Getting Started with CoaSim/GUI

An introduction to the simulator CoaSim

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About CoaSim

CoaSim is a tool for simulating the coalescent process with recombination and geneconversion, under either constant population size or exponential population growth. It effectively constructs the ancestral recombination graph for a given number of chromosomes and uses this to simulate samples of SNP and micro-satellite haplotypes or genotypes.

CoaSim comes in two flavours: A graphical user interface version for easy use by novice users, and a scripting based version (using either Guile-Scheme or Python) for efficient batch simulations. This document is an introduction to the GUI version.

Installing CoaSim

CoaSim is distributed as RPM files or as source code. For most users, we recommend installing from the RPM files, since building the tool from source requires setting up the right build environment and having access to the needed development tools. If you are not familiar with UNIX C++ development—using the Automake suite of tools—and with Qt development we do not recommend that you try building from source.

Installing the RPM Files. The RPM file, `coasim-gui-x.y.z-r.i386.rpm`, contains a binary version of the program, compiled to an Intel x86 Linux platform. To install the graphical user interface version from the RPM package, run

```
> rpm -Uvh coasim-gui-x.y.z-r.i386.rpm
```

where `x.y.z-r` is the version number of CoaSim. Since the RPM files installs in the directory `/usr/local/`, installing the RPM package requires root access.

Installing from the Source Files. The source code is distributed in two tar-files:

- `coasim-core-x.y.z.tar.gz`, and
- `coasim-gui-x.y.z.tar.gz`.

To build the source files, first untar the core module and place it in a directory called Core:

```
> tar zxf coasim-core-x.y.z.tar.gz
> mv coasim-core-x.y.z Core
> cd Core
> ./configure
> make
```

To build the graphical user interface to this simulation core, untar the GUI source files next to the Core module, install the designer plugins used, then qmake and build:

```
> cd ..
> tar zxf coasim-gui-x.y.z.tar.gz
> cd coasim-gui-x.y.z/designer_plugins
> qmake
> make install
> cd ..
> qmake
> make
> make install
```

If you do not have write access to `QTDIR/plugins`, you will need to install the plugins locally, e.g. use qtconfig to add `$(HOME)/.qt/plugins` to the plugin path and do:

```
> cd ..
> tar zxf coasim-gui-x.y.z.tar.gz
> cd coasim-gui-x.y.z/designer_plugins
> qmake
> INSTALL_ROOT=~/.qt make install
> cd ..
> qmake
> make
> make install
```

Running CoaSim

Installing the graphical user installing version should, on GNOME or KDE desktops, add an icon in the start menu for running CoaSim. If this is not the case, the tool can be started on the command-line with the command

```
> coasim_gui
```

Using CoaSim

Running CoaSim will in most cases consist of three steps: Set up the simulation parameters, including the markers (type of marker, mutation rates and similar), demographic parameters, rates for recombination, etc.; running the simulation obtaining and ARG; and extracting the needed information from the ARG (*Ancestral Recombination Graph*), e.g. the resulting sequences, the timing of the various events, or the local coalescent trees embedded in the ARG.

The graphical user interface for CoaSim makes it possible for the casual user to perform simple simulations; for more advanced use the scripting facilities of the Scheme or Python based versions are needed.

In future releases we plan to build more power into the GUI version, but at this moment limited resources forces us to focus our efforts on one of the versions, and therefore the GUI version is limited compared to the Guile Scheme version.

Once CoaSim has been install, on most platforms it will appear in the menu, as shown in Fig. 1. If it does not, however, it can be started from the command line as

```
> coasim_gui
```

Figure 1: The CoaSim icon in the menu.

Once started, the main window, shown on Fig. 2, appears. This window is used to specify the markers to use in a simulation. Using the tabs, different kinds of markers can be specified: trait markers, used for specifying a trait of interest; SNP markers, similar to trait markers, but with a different ascertainment bias; and micro-satellite markers, with a different mutation model than the other two. Additional parameters for the simulation can be set in the *ARG Simulation Parameters* dialogue, shown in Fig. 3, opened from the *Simulation* menu in the main window.

Once the parameters have been set, the simulation can be started from the *Simulation* menu. This opens the simulation monitor, shown in Fig. 4 and runs the simulation. Once the simulation has completed, the result is shown in the result dialogue shown in Fig. 5. From this dialogue it is possible to save the result as a simple text file.

Contact

For any comments or questions regarding CoaSim, please contact Thomas Mailund, at mailund@mailund.dk or mailund@birc.au.dk.

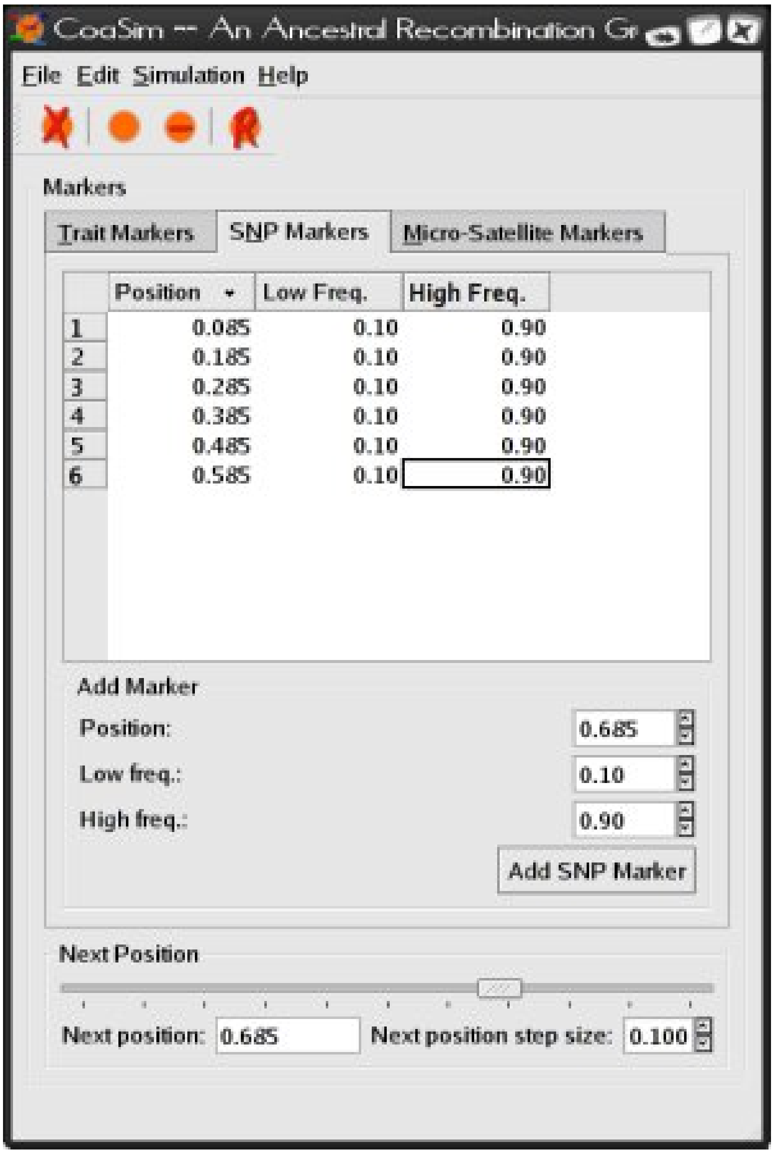

Figure 2: The CoaSim main window. Used to set up markers for simulation.

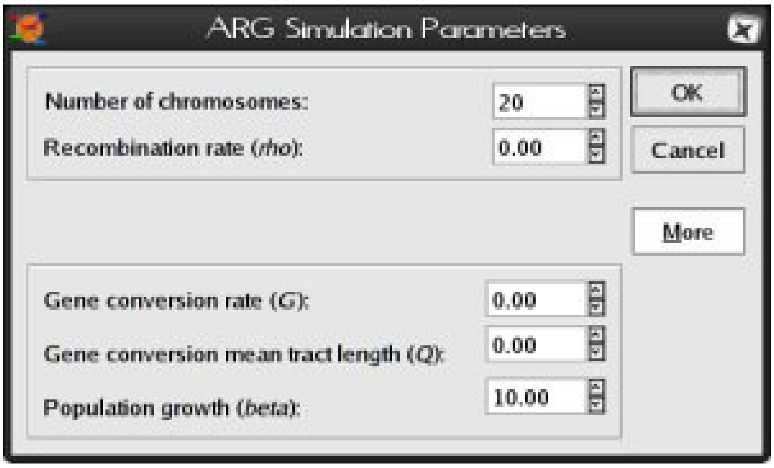

Figure 3: Dialogue for setting ARG simulation parameters.

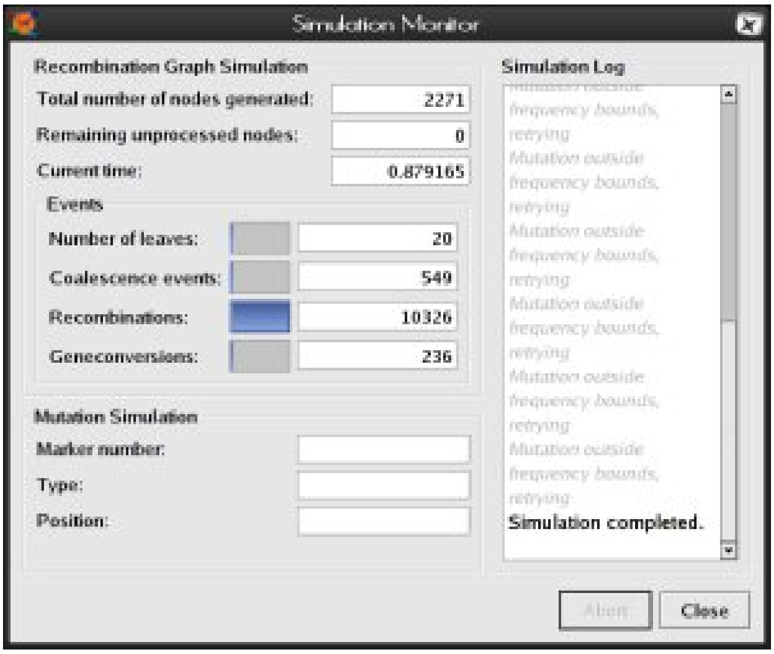

Figure 4: Simulation monitor, showing the progress of the monitor and different statistics about the simulation.

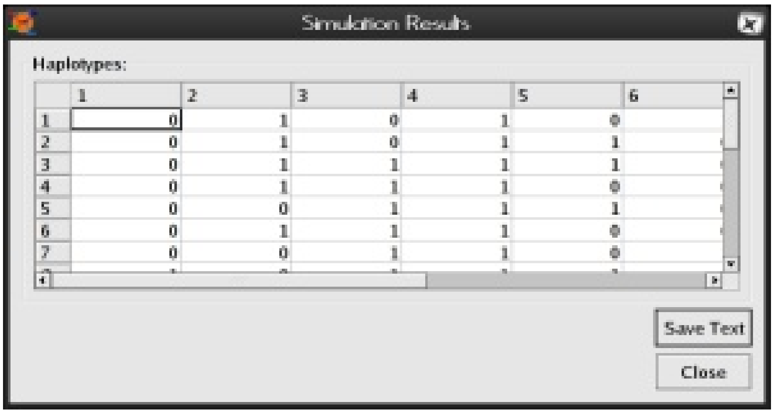

Figure 5: Simulation results.