PedApp 2.00 [Beta] is an early release of a substantial revision of **Version 1.0**. The documentation is confined to a description of the use of the current version for calculations appearing in the manuscript "On the choice of prior density for the Bayesian analysis of pedigree structure", Almudevar and Lacombe.

Files for 4 generation examples

Data for the 5, 10, 15, 20 replication pedigrees is available in files *PedB05repData.dat*, …, *PedB20repData.dat*, which use the following column formats:

Columns 1-2: Pedigree structure matrix
Column 3: Age (generation)
Column 4: Output flag
Columns 5 - 20: Genotype data

Running the software

1. Select **Data Form** (use **View** menu if needed).

2. To import data, select the **Data Table** tab. Use the **Open Data File** button to import file, then specify the correct columns using the **File Layout** group box. To double-check formatting, press **Relabel Columns**. To run the job, select the **Control Form** (use **View** menu if needed).

3. Select **Likelihood** in the **Model Type** group box.

4. Select the appropriate structural prior model in the **Structural Pedigree Prior** group box.

5. Select **Sample from posterior** from the **Inference Type** group box.

6. When using **Uniform** or **Edge Code** priors, set **Sample Size for Posterior** equal to 1000, when using the **Block Code** prior, set **Total Transitions**, **Burn-in Transitions** and **Total in Sample** equal to 10,000,000, 5,000,000 and 1,000 respectively (don't include commas, and don't adjust for 1,000s).

7. In the **Allele Frequency Source** group box, select **Estimate from data.**

8. Uncheck **Use available sex data** if it is checked.

9. In the **Select Output Statistics** group box, select **Descendants** and **Use output flag**. Currently, selecting **Optimal Block Estimate** causes the minimum scoring pedigree to be appended to the end of any posterior sample file. For the example here, the sample R file assumes that this option is not checked.

10. The job is started by pressing the **Go** button.

The JOBNAME conventions used in the project were *pedb05_uniform, pedb05_edge, pedb05_block,…, pedb20_uniform, pedb20_edge, pedb20_block.*

Posterior samples are stored sequentially in files using the following name conventions. For fitness, descendants and offspring, if **Use output flag** in the **Select Output Statistics** group box is selected, output is provided only for those individuals with a '1' in the **Output Flag** column in the **Data Table**.

JOBNAME_FIT.txt (Fitness)
Number of offspring for individual.

JOBNAME_DES.txt (Descendant)
Total number of descendants for individual.

JOBNAME_OFF.txt (Offspring)
List of offspring (number of offspring followed by that number of IDs).

JOBNAME_DIS.txt (Distance)
Pedigree distance from pedigree specified in Data Table (Pedigree columns in File Layout group box must be specified).

JOBNAME_COM.txt (Complete pedigree)
Given as consecutive parent pairs. Missing parents are given as 0.

JOBNAME_SCO.txt (Score)
Pedigree score.

Once the examples are complete, use the R script in the *SummarizeA.txt* file to produce the summary.