogenetic services for non-specialists. *Nucleic Acids Research* 2019.

PastView

www.pastview.org

Chevenet F, Castel G, Jousset E, Gascuel O. PastView: a user-friendly interface to explore ancestral scenarios. *BMC Evolutionary Biology* 2019. 10.1186/s12862-019-1490-4.

ImJoy

<https://imjoy.io>

Ouyang W, Mueller F, Hjelmare M, Lundberg E, Zimmer C. ImJoy: an open-source computational platform for the deep learning era. *Nature Methods* 2019. 10.1038/s41592-019-0627-0.

DIVA

<https://diva.pasteur.fr/>

El Beheiry M, Godard C, Caporal C, Marcon V, Ostertag C *et al.* DIVA: Natural Navigation inside 3D Images Using Virtual Reality. *J Mol Biol* 2020;432:4745. doi: 10.1016/j.jmb.2020.05.026.

Genuage

Blanc T, El Beheiry M, Caporal C, Masson JB, Hajj B. Genuage: visualize and analyze multidimensional single-molecule point cloud data in virtual reality. *Nat Methods* 2020;17:pp. <https://doi.org/10.1038/s41592-020-0946-1>

LR_EC_analyser

Lima L, Marchet C, Caboche S, da Silva C, Istace B *et al.* Comparative assessment of long-read error correction software applied to Nanopore RNA-sequencing data. *Brief Bioinform.* 2020 Jul 15;21(4):1164-1181. doi: 10.1093/bib/bbz058.

yacrd

Marijon P, Chikhi R, Varré JS. yacrd and fpa: upstream tools for long-read genome assembly. *Bioinformatics* 2020;36: 3894. <https://doi.org/10.1093/bioinformatics/btaa262>

fpa

Marijon P, Chikhi R, Varré JS. yacrd and fpa: upstream tools for long-read genome assembly. *Bioinformatics* 2020;36: 3894. <https://doi.org/10.1093/bioinformatics/btaa262>

ESSCompress

Rahman A, Chikhi R, Medvedev P. Disk Compression of k-mer Sets, WABI (2020)

JASS

Julienne H, Lechat P, Guillemot V, Lasry C, Yao C *et al.* JASS: command line and web interface for the joint analysis of GWAS results. *Nar Genomics and Bioinformatics* 2020;2:lqaa003. <https://doi.org/10.1093/nargab/lqaa003>

Quicksom

Mallet V, Nilges M, Bouvier G. quicksom: Self-Organizing Maps on GPUs for clustering of molecular dynamics trajectories. *Bioinformatics* 2020;btaa925. doi: 10.1093/bioinformatics/btaa925

ARIAweb

Allain F, Mareuil F, Ménager H, Nilges M, Bardiaux B. ARIAweb: a server for automated NMR structure calculation. *Nucleic Acids Res* 2020 48:W41. doi: 10.1093/nar/gkaa362

REINDEER

Marchet C, Iqbal Z, Gautheret D, Salson M, Chikhi R. REINDEER: efficient indexing of k-mer presence and abundance in sequencing datasets. *Bioinformatics* 2020;36:i177. doi: 10.1093/bioinformatics/btaa487.

Cell Tracking Profiler

Mitchell C, Caroff L, Solis-Lemus JA, Reyes-Aldasoro CC, Warburton F *et al.* Cell Tracking Profiler: a user-driven analysis framework for evaluating 4D live cell imaging data. *J Cell Sci* 2020;133:jcs241422. doi: 10.1242/jcs.241422.