

Readme for SSG1to3 program

The “**Stage Selection Gain 1to3**” (SSG1to3) in R (SSG1to3_R) or SAS (SSG1to3_SAS) is a simple program to determine the response to selection in standardized units (R) after 1-stage selection with up to three seasons of testing, 2-stage selection with two seasons of testing, and 3-stage selection with three seasons of testing.

The **required input** SSG1to3_R and SSG1to3_SAS is identical and comprising a vector of 17 numbers; note in SSG1to3_R these numbers must be separated by a “,” (see examples below).

1. A qualifier for 1, 2, or 3 stage selection (1, 2, or 3), with 1 for 1-stage selection, 2 for 2-stage selection, and 3 for 3-stage selection.
2. The total test capacity as number of plots for the entire multiple environmental trial series (for example 540, 1080, or 2268)
3. Number of finally selected clones. For later breeding stages we recommend 2, 3, 4, or 5.
4. The variance component ratios for σ_G^2 , σ_{GxL}^2 , σ_{GxS}^2 , σ_{GxLxS}^2 , and σ_ϵ^2 , relative to σ_G^2 , where G denotes genotype, L is location, and S is season. The first number for σ_G^2 must be 1 and all other numbers must be entered relative to the variance component estimate σ_G^2 from the analysis of variance (for example 1, 0.189, 0.103, 0.603, 1.162).
5. Three numbers for the number of clones tested in each season, in case you test no genotypes at season 3 set the 3rd number to “NA” (for example 42, 42, NA) or no genotypes at season 2 and 3 set the 2nd and 3rd number to “NA” (for example 42, NA, NA).
6. Three numbers for the number of locations at each season, in case you test no locations at season 3 set the 3rd number to “NA” (for example 3, 12, 0) or no locations at season 2 and 3 set the 2nd and 3rd number to “NA” (for example 6, 0, 0).
7. Three numbers for the number of plot replications at each season, in case you test no locations at season 3 set the 3rd number to “NA” (for example 1, 3, NA) or no locations at season 2 and 3 set the 2nd and 3rd number to “NA” (for example 3, NA, NA).

Example 1:

SSG1to3_R (1,2268,3,1,0.189,0.103,0.603,1.162,42,42,42,9,9,9,2,2,2)

A one stage selection after three seasons of testing, using a total test capacity of 2268 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 42 genotypes tested at 9 locations, and 2 plot replications at each season across all locations.

Example 2:

SSG1to3_R (1,2268,3,1,0.189,0.103,0.603,1.162,63,63,NA,9,9,NA,2,2,NA)

A one stage selection after two seasons of testing, using a total test capacity of 2268 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 63 genotypes tested at 9 locations, and 2 plot replications at both seasons across all locations.

Example 3:

SSG1to3_R (1,2268,3,1,0.189,0.103,0.603,1.162,126,NA,NA,9,NA,NA,2,NA,NA)

A one stage selection after one seasons of testing, using a total test capacity of 2268 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 126 genotypes tested at 9 locations, and 2 plot replications in a single season across all locations.

Example 4:

SSG1to3_R (2,540,3,1,0.189,0.103,0.603,1.162,144,9,NA,3,6,NA,1,2,NA)

A two stage selection after two seasons of testing, using a total test capacity of 540 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 76 and 7 genotypes tested at the 1st and 2nd selection stage with 3 and 6 locations, respectively, and 2 plot replications at each season across all locations.

Example 5:

SSG1to3_R (3,2268,3,1,0.189,0.103,0.603,1.162,499,77,8,1,7,12,2,2,2)

A three stage selection after three seasons of testing, using a total test capacity of 2268 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 499, 77, and 8 genotypes tested at the 1st, 2nd, and 3rd selection stage with 1, 7, and 12 locations, respectively, and 2 plot replications at each season across all locations.

Example 6:

SSG1to3_R (3,540,3,1,0.189,0.103,0.603,1.162,138,11,5,3,3,6,1,2,2)

A three stage selection after three seasons of testing, using a total test capacity of 540 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 138, 11, and 5 genotypes tested at the 1st, 2nd, and 3rd selection stage with 3, 3, and 6 locations, respectively, and 1 plot replication and 2 plot replications at the 1st, 2nd and 3rd selection stage across all locations, respectively.

Example 7:

SSG1to3_R (2,2268,3,1,0.189,0.103,0.603,1.162,500,32,NA,3,12,NA,1,2,NA)

A two stage selection after two seasons of testing, using a total test capacity of 2268 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 500 and 32 genotypes tested at the 1st and 2nd selection stage with 3 and 12 locations, respectively, and 1 plot replication and 2 plot replications at the 1st and 2nd selection stage across all locations, respectively.

Example 8:

SSG1to3_R (2,540,3,1,0.189,0.103,0.603,1.162,144,9,NA,3,12,NA,1,2,NA)

A two stage selection after two seasons of testing, using a total test capacity of 540 plots, variance component ratios of 1 : 0.189 : 0.103 : 0.603 : 1.162, and 144 and 9 genotypes tested at the 1st and 2nd selection stage with 3 and 12 locations, respectively, and 1 plot replication and 2 plot replications at the 1st and 2nd selection stage, respectively, across all locations.

Output:

R the response to selection in standardized units. In case you want the response to selection in unstandardized units multiply R with $\sqrt{\sigma_G^2}$ from variance component estimations.

Reference:

Diaz F. et al. (to be submitted) Selection of High Dry Matter Orange Fleshed Sweetpotato [*Ipomoea batatas* (L.) Lam.] and Allocation of Breeding Resources in the Humid Tropics of Peru