

New and updated features in the VUler™ 2019a release:

All

- Peak labels from neighboring loci no longer overlap.
- Primer peaks have less influence on the Y-axis (rfu) scaling.

Analyze

- Bayesian method tracks size standard data.
- The *size_standard_autotracking.txt* preference file provides and records parameters used for Bayesian tracking.
- The AutoEdit Sizing interface includes updated features and tables.

Data

- Batch upload (Upload > Request) supports 4 and 5 unknown contributor requests.
- Batch upload allows for adding a *prefix*, such as a case number, to each request.

Request

- The software automatically appends '*_rep1*' to the request name for replicate request. When a replicate request already exists, the software automatically increments the new replicate request's name.
- The Request window now provides scroll bars when a large number of requests are present.

Report

- The *Load unchecked* preference deselects all genotypes when the Genotype Selector window opens. This option defers match computation; helpful when loading large spec files.
- The *Enable CYB* preference deselects the CYB Population when the Genotype Selector window opens. Match statistics relative to CYB are not calculated. However, CYB is still downloaded for contributor and noncontributor computation.
- The *show_GR* preference allows the GR (Gelman-Rubin) statistic to be displayed for each mixture genotype in the Match table.
- Additional file options are available for saving the Match table.
- Report *.tas* files include timing information.

Tools

- On a computer with ssh access, an owner can *terminate* a currently solving request. Stopping the request frees up processing for another request..
- The Request Processing table provides the *user name* and the *estimated processing time* for each active request.