

Quick Start 1 – PRT 2.22 – Estimation 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 read data and obtain an estimate.

Figure 1

- Start from the **Genotype Chart** in the **Control Panel**, press the **Open** button, and read in the **UnlikelyGenotypeExample.dat** file. Select **Genotype Chart** tab if necessary.

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	5	6	4	7	4	6	1	3	3	8
2	5	6	2	4	4	6	1	3	2	8
3	6	8	2	7	4	6	3	5	3	4
4	5	6	2	4	6	7	1	3	2	8
5	5	6	4	7	4	6	3	5	3	8
6	6	8	2	7	4	6	3	5	3	8
7	5	6	2	4	4	6	3	5	3	8
8	6	8	4	7	4	6	1	3	3	8

Rows: 20
Columns: 13
Col Width: 45
Clear
Rotate
Open
Save
Relabel

Genotypes in rows: 1 to 20
Indiv labels in columns: 0 to 0
Genotypes in columns: 1 to 12
Group labels in columns: 0 to 0
Estimated SG labels in column: 13

Grid Title: C:\Users\super\Desktop\distribution PRT_2_21\UnlikelyGenotypeExample.dat

☒ 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 window should look like this. Make sure the genotype column and row indices are correct, and press **Relabel** to double check.

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: 200

☒ 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: 1

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: 6

Alleles per Locus: 8

Sibling Group Sizes

	N	Gr1	Gr2	Gr3	Gr4	Gr5
1						
2						
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 3

- Selecting the **Single Generation Tasks** tab should lead to this window. Select the options as indicated. Note that the panel labels are in bold font only those panels which are needed for this task. Make sure the **Output MSG List** option is selected in the **Output Options** panel. After pressing the **Go** button the progress bars should be filled as shown above.

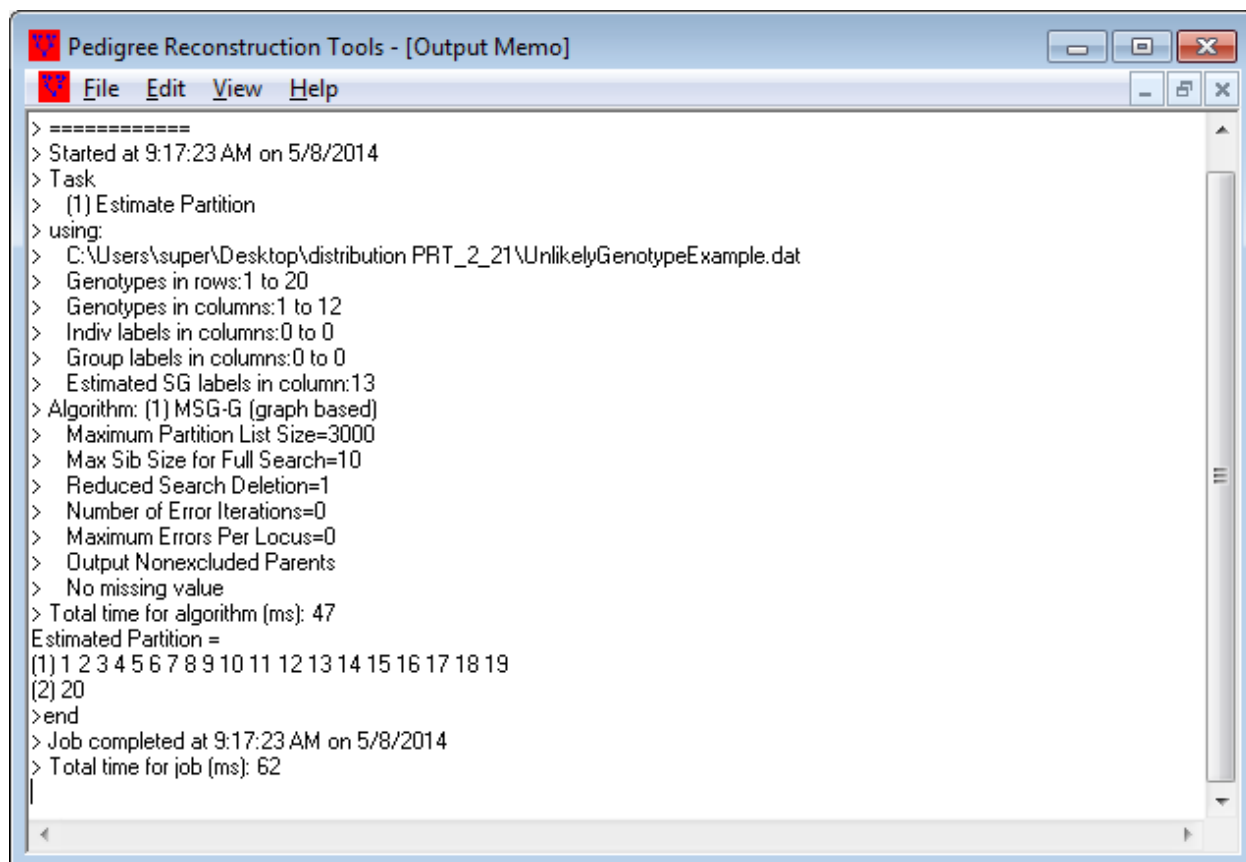


Figure 4

- 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. Notice that the estimated pedigree places individuals 1-19 in one sibling group and 20 in the other. The computation time was about 0.062 seconds.

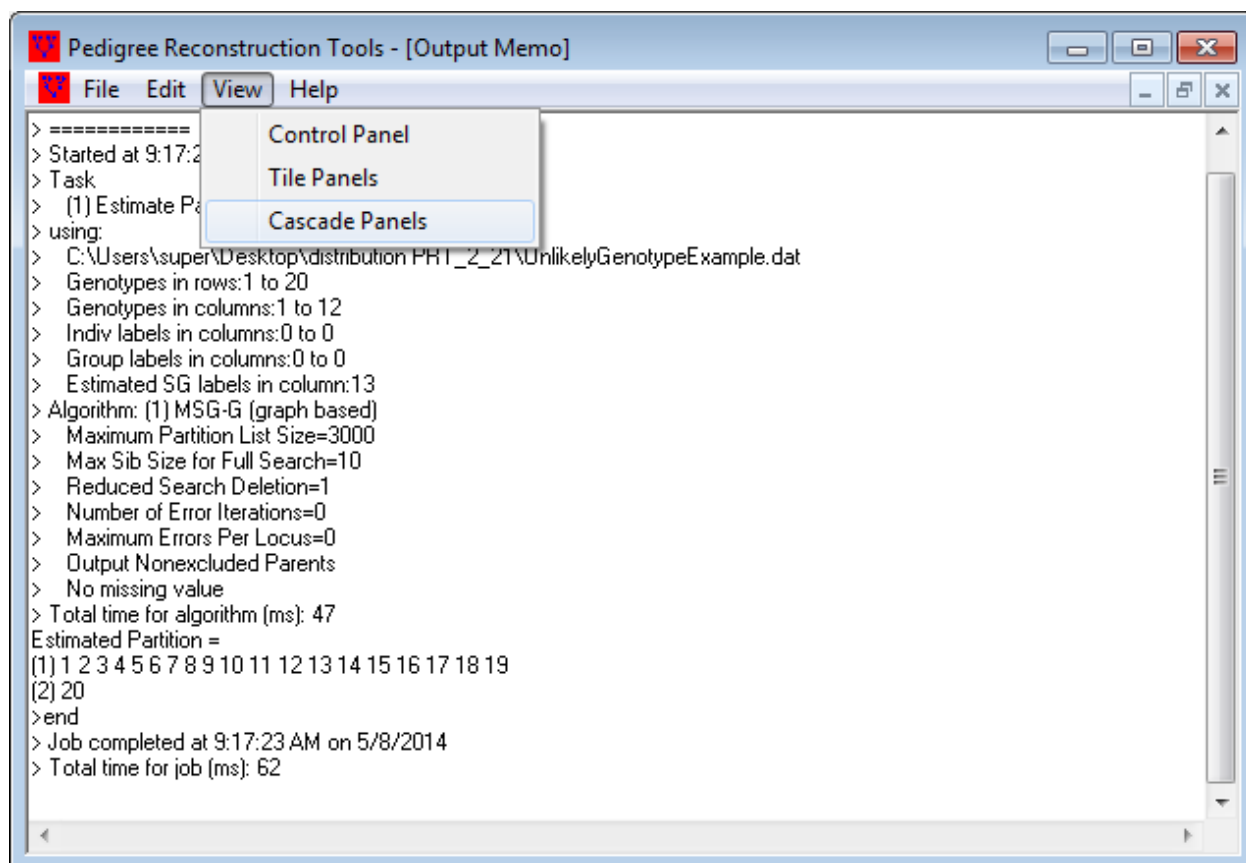


Figure 5

- To go next to the **Output Grid** select, for example, the **Cascade Panels** function.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	1	3	4	7	12	15	16	5	10	11	13	14	17	18	19	2	6	8	20	9
2																				
3																				
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20																				

Figure 6

- Expand the **Output Grid** to see the entire output. This is the set of all MSGs. There is only one of size twenty, which means that the entire data set forms a feasible sibling group. The algorithm decided, however, that individual 20 is not part of the same sibling group as the remaining 19. This is because the genotypes of individual 20 at loci 1 and 4 are 1/8 and 1/2 while the genotypes of the other individuals are about equally divided between 5/6 and 6/8 at locus 1 and 1/3 and 3/5 at locus 4 (this can be seen in the **Genotype Chart**). Therefore, the 20 individuals are not genetically excluded as a sibling group, but it is statistically unlikely that they are a true sibling group.