Analysis Power Tools: CHANGE LOG

Version:
apt-2.11.8
Date:
Friday February 24, 2023

The 2.11.8 release of APT contains 3 new applications as well as updates to the genotyping engine. APT 2.11.8 is a full release to support AxAS 5.3.

Changed Applications:

- **apt-summary-genotype-axiom**
  - A warning is reported for the first 20 unexpected probesets. An unexpected probeset_id is not in the input summary or cdf files but appears in snp-specific-param-file, snp-priors-input-file, or copynumber-probeset-calls-file.
- **apt-genotype-axiom**
  - artifact reduction parameter has been updated to support new values found in the cel header; pvcam or qcam
  - Update artifact reduction options:
  - Add new option: artifact-reduction-clip-pvcam create alias for option artifact-reduction-clip called artifact-reduction-clip-qcam
  - Set APT default for artifact-reduction-clip-pvcam = 0.43 Change APT default for artifact-reduction-clip-qcam = 0.4 (was 2.0)
- **apt-format-result**
  - Performance has been improved for single sample export of VCF files

New Applications:

- **ps-update**
  - A tool that merges genotyping results from 2 different genotyping analyses
- **apt-geno-qc-axiom**
  - Replaces apt-geno-qc as single sample quality tool. Plate barcode information has been added to the report.txt file

- **apt-summary-plate-norm**

    - A new engine that minimizes plate effects by adjusting signals for subsets of probesets over entire plates.

Version:
apt-2.11.7
Date:
Tuesday February 14, 2023

The 2.11.7 release of APT contains updates to the copy number engine. APT 2.11.7 is a full release to support ChAS 4.4.

Changed Applications:

- **apt-copynumber-cyto-ssa**

    - Feature addition where both the new whole genome segmentation and the xon segments shall be generated by default.
    - There shall be a new library regions file (CytoXON-chrARMRegions.txt) containing the start and stop for each arm of every chromosome. There will be a file for hg19 and one for hg38.

      parameters are analogues of existing parameters. So what ever the old description holds true, except that it applies to the WG segmentation

Version:
apt-2.11.6
Date:
Tuesday March 22, 2022

The 2.11.6 release of APT contains updates to the copy number, export, genotyping, probeset metrics and classification, as well as utility engines. It also includes two new utilities, apt-a5-table-converter and apt-copynumber-cnvmix-util. APT 2.11.6 is a full release to support AxAS 5.2.

Changed Applications:

- **apt-a5-table-converter**

    - New utility that converts a single table in a .txt file to new .a5 file (HDF5 format), or converts a .a5 file containing expected Datasets to new .txt file

- **apt-copynumber-axiom-cnvmix**
  - Affymetrix-scan-date is now included in the report.txt file.
- **apt-copynumber-axiom-hmm**
  - Fix to Autosomal LOH calculation
  - Fix to sometimes reporting segments smaller than min-seg-size parameter in hmm_regions.txt
  - Add mosaicism algorithm support for HT-CMA array
  - New filtering parameters for segments:
    - --seg-min-bases-CN-one default: 50000
    - --seg-min-bases-CN-two default: 50000
    - --seg-min-bases-CN-three default: 100000
    - --seg-min-bases-CN-fourormore default: 100000
    - --seg-min-probesets-CN-one default: 50
    - --seg-min-probesets-CN-two default: 50
    - --seg-min-probesets-CN-three default: 100
    - --seg-min-probesets-CN-fourormore default: 100
  - Old filtering parameters for segments:
    - --seg-min-bases-CN-oneormore
    - --seg-min-probesets-CN-oneormore
  - Support for .cn_models probeset flag identifying probesets to use for segment calling
  - New folded BAF metric to evaluate CN gain segment calls
  - Affymetrix-scan-date is now included in the AxiomHMM.report.txt file
- **apt-copynumber-axiom-ref**
  - Number of waves to store in reference can be determined automatically if wave-count < 0.
    - --wave-count is the number of waves to save to models file. If wave-count <0, it is computed as number of unique plates + wave-count-offset.
    - --wave-count-offset is number of waves to add beyond plate count, when computing wave-count.

      `/n`
      --max-wave-count is upper limit on number of waves to store in models file if input parameter wave-count <0
  - Approximate MAPD and WavinessSD are now calculated by supplying input parameters

    - --mapd-max
    - --waviness-sd-max

- **apt-copynumber-axiom-safer**
    - Affymetrix-scan-date is now included in the report.txt file

- **apt-dmet-translation**
    - Ability to run up to 5000 samples has been enabled in apt-dmet-translation

- **apt-format-result**
    - Option to include qc columns from the ps.performance file
    - vcf export updates:
        - Special characters are now supported in the INFO column
        - rsID and extended_rsID can be included in the INFO column
        - CN regions are now listed in correct chromosomal order in the DATA table
        - Option to filter pass probesets with –filter-pass-probeset parameter

- **apt-geno-qc**
    - Affymetrix-scan-date is now included in the .report.txt file
    - IQR is now correctly identified as MQR and the following has been updated:
        - axiom_signal_contrast_AT_B_IQR to axiom_signal_contrast_AT_B_MQR
        - axiom_signal_contrast_AT_FLD to axiom_signal_contrast_AT_MLD
        - axiom_signal_contrast_AT_S_IQR to axiom_signal_contrast_AT_S_MQR
        - axiom_signal_contrast_GC_B_IQR to axiom_signal_contrast_GC_B_MQR
        - axiom_signal_contrast_GC_FLD to axiom_signal_contrast_GC_MLD
        - axiom_signal_contrast_GC_S_IQR to axiom_signal_contrast_GC_S_MQR

- **apt-genotype-axiom**
    - Lambda parameter controlling sharing of posterior variance can now also be read from the SNP Specific parameter file
    - Affymetrix-scan-date is now included in the report.txt file

- **apt-package-util**
    - apt-package-util now accepts custom file names for AxiomHMM.cnv.a5 and AxiomHMM.report.txt files for HMM analysis batches
- **apt-summary-genotype-axiom**
    - Affymetrix-scan-date is now included in the report.txt file
    - Rare het adjustment has been enabled
    - Lambda parameter controlling sharing of posterior variance can now also be read from the SNP Specific parameter file
- **otv-caller**
    - Option to set OTV to no calls with parameter otv-to-nocall
    - Column of number of OTV calls, n_OTV may be added to ps-metrics and ps-performance files if in the input calls file exists at least one OTV call code for any of probesets
- **ps-call-adjust**
    - The threshold calls file now contains a call-translation table in the pre-header.
- **ps-classification**
    - Probeset specific classification has been enabled via psct library file. This file will have classification threshold values only for specific probesets and will override the global thresholds values for those probesets. When the file is supplied, there will be an additional column titled psct in the ps.performance file
    - Probesets that are classified as MHR or NMH in the diploid sections and which also pass the copy number classification checks on haploid and/or CN0 cluster locations will now be classified as PHR.
    - Check for het only diploid samples will now be done for all species. Previously, X probesets with only het females and both hap cluster male samples were sorted into MHR instead of Other for non-human species. These probesets will now be classified as Other.
- **ps-extract**
    - Report.txt file support has been added to ps-extract

- **ps-metrics**
    - A column of number of OTV calls, n_OTV may be added to ps-metrics files if in the input calls file exists at least one OTV call code for any of probesets

Bug Fixes

- Warnings reporting about amount of male, female samples in the run are not correct.
- fBAF_median, fBAF_stdev, fBAF_marker_count for segment is not correct.
- Exception running wave correction in the 'pca' mode.
- Node name has been changed between apt2.11.4 and 2.11.6.
- Cannot run safer with input wrapper arg-file in master.
- Differences in the cnvmix results under: Reference has no wave table, one test --use-wave-correction false, another test --use-wave-correction true.
- memory leak in BlobWriter.
- Segmentation fault ruuning chimeric run with waves.
- APT-package-util for HMM batches should not require genotype-data-dir.
- Run-time exception running chimeeric reference.
- Error running chimeric ref run, that does not exist before in apt2.11.3.
- Differences in cnpscalls file when running cnvmix from master. apt2.11.3.
- Apt-genotype-axiom does not remove always "IntensityScratchPadFileName_..." file under condition "do-rare-het-adjustment true".
- Error in LOH when running cnvmix.
- Marker count is not consistent for some segments in the hmm output a5 file.
- Difference in hmm report file between 2.11.2 and master in CN count columns reporting.
- apt-copynumber-axiom: Change the default value to no calls when initializing mmap block data.
- If input --wave-count value > wave count in the ref table, app will proceed execution with no error or warning in the log file.
- If any of the wave parameters has empty value, then no error reported in the log file.
- Segmentation fault when input summary does not have both alleles for the snp. It used to run to the end.

Version:

apt-2.11.5.2

Date:

Monday November 08, 2021

The 2.11.5.2 release of APT is a point release to update apt-copynumber-cyto-ssa and apt-copynumber-familial to support Mosaicism and to fix a defect in apt-copynumber-axiom-hmm.

Changed Applications:

- **apt-copynumber-cyto-ssa**
  - Implements the copynumber, mosaic segmentation and loss of heterozygosity (LOH) analysis pipeline for the CytoScan family of arrays on a a per sample basis with respect to a reference set of samples.
- **apt-copynumber-familial**
  - Enabled RHCHP file support.
- **apt-copynumber-axiom-hmm**
  - Bug fix.

Bug Fixes

- Fix to Autosomal LOH calculation in apt-copynumber-axiom-hmm.

Version:
apt-2.11.4
Date:
Monday January 25, 2021

The 2.11.4 release of APT is a point release to update apt-package-util to package HMM output into Axiom Analysis Suite compatible batches and to fix a defect in apt-summary-genotype.

Changed Applications:

- **apt-package-util**
  - Enable HMM output to be packaged into batches suitable for viewing in AxAS 5.0 or higher.
- **apt-summary-genotype-axiom**

- bug fix: previously an “fseek” error would occur if probeset_id file had probesets sorted in different order than the summary.txt file.

Bug Fixes

- Fix to the pption '--@acr-ad-interm-output' which did not work correctly.
- Fix to apt2-sdk to check the return values of client call backs.
- Fix to apt-package-util so that it does not return zero exit code when application finished with error.
- New output files for "Remote Copy Number-Influenced" Genotyping added to CNVmix.
- Fix to apt-package-util crash when input genotyping data directory contains AxiomCN.cnregions.summary.txt and AxiomGT1.summary.txt files at the same level.
- Fix to segmentation fault running cnvmix.
- Fix to fseek in runing apt-summary-genotype-axiom

Version:
apt-2.11.3
Date:
Tuesday June 02, 2020

The 2.11.3 release of APT enables use of a set of metrics to distinguish rare heterozygous genotyping calls for the Axiom family of arrays. APT 2.11.3 supports AxAS 5.1.

Changed Applications:

- **apt-dmet-translation**
  - Bug fix: Allele Translation will now run to completion even if there are samples in the batch that have many haploid No Calls.
- **apt-format-result**
  - Bug fix: For VCF File export, the INDEL position is off by 1.
- **apt-summary-genotype-axiom**
- **apt-genotype-axiom**
  The genotyping algorithm has been updated to include option of using a set of parameters for rare heterozygous calling. The parameter ‘do-rare-het-

adjustment' is defaulted to 'false'. When turned on, if the heterozygous call fails the rare het adjustment test, it will be changed to a 'NoCall'. When enabled, there will be 2 additional output files: AxiomGT1.rare_het.report and AxiomGT1.rare_het_maj_hom.report.

Bug Fixes

- apt-format-results --export-vcf-file: INDEL position is off by 1.
- Update Rare Het Parameter Threshold Values.
- Changed some rare het parameters from developer option.
- Rare het report has different intensities for same probeset when using probeset-ids file vs cdf.
- Add rare-het-calling dev parameter to the header of the output files as usual.

Version:
apt-2.11.2.1
Date:
Friday April 10, 2020

The 2.11.2.1 APT release is a point release to update apt-format-result to fix a critical defect.

Changed Applications:

- **apt-format-result**
  - Bug fix: For VCF File export, the INDEL position is off by 1.

Bug Fixes

- apt-format-results --export-vcf-file: INDEL position is off by 1.

Version:
apt-2.11.2
Date:
Thursday February 27, 2020

The 2.11.2 APT release is a point release to update apt-copynumber-axiom-ref, apt-copynumber-axiom-safer, apt-copynumber-axiom-cnvmix, apt-copynumber-axiom-hmm, apt-copynumber-cyto-ssa and apt-copynumber-familial to support ChAS 4.1.

Changed Applications:

- **apt-copynumber-axiom-ref**
    - Enabled wave correction when creating a reference model file for AxiomCN
    - Added parameter to enable SNPQC calculation
    - Added parameters to input a covariate adjustment file
- **apt-copynumber-axiom-safer**
    - Enabled wave correction for copy number analysis
    - Added allele difference calculation to Axiom Copy Number analysis
    - Added parameter to enable SNPQC calculation
    - Added Y-target parameters from Cyto pipeline
    - Added parameters to input a covariate adjustment file
- **apt-copynumber-axiom-cnvmix**
    - Enabled wave correction for copy number analysis
    - Added allele difference calculation to Axiom Copy Number analysis
    - Added parameter to enable SNPQC calculation
    - Added Y-target parameters from Cyto pipeline
    - Added parameters to input a covariate adjustment file
- **apt-copynumber-axiom-hmm**
    - Enabled wave correction for copy number analysis
    - Added allele difference calculation to Axiom Copy Number analysis
    - Added parameters for allelic call reject, which uses the allele difference data to reduce false copy number segment calls
    - Added parameter to enable SNPQC calculation
    - Added Y-target parameters from Cyto pipeline
    - Added Y-gender calling algorithm
    - Added parameters to input a covariate adjustment file
- **apt-copynumber-cyto-ssa**
    - Added parameter to enable manual adjustment of the log 2 ratio.
    - Added parameter to input the user defined log2 ratio which will be recentered as log 2 ratio of 0.
- **apt-copynumber-familial**

- Enable analysis of CytoScan XON xnchp files.

- **apt-sample-util**
  - Added parameter to allow users to select plates to be combined into single file.

- **apt-package-util**
  - Enabled apt-copynumber-axiom-hmm output files to be converted to AxAS usable batches.

- **apt-summary-genotype-axiom**
  - Fixed defect where the application does not errors out if probeset list does not contains probeset from snp_specific_parameters file.

Bug Fixes

- Report error if the Probesets are different (and/or the ps order, if that's required) between the call and summary file.
- If combine file contains barcode that does not exist, then it will be ignore by application without any warnings or error.
- Wave node received wrong l2R if ref run is chimeric.
- MedianSignal between chimeric reference and probeset-covariates table of the output model file are not the same.
- Add allelic differences demodulation (port from Cyto).
- App does not report a warning message for chimeric run if sample name from regions file does not exist in the call or summary for one of the chimeric regions. It used to be warning in all previous releases.
- apt-package-util should also be able to import apt-copynumber-axiom-hmm output files.
- App should allow duplicate barcodes in the different folders under -- combine option.
- Application errors out if probeset list does not contains probeset from snp_specific_parameters file. Apt-genotype-axiom is working fine in this case.
- Hmm does not delete file AxiomCN.cnv.a5_00002f26-5717-42b6-2570-005cb1006816 at the end of the run.
- Unexpected error when running cn ref application on Win OS only.
- Removing QC failures from CNV Mix output.
- Allow user-defined flags in the AxiomCN covariate adjustment.
- apt-package-util: when creating batch_info.xml only put arraytypename as single value.

- APT-External: mmap: Investigate and fix the issue with remapping on linux-based OS.
- Add parameter consistency checks to ACR2.0 in HMM.
- Discrepancy between apt AD temp output and gold data generated by R script.
- snpqc output is not created for cnvmix and safer.
- Need a warning in the log if --snp-qc-snp-list is specified, but ref does not have AAMedianSignalLog, ABMedianSignalLog, BBMedianSignalLog.
- Change warning about clean allelic differences missing from temp file into an informational message.
- Add Y-gender call to HMM in AxiomCN.
- Add Y-target to AxiomCN.
- Add SNPQC to AxiomCN (port from Cyto).
- New cn-qc-report parameter added in CNVMIX.
- Add allelic differences (incl. allele peaks filtering) to AxiomCN.
- apt-sample-util: add 'combine' parameter.

Version:

apt-2.11.1

Date:

Wednesday January 08, 2020

The 2.11.1 APT release is a point release to update ps-classification and apt-copynumber-axiom-ref executables. APT 2.11.1 supports Axiom Analysis Suite 5.0.1.

Changed Applications:

- **ps-classification.exe**
- **apt-copynumber-axiom-ref.exe**

Bug Fixes

- Additional filter of BestandRecommended =1 has been added. One probeset will be written to the recommended.ps file and in any additional .ps files whose conversion type is listed in the recommended parameter.
- Metric HomMSBD has been deprecated. Hom-ro-ma-cutoff and hom-ro-ma-2-cutoff are to be used instead.
- Region based copy number reference generation has been updated to allow 5000 samples using up to 11 regions (parameter –fixed-cn-region-calls-file).

Version:

apt-2.11.0

Date:

Monday November 18, 2019

The 2.11.0 release of APT is a full release that includes substantial number of bug fixes, changed applications and new application. The details are given below.

Changed Applications:

5000 sample batches has now been enabled on all Axiom copy number applications. See table below for space, memory and runtime estimates on UKBBv2 sample batch

Workflow	32GB Operating System	Total Space	Memory	Runtime
Reference Creation	Linux	317GB	3.465MB	24hrs
CNVMix	Linux	124GB	11,944MB	30hrs
HMM	Linux	124GB	13,402MB	36hrs
Reference Creation	Win7	317GB	3,294MB	42hrs
CNVMix	Win7	124GB	10,125MB	44hrs
HMM	Win7	124GB	14,273MB	61hrs

Axiom copy number applications now support wave correction for advanced signal normalization array types that support wave correction.

- **apt-copynumber-axiom-hmm**
  CN QC metrics have been updated to include option of MAPD and WavinessSD calculation after plate based signal correction.
  Median log2ratio and standard deviation are now reported for each segment .
- **apt-copynumber-axiom-ref**
  checks added that warn or error:
  - If the ProbeData table contains any probeset with AxiomProcessFlag<>0 that is not in the input data (via supplied summary file or supplied CELs/CDF).
  - If any probeset in the ProbeData table is NOT in the Reference table.
  - If a probeset is not written to Reference table only because of missing position information
  - Errors out if a probeset in ProbeData with CN_Region<>NA is not in Reference table.

- **apt-format-result**
  - Ability to export one sample per file has been enabled as well as the ability to export alternate marker names instead of probeset_id.
  - Updates to VCF export:
    - Addition of RSID in INFO column when probeset_id is used as ID.
    - In Metadata section: ##INFO=ID=RSID,Number=1,Type=Integer,Description="dbSNP RS ID"
    - Contig information added to the #CHROM column.
    - ##CONTIG="ID=X"
  - Updates to PLINK export:
    - Export of chromosome short names for .ped and .tped formats.
    - Sample filtering to export selected samples for .tped and .tfam formats.
- **apt-genotype-axiom**
- **ps-metrics**
  - ps-metrics has been updated with new metrics for multi allelic probesets.
  - Z/W probesets are now handled as special SNPs for avian species.
  - ps-metrics can now take a list of samples as an input argument and calculates metrics only on those samples.
  - The Hardy-Weinberg test statistic and p-value have been updated in ps-metrics. The test statistic and p-value are produced when the chi-squared test is used, and only the p-value is produced when the exact test is used (with small sample sizes).

- **ps-classification**
  - ps-classification has been updated with improved classification for multi allelic probesets.
  - ps-classification selects the best probeset for a multi allelic SNP id when a 4-column ps2snp file is supplied.

New Applications:

- **apt-sample-util**
  - Application that splits samples by plate barcode from report, summary, confidence and calls files.
- **apt2-summary-file-util**
  - Utility that converts summary.a5 to summary.txt file and summary.txt files to summary.a5 format.

- **ps-bac**
  - Application that is used to determine batch effects for samples that are genotyped together.
- **ps-call-adjust**
  - This function takes in a calls file and a confidences file and changes any assigned calls to NoCall when the matching confidence value is larger than a threshold.
- **ps-extract**
  - When a list is provided, the application extracts selected samples, probesets or combination of both, from the calls, confidences, summary, posteriors, multi-posteriors, priors, multi-priors, or reference files.

Bug Fixes

- apt-format-result fails with unhandled error when almost all available options were used with export-single-samples.
- apt-format-result can't generate output TXT files when snp-identifier-column and export-single-samples options are used together.
- apt-format-result generates incorrect data when pedigree file has used with export-single-samples option.
- When splitting summary.a5 file, we will not create header inside each of the output .a5 files.
- Cannot create ref with waves from summary file: ERROR Failed to open the temporary gender info file.
- Error running cn reference creation for 7500 UKB samples.
- apt-summary-genotype-axiom: 'ERROR Cannot open file' with any explanation which one.
- Support missing genotype calls when sample fails QC call rate.
- HMM --exclude-failed-samples parameter: change default setting.
- Could we remove temp files after run is done: GenderInfo_6b2d5372-a621-4b6b-c537-317c5a0d9d3d, Log2RatiosScratchPadFileName_0c71771e-4eb3-4b09-1066-d2d3d8d9e326, WaveCorrection_4aafe45f-8244-4355-3013-7bbcd0c6e469.
- Error in the application instead of warning.
- ERROR: Exception occurred in multi-allele genotyping node when I remove version row from input multi-posteriors file.
- apt-format-result is too slow while exporting 5000 samples with --export-single-samples option set to True.
- MainNode::standardMain(): Unhandled std::exception (stof) in cnvmix if summary intensity is not a float.

- apt-format-result fails with unhandled error while processing input-plink-file with enabled export-single-samples key.
- apt-format-result should use exactly the same sample name as a part of the filename as in the input data when --export-single-samples option is used.
- apt-format-result: unexpected file created in the output directory when --export-single-samples option is used with --sample-filter-file.
- apt-format-result with --export-single-samples attempts to create temp files in the cwd.
- There is some circumstance where a call to translateCall() returns an empty string, which causes a set fault.
- apt-sample-util: Samples order reporting only for call files is not correct.
- reproductive risk values are inaccurate when larger than int max.
- apt-format-result: short names for some chromosomes are missing in output PLINK files when export-chr-shortname is set to True
- Validation of chromosome table
- Cannot run hmm with reference with relative path.
- ap-format-result: VCF #CHROM column contains empty strings for 2147483648 when --export-chr-shortname option is used
- apt-format-result silently skip sample columns while creating VCF file when sample-attributes-file contains duplicated alternate sample names
- ERROR\tFailed to open the temporary wave file' when trying to create regular reference model file without wave correction
- apt-format-result: EMBL-EBI VCF validator reports 'Reference and alternate alleles must not be the same' error
- Please change the expected column name for the 2nd column in the --export-alternate-probeset-ids file
- apt-format-result: wrong sorting order of the values in the POS column
- apt-format-result: EMBL-EBI VCF validator reports duplicated variant errors
- apt-format-result fails with unhandled error while processing input-plink-file with sample-filter-file
- apt-format-result terminates with error status when --performance-file option has used with batch folder which contains Ps.performance.txt file in the SNPolisher subfolder
- 5000 samples cnvmix run: Segmentation fault with Version: master-dev stash.amer.thermo.com/ma-alg/apt2-genotyping.git/master@1416055794(1e6f82bbdd) 2019-01-28-13:13
- Difference in LOH of the report file for sample a550484-4209460-021415-140_C01.CEL between apt2.10.2.2 and current master
- apt-format-result: VCF output may not match specification due to arbitrary alternate probeset names

- apt-format-result: not all data of --additional-snp-information-file are exported when --export-chr-shortname option is used
- ap-format-result: alternate is not a single dot or a comma-separated list of bases in the VCF output file
- apt-format-result: remove space before Description in the FILTER meta-information field
- apt-format-result: Issue with 20-min socket timeout due to slow VCF export of 5000 samples.
- App could not handle special-snps option without node name with --analysis-files-path.
- apt-format-result should not report an error if a probeset_id in the --export-alternate-probeset-ids is missing
- When the annotation file is missing not all --additional-snp-information-file are exported
- APT2-Core: util-affx: Fix decimal issue with formatDouble in AffxConv.
- We need --@force-missing-probeset-in-region-error-to-warning option, default false
- All warnings and error messages produce by aptng 2173-2176 should be related to final output model file. All region reference files for chimeric run should be ignored.
- apt-format-result: Fix single quote issue in VCF format for EBI compliance on filter header lines.
- apt-format-result: help topic for the --plink-sort-by-chrpos parameter doesn't reflect all possible file formats
- apt-format-result: PLINKT output *.tped file contains unexpected lines
- apt-format-result: PLINK Export: selected samples in tped and tfam
- apt-copynumber-familial: Input mother or father files should not be required, because it is possible to run index and only one of them
- apt-copynumber-familial: Change the default value for role validity threshold to 1000.
- report.txt file has 2 extra tabs at the ends of each line of data
- APT2-Build: Must poll relevant Git submodules for apt2-tools in order to trigger Jenkins builds to run.
- apt-dset-compare: Allow --exclude-dataset-row to work if one file contains row and another doesn't.
- CachedVectorVector should not create the cache folder in the current working directory
- Segmentation fault running safer for PharmacoScan, 24 samples
- Running time for reference creation of 5000 samples is not acceptable for PMRA array
- Could we remove 'ProbeSetBAFs' folder from the cn apps output

- No error if empty string value in the chr column of the hmm region file
- Error while reading file in Dset::IO_TsvFile_Cursor::seek1008 when snp list has different order, than summary file
- Cannot create cn reference for 500 samples Transplant array only on OS-X. ERROR 1 4076 MainNode run failed with one or more errors. ErrCode: 1000
- Reduce .cnv.a5 file size by changing strings in the probeset dataset from variable length to fixed length
- apt-copynumber-onco-ssa: Investigate bad memory allocation and re-enable OncoScan r1_NDFLD6wave and v3db_NDFLD6wave tests for Linux.
- apt-copynumber-axiom-ssa: Temporarily disable copynumber a5/txt summary tests. Todo: Re-enable once all of vector out-of-range exceptions are fixed and gold data are updated.
- Strange error message running option '--summaries-only true' in eureka
- App does not report any errors in gender value is unknown - 'abc'
- Error message is not correct when gender or report file is empty - does not have any gender data.
- Reading PharmacoScan_96F.r6.spf for AxiomEngineTest produces different results than reading PharmacoScan_96F.r6.cdf
- Application should run if all samples have blank gender value
- Application should run if not all samples gender is 'unknown'
- Reference file chr value is not correct for chicken array.
- apt-copynumber-axiom-ref must preserve the probeset_id order from the unadjusted summary file in the adjusted summary file

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