Getting Started with vPhyloMM (Bacheler Dataset)

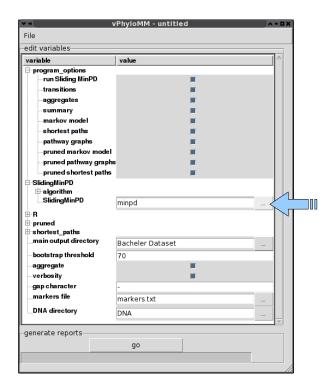
- 1. Make sure to have installed vPhyloMM and its dependencies (see Installation/).
- 2. In the command line, terminal, or shell run:

cd PATH/TO/vPhyloMM/
perl vPhyloMM.pm

where PATH/TO/vPhyloMM is the directory in which vPhyloMM.pm has been installed.

- 3. Once the vPhyloMM window has loaded, it will be ready to run the vPhyloMM algorithm on the included sample "Bacheler dataset" which should be present in the same directory as vPhyloMM.pm (the directory which contains the dataset is called DNA).
- 4. Select which reports will be generated in the "program options" section.
- 5. The executable for Sliding MinPD is called minpd or minpd.exe on Windows machines (Important! See Installation/Sliding MinPD.pdf for instructions on setting up minpd properly). If it is not in your system path (if typing minpd at the command prompt does not run Sliding MinPD) then you will need to tell vPhyloMM where to find it by setting the SlidingMinPD variable:

click on the "+" symbol to the left of "SlidingMinPD" and then either typing the path or clicking the box labled "..." and browsing there. This will be the same directory that you chose in step 5 of Sliding MinPD installation.



- 6. The same applies for the R executable, although the default setting here should work if R has been properly installed.
- 7. Choose the main output directory. This can be an absolute or relative path and is the directory where the results will be stored. If it does not exist, vPhylomm will create it if possible. The default is "Bachelor Dataset".
- 8. The settings are reset each time vPhylomm is loaded. To save your settings and recall them later click on File->Save As... In the upper left-hand corner of the window. Choose a folder and a name for the setting and click Save. The next time vPhylomm is loaded you can recall these settings by clicking on File->Open... and choosing your saved file.
- 9. Click the "go" button at the bottom to generate the selected reports.
- 10. The output files will be placed in the "Bacheler Dataset" directory unless you have changed the main output directory.