

## Quick Start 2 – PRT 2.22 – Simulation 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 which illustrates the simulation features.

The screenshot shows the 'Control Panel' window for PRT 2.22. The 'Task' tab is selected, showing options for estimating, bootstrapping, or evaluating partitions. The 'Select Enumeration Algorithm' section has 'MSG-G (graph based)' selected. 'Bootstrap Options' include 200 replications and 'Condition on Alleles'. 'Partition Options' show a maximum list size of 3000. 'Randomization' has a seed of 1234567890. 'Genotype Error Iteration' is set to 0. 'MSG Algorithm Options' include 'Use Suggested Settings'. 'Triplet Enumeration Options' have 'Unlimited Triplet Iterations'. 'Output Options' include 'Output Genotype Error Screen'. 'Simulation Type' is 'Single Trial' with 50 repeated trials. 'Sample From Individuals' is 'N Indiv in Sample' (10). 'Frequency Properties' show 6 loci and 8 alleles per locus. 'Sibling Group Sizes' table is shown below.

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

Buttons at the bottom include 'Go', 'Show Main Form', 'Run Script', 'Hide Control Panel', and 'Cancel'. System settings show 1000 MB tree memory, 3000 max MSG, and 6000 max partition list. Simulation options on the right are all 'On'.

Figure 1

- Set the options as in Figure 1, then press the **Go** button.
- To make output visible (if it isn't), press the **Show Main Form** button.
- In this mode, one single set of simulated data is produced. This can be seen using the **Genotype Chart** tab (Figure 2).

**Control Panel**

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

	L 1a	L 1b	L 2a	L 2b	L 3a	L 3b	L 4a	L 4b	L 5a	L 5b
1	2	5	1	2	4	7	1	8	4	7
2	2	5	2	7	4	7	5	8	4	6
3	5	5	2	7	1	6	5	8	6	7
4	2	5	1	2	4	7	1	8	7	7
5	5	5	2	7	4	7	5	8	4	6
6	2	5	1	8	6	7	5	8	4	6
7	2	5	2	7	6	7	5	8	4	7
8	5	5	1	8	4	7	5	8	4	7
9	2	7	1	4	2	4	2	4	4	4

Rows: 28  
Columns: 15  
Col Width: 45

Clear  
Rotate  
Open  
Save  
Relabel

Genotypes in rows: 1 to 28  
Indiv labels in columns: 0 to 0  
Genotypes in columns: 1 to 12  
Group labels in columns: 13 to 14  
Estimated SG labels in column: 15

Grid Title: Simulated Data

☒ Numerical Validation

**Missing Values**  
☐ Use Missing Value  
Missing Value Code: 999

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 2

- The data may be saved (press **Save** button) for later use (use the **Open** button).
- From the original control panel (select **Single Generation Tasks** tab) uncheck the **Single Trial** check box. This will result in 50 simulations of the model after pressing the **Go** button (or whatever number is in the **Repeated Trials** text box).

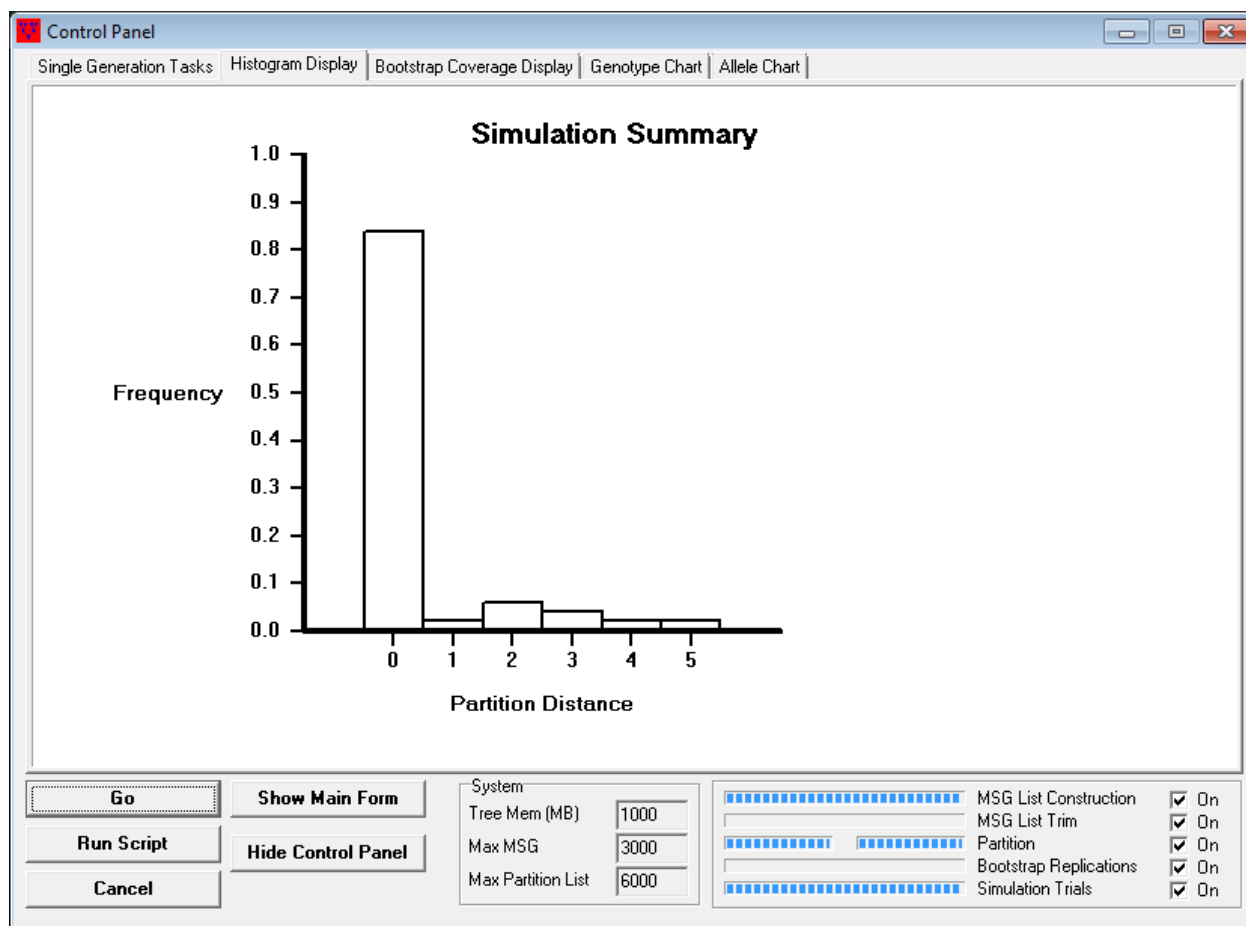


Figure 3

- Select the **Histogram Display** tab. A histogram of the partition distances resulting from the simulated trials is shown (Figure 3).

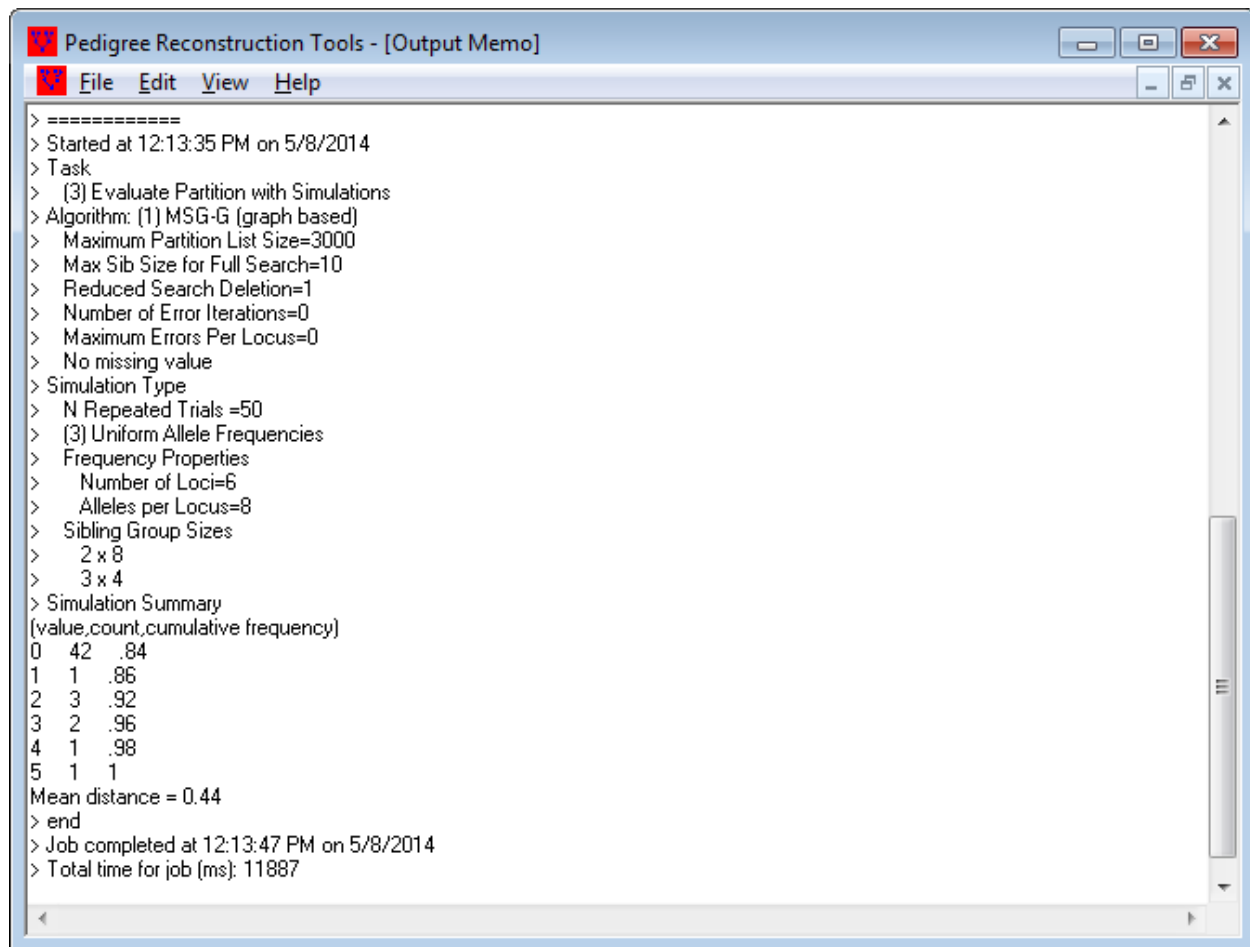


Figure 4

- 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. A numerical summary of the simulation results is given. For example, of the 50 trials, 42 yielded an estimate with 0 errors, whereas a proportion of 0.98 yielded errors of no greater than 4. The mean partition distance is also given, in this case equal to 0.44.