

chromEvol package

This document details the contents and usage of the chromEvol package. Please read this document carefully before running the software. Also refer to the chromEvol usage manual for further details.

The package includes the following items:

- A Linux-compiled version of chromEvol v2.0
- The Ploidy Inference Pipeline (PIP) perl scripts and files
- A usage example for chromEvol inference
- A usage example for chromEvol simulation
- A usage example for PIP

chromEvol inference usage example

This dataset exemplifies the use of chromEvol in order to infer the chromosome number evolution of a hypothetical group of species, and the likelihood of 10 evolutionary models is compared (details about these models can be found in the manual).

To run the inference example, follow these steps:

1. Browse (cd) to the package directory, for example:
`$ cd /user/chromEvol_package`
2. Use the provided chromEvol_control file, located in the chromEvol_example directory, to run the inference with the chromEvol executable:
`$./chromEvol ./chromEvol_example/chromEvol_control`

If the program does not run, you might have to download the chromEvol source and compile it on your system. See compilation instructions in the chromEvol manual.

You can view the inference results in the chromEvol_out directory. Detailed explanation of the output files can be found in the manual.

chromEvol simulation usage example

Here we exemplify the use of chromEvol in order to simulate chromosome-number evolution.

To run the simulation, follow these steps:

1. Browse (cd) to the package directory, for example:
`$ cd /user/chromEvol_package`
2. Use the provided simulation_control file, located in the chromEvol_example directory, to run the simulations with the chromEvol executable:
`$./chromEvol ./chromEvol_example/simulation_control`

If the program does not run, you might have to download the chromEvol source and compile it on your system. See compilation instructions in the chromEvol manual. You can view the results in the simulation_out directory. Detailed explanation of the output files can be found in the manual.

PIP usage example

Here we exemplify the use of the external ploidy inference pipeline.

To run the pipeline, follow these steps:

1. Browse (cd) to the package directory, for example:
`$ cd /user/chromEvol_package`
2. Make sure all requirements are installed on your machine (see manual).
3. Use the provided PIP_control file, located in the PIP_example directory, as input for the PIP.pl script:
`$ perl PIP/PIP.pl PIP_example/PIP_control`

You can view the results in the PIP_out directory. Detailed explanation of the output files can be found in the manual.