

Quick Start 3 – PRT 2.22 – Run Script and Bootstrap Task

- There is no installation script. Put application and help file in one single folder.
- This version of PRT 2.22 is for Windows.
- More detailed instructions are given in the help file, accessible from the application itself (at the **Help** menu item).
- A quick introduction is given below, showing how to run a script file and perform a bootstrap procedure.
- The file **SampleScript.txt** which is included in the PRT 2.22 distribution contains the following script commands:

```
task 4
number_of_bootstrap_replications 100
select_enumeration_algorithm 3
use_suggested_settings false
minimum_msg_size 3
number_of_msg_iterations 2
min_msg_size_increment 5
single_trial true
simulation_type 4
number_of_loci 4
alleles_per_locus 6
clear_sibling_group_sizes
add_sibling_group_sizes 2 5
add_sibling_group_sizes 3 4
go
save_genotype_chart sampleData.txt
```

- The script command `task 4` sets the **Task** option in the **Single Generation Task** tab to **(4) Evaluate Bootstrap with Simulations**. The bootstrap will use 100 replications. The MSG enumeration algorithm is specified with the commands:

```
select_enumeration_algorithm 3
use_suggested_settings false
minimum_msg_size 3
number_of_msg_iterations 2
min_msg_size_increment 5
```

- The **(3) MSG-MG (large SG modification)** algorithm is selected. The default options are not used, and new settings are specified.

- The simulation model is specified with the commands:

```
single_trial true
simulation_type 4
number_of_loci 4
alleles_per_locus 6
```

- Only one simulated data set will be used, using 4 loci with 6 alleles each. The allele frequencies follow a Zipf distribution.

- The sibling group structure is specified with the following commands:

```
clear_sibling_group_sizes
add_sibling_group_sizes 2 5
add_sibling_group_sizes 3 4
```

- This will result in 2 sibling groups of size 2 and 3 sibling groups of size 4. The `add_sibling_group_sizes` command appends the specified numbers to the **Sibling Group Sizes** grid sequentially. A single command can add up to 6 numbers to a row (see documentation for more on this feature). It is advisable to precede these commands with a `clear_sibling_group_sizes` command, which will clear the **Sibling Group Sizes** grid. Otherwise, the entries will be appended to whatever already exists in the grid.

- Finally, the following commands are included:

```
go
save_genotype_chart sampleData.txt
```

- The `go` command begins the task, then the simulated data is saved into the file **sampleData.txt** (do not use filenames with embedded blanks). The `save_genotype_chart` command should come last, since the data is not generated until after the `go` command is executed.

Control Panel

Single Generation Tasks | Histogram Display | Bootstrap Coverage Display | Genotype Chart | Allele Chart

Task

☐ (1) Estimate Partition
☐ (2) Bootstrap Partition
☐ (3) Evaluate Partition with Simulations
☒ (4) Evaluate Bootstrap with Simulations

Bootstrap Options

Number of Bootstrap Replications: 100

☒ Condition on Alleles
☐ Condition on Genotypes
☐ Unconditional Bootstrap

Partition Options

Maximum Partition List Size: 3000

Max Sib Size for Full Search: 10

Reduced Search Deletion: 1

Randomization

☐ Specify Random Seed: 1234567890

Genotype Error Iteration

Number of Error Iterations: 0

Maximum Errors Per Locus: 0

Select Enumeration Algorithm

☐ (1) MSG-G (graph based)
☐ (2) MSG-T (triplet enumeration)
☒ (3) MSG-MG (large SG modification)

MSG Algorithm Options

☐ Use Suggested Settings
 Minimum MSG Size: 3
 Number of MSG Iterations: 2
 Min MSG Size Increment: 5

Triplet Enumeration Options

☒ Unlimited Triplet Iterations
 Maximum Triplet Iterations: 100

Output Options

☐ Output Genotype Error Screen
☐ Output Alternative SG Assignments
☐ Output Nonexcluded HSGs
☐ Output Nonexcluded Parents
☐ Output Bootstrap Plot:XY Data
☐ Output MSG List
☐ Use Labels for Partition Summary

Simulation Type

☒ Single Trial N Repeated Trials: 50

☐ (1) Sample from Individuals from Genotype Chart
☐ (2) Use Allele Frequencies from Allele Chart
☐ (3) Uniform Allele Frequencies
☒ (4) Zipf Allele Frequencies

Sample From Individuals

N Indiv in Sample: 10

Frequency Properties

Number of Loci: 4

Alleles per Locus: 6

Sibling Group Sizes

	N	Gr1	Gr2	Gr3	Gr4	Gr5
1	2	5				
2	3	4				
3						
4						
5						
6						
7						
8						

Go Show Main Form

Run Script Hide Control Panel

Cancel

System

Tree Mem (MB): 1000

Max MSG: 3000

Max Partition List: 6000

MSG List Construction: ☒ On

MSG List Trim: ☒ On

Partition: ☒ On

Bootstrap Replications: ☒ On

Simulation Trials: ☒ On

Figure 1

- Press the **Run Script** button, then select the file **SampleScript.txt** included in the PRT 2.22 distribution. The options specified in the script file should be shown in **Single Generation Tasks** tab of the **Control Panel**.
- The task will have finished when the **Bootstrap Replications** progress bar is filled.

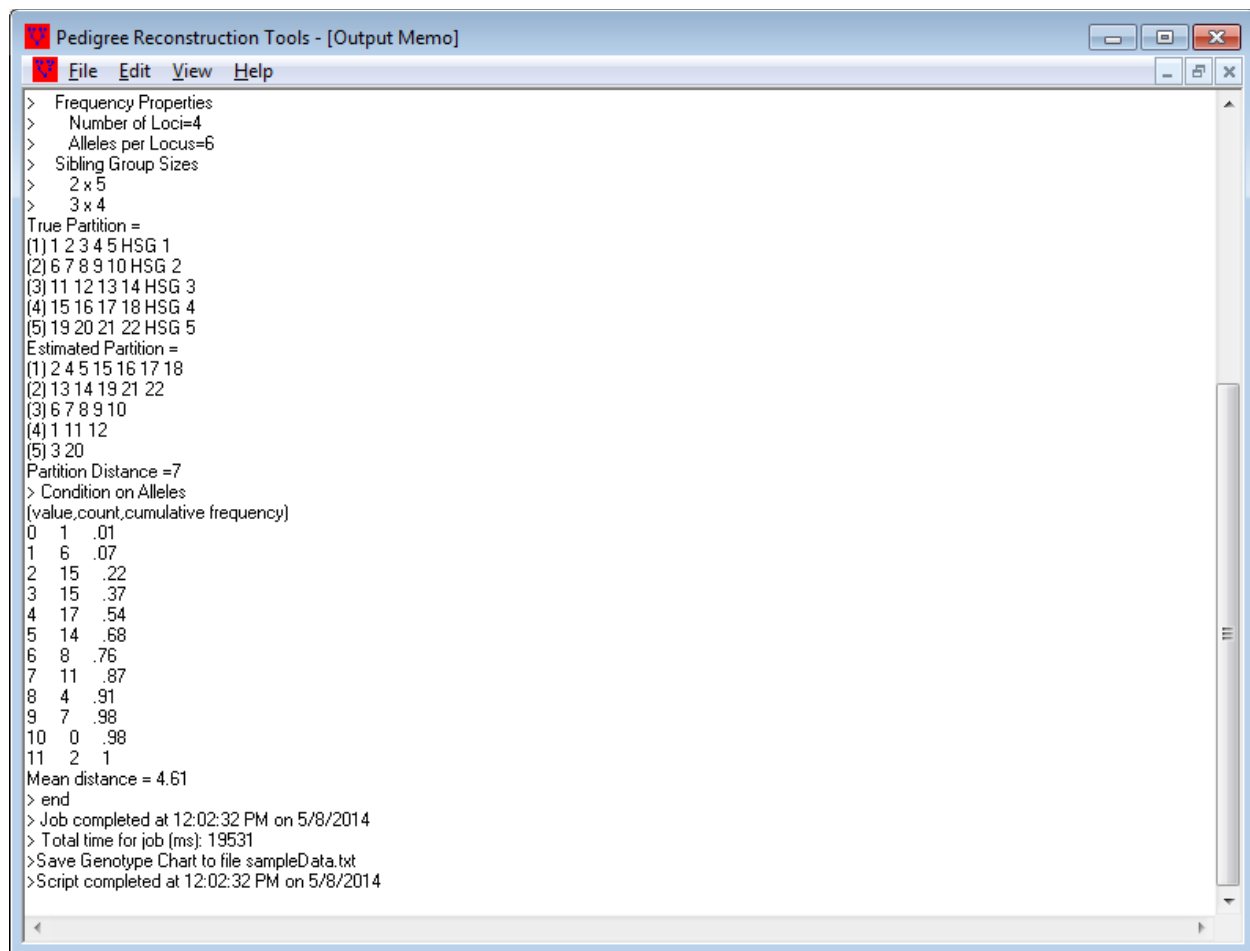


Figure 2

- Next, go the **Pedigree Reconstruction Tools** window. Press the **Show Main Form** button on the **Control Panel** window if needed. It might be helpful to maximize the **Output Memo** to view the output.
- Because only one simulation trial was specified, we may examine the true and estimated pedigrees. In this case the partition distance between the true and estimated partition was 7. The bootstrap estimate of the partition distance sampling distribution follows. A 98% upper confidence bound for the partition distance was estimated to be 9.

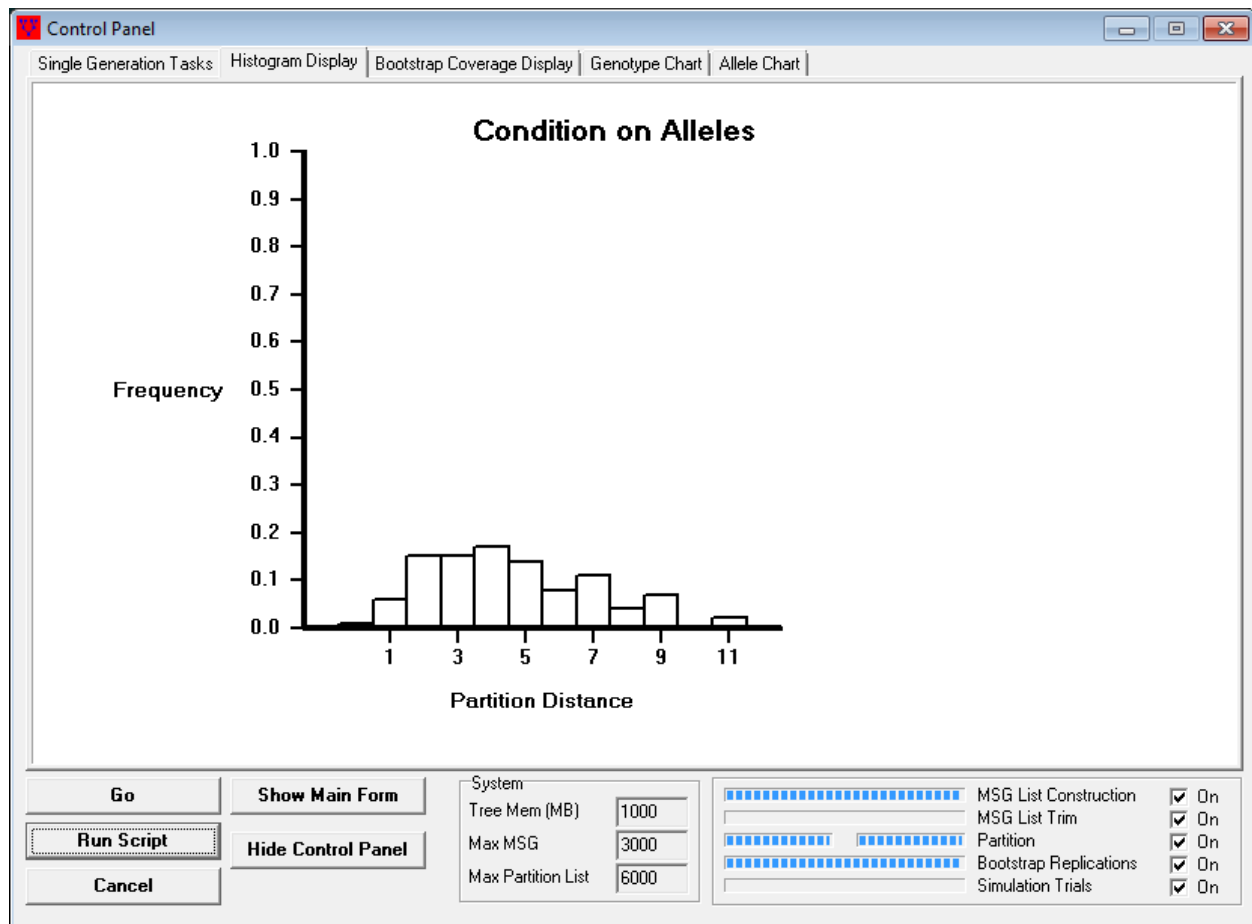


Figure 3

- Select the **Histogram Display** tab from the **Control Panel** of the **Pedigree Reconstruction Tools** window. If necessary, select the **Control Panel** option from the **View** menu. A histogram of the partition distances resulting from the simulated trials is shown (Figure 3).