cgatools Release Notes

Version 1.1.1

Related Documents

Customers should consult the *cgatools Methods* document for detailed information on specific tools. This document can be downloaded at: http://cgatools.sourceforge.net.

New Features and Enhancements

The following new features and enhancements are provided in this release by comparison with previous **cgatools** released by Complete Genomics:

1. Fixed crash in join tool when reading `geneVarSummary` file.
2. Added Mac OS X binary tarball.

Changes to Version 1.1.0

1. Enhanced the calldiff tool to allow users to identify somatic variants from a tumor/normal pair (beta). This tool takes two variant files—genome A (tumor) and genome B (normal)—as inputs and produces:
    - a report ("SomaticOutput ") that lists variants found only in genome A

   - a score that indicates the likelihood that each variant is truly somatic
2. Added listvariants (beta) and testvariants (beta) tools for comparing variants across multiple genomes, allowing users to determine whether a variant was found in a given genome and the frequency of the variant across the set of tested genomes. listvariants generates a list of all fully called variants found in at least one genome within the tested set. testvariants uses this list as input and reports for each variant whether the allele called in each genome is 1) inconsistent with the variant, 2) is fully called and is consistent with the variant, or 3) has no-calls and allele is consistent with the variant.
3. Added the join (beta) tool, allowing users to combine information from two tab-delimited files by specifying column(s) within the files to be used for determining overlap and column(s) from each file to be included in the merged file.
4. Changed parameters for snpdiff and calldiff tools. In previous releases of **cgatools**, separate parameters were required to output each report (such as Stats, Output, and SuperlocusOutput) to a specific location. These parameters were replaced with two new ones: a parameter that allows you to specify multiple reports to be output and a parameter that allows you to specify a path to the directory to which all output reports will be saved.

Changes to Version 1.0.0.15

1. Fixed snpdiff and calldiff failure processing male build 37 genomes.

Changes to Version 1.0.0.14

1. Fixed evidence2sam to be able to support genomes from assembly format version 1.0.

Changes to Version 1.0.0.13

1. Changed to dynamic linkage on Mac OS X.

Changes to Version 1.0.0

1. Renamed cgi2sam to map2sam.
2. Added evidence2sam (beta).

Changes to Version 0.5.0 (Initial Version)

1. The initial version of **cgatools** included:
   - Reference tools
   - snpdiff
   - calldiff
   - cgi2sam

