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ForenSeq Universal Analysis Software v1.2 Release Notes
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Software Release Notes

ForenSeq Universal Analysis Software v1.2

02/AUG/2016

Introduction

These release notes describe notes on the software and known issues of software components of the MiSeq FGx Forensic Genomics Software Package for the v1.2 update. Only changes from the v1.1.1 release are described in this section.

The detail level of the release notes is meant to describe the bug fixes and features added from a cursory level. Additional details on the software is provided in the accompanying User Guide (PN 15053876).

The MiSeq FGx software includes:

- MiSeq FGx Control Software version 1.0.15.0
- BaseSpace Broker version 2.4.0.29
- MiSeq Reporter (MSR) version 2.5.1.3
- Real Time Analysis (RTA) version 1.18.54
- Recipes version 3.0.10
- Genomes version 1.1.0
- ForenSeq UAS Service Broker 1.0.15063.0844

The ForenSeq Universal Analysis Software includes:

- ForenSeq Universal Analysis Software version 1.1.15190 to 1.2.16173
- Management Module Version 1.1.15190 to 1.2.16173
- Web Module Version 1.1.15117 to 1.2.16106
- Secondary Analysis Module Version 1.1.15190 to 1.2.16173
- Forensic Genomics Secondary Analysis Module 1.0.15119

I. MiSeq FGx Control Software

NEW FEATURES:

- No updates

DEFECT REPAIRS:

- No updates

KNOWN ISSUES:

- No updates

ADDITIONAL NOTES:

- No updates

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II. ForenSeq Universal Analysis Software

NEW FEATURES:

- The data repository for sequencing runs and analyses can be configured to allow storage of data off the UAS server.

- When an analysis errors out, a new message window appears with information on where to find the log files.

- The QC indicators update based on user modifications to genotypes.

- The Single Source Sample indicators update based on user modifications to genotypes.

- The Low Coverage QC Indicator was removed for new analyses.

- An Analytical Threshold QC Indicator was added to indicate loci with an allele below the analytical threshold and no signal greater than the interpretation threshold.

- A Not Detected QC Indicator was added to indicate loci for which no signal is present.

- The Interpretation Threshold QC Indicator was updated to indicate when any non-stutter allele is present between the analytical and interpretation thresholds.

- Initial gender determination was updated so that samples with less than 3 of each X and Y STR loci that don't have an allele to exceed the analytical threshold will assign a gender of Inconclusive.

- The project report was updated with new worksheets that list the detailed coverage information for all typed alleles in the report.

- Isometric alleles have the SNPs highlighted in the reports with a font size difference.

- The analytical and interpretation threshold values for STR loci are reported by clicking on an information icon above the seq-o-gram.

- A phenotype estimation report was added that summarizes the phenotype estimation as well as the genotypes and coverage for the aiSNPs and piSNPs.

- A ReadMe file is now installed on the server describing the license information for the third party components used in the software.

DEFECT REPAIRS:

- Alleles with an intensity equal to a threshold will be correctly colored in the seq-o-gram.

- Alleles with an intensity less than the analytical threshold can no longer be typed.

KNOWN ISSUES:

- The genotypes displayed for a phenotype estimation represent the current state of the data, not necessarily the data that was used to create the estimation. To confirm the estimation, perform the estimation again.

- Creation of a run where the header row of the first column of the uploaded sample sheet is not an allowed field name, the system will display an unhandled exception. Fixing the sample sheet and re-uploading to create the run will solve the issue.

- The figure plots in the sample reports are not visible for reports only opened on a Mac.

ADDITIONAL NOTES:

- The updates related to QC indicators were implemented in the Management Module, not the Forensic Genomics Secondary Analysis Module. The Forensic Genomics Secondary Analysis Module is responsible for the calling of genotypes and any logic related to QC indicators is ignored and recalculated in the Management Module.

- The new QC indicators will be calculated on new analyses and loci that are user modified after the install. Results that were obtained prior to the new version will not be modified.

- The interlocus balance indicator for a sample is not updated when an assigned gender is updated.

- If the Q indicator for runs on the dashboard is grey for all the runs, the system is likely unable to access the run and analysis data repository. Check the network, configuration, and security settings to re-establish the connection.

- When running the installer on a system that is running v1.2, the configuration file that denotes the data repository will be replaced with the default configuration file. The data repository will need to be re-configured if it was changed from the default location on the UAS server.

- The installer was designed to update v1.1.1 installations. If the server is not running v1.1.1, update the UAS through the release history in order (i.e. v1.0, v1.1, v1.1.1, v1.2) to prevent deleterious database implications.

III. Forensic Genomics Secondary Analysis Module

NEW FEATURES:

- No updates

DEFECT REPAIRS:

- No updates

KNOWN ISSUES:

- No updates

ADDITIONAL NOTES:

- No updates