

ASRgenomics change log

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To report bugs and new features, please send a message to *salvador.gezan@vsni.co.uk*

Changes in ASRgenomics 1.1.1 - July 21th

Improvements:

- Small internal changes for better integration with ASRgwas.

Changes in ASRgenomics 1.1.0 - May 25th

New Features:

- The function `snp.pruning` for marker pruning based has been added.
- The function `synthetic.cross` for obtaining the genotypes of offsprings off of a set of crosses has been added.
- The function `snp.recode` for marker recoding has been added.
- The function `H.matrix`, which is a simplification of `H.inverse`, has been added.
- In `kinship.diagnostics`, an option to determine the proportion of data points to use for plotting has been added to improve processing time.
- Two new filters for markers have been added to `qc.filtering`, one based on inbreeding and one based on the observed heterozygosity (suggested by Simon Nadeau).
- An option to draw group-dependent ellipses has been added to both `snp.pca` and `kinship.pca`.
- Now the markers map can be passed to `qc.filtering` and will also be filtered.

Improvements:

- Relevant attributes of an object (such as `INVERSE`) are preserved after using `full2sparse` and `sparse2full`.
- Now `qc.filtering` can better deal with markers with all samples missing. These markers are removed first thing when the function is called.
- Plot generation in `match.G2A` processing time has been reduced by a factor of ~3.
- The recoding section of `qc.filtering` has been put into another function (`snp.recode`). The arguments related to recoding in the first have not been removed, but if used will generate a stop suggesting the usage of the latter. Consequently, the `M.recode` output has been removed.
- More message control with `message = TRUE/FALSE` has been added to several functions.
- Some internal linear algebra has been changed to improve processing time.
- Error handling has been improved in `G.inverse` to provide more informative messages to the user.
- Help files have been reviewed and improved.

Bug Fixes:

- Now the `colNames` attribute is correctly assigned in `full2sparse`.