Analysis Power Tools (APT) -- Release 2.11.4

The Analysis Power Tools (APT) is a collection of command line programs for analyzing and working with Affymetrix microarray data. These programs are generally focused on CEL file level analysis. APT also refers to the underlying C++ source code. Binaries and source code are available from the main APT website, http://www.affymetrix.com/support/developer/powertools/index.affx.

Power User Manuals

Power user manuals are available for specific command line applications:

- Main Applications:
  - apt-genotype-axiom: A program for performing recommended genotype calling analysis on Axiom arrays.
  - apt-summary-genotype-axiom: A program that enables genotyping using a summary.a5 or .txt file as input, rather than CEL files.
  - apt-geno-qc: A program for doing single chip QC of WGSA genotyping arrays.
  - apt-probeset-genotype: A program for analyzing mapping arrays. Supports BRLMM-P, Birdseed, and BRLMM methods for genotype calling.
  - apt-copynumber-axiom-cnvmix: A program that reports copy number in predefined regions with dynamic copy number state thresholds. Also reports loss of heterozygosity states.
  - apt-copynumber-axiom-hmm: A program that reports copy number and loss of heterozygosity states using a hidden Markov model.
  - apt-copynumber-axiom-ref: A program that generates a copy number reference model library file used by other copy number engines.
  - apt-copynumber-axiom-safer: A program that reports copy number in predefined regions with fixed copy number state thresholds. Also reports loss of heterozygosity states. Renamed from apt-copynumber-axiom-ssa.
  - apt-dmet-genotype: A program to compute genotypes and copy number variation from DMET Plus CEL files. DMET CHP files are generated.
  - apt-dmet-translation: A program to compute star allele translation reports from DMET Plus CHP files.
  - apt-copynumber-cyto-ssa: A program to run single-sample copynumber and LOH analysis on CytoScan family of arrays.
  - apt-copynumber-cyto-ref: A program to generate reference model files for copynumber and LOH analysis of CytoScan family of arrays.
  - apt-copynumber-wave: A program to add additional waves to copynumber reference file. Most users should use default wave corrections provided by ThermoFisher.
  - apt-canary: A program to compute copy number variation calls given a known set of CNV regions.
  - apt-copynumber-onco-ref: A program to generate copynumber reference model files for OncoScan arrays.
  - apt-copynumber-onco-ssa: A program to perform copynumber analysis on OncoScan arrays and matched normal/tumor pairs.
  - apt-copynumber-onco-som-ref: A program to generate somatic mutation reference model files for OncoScan arrays.
  - apt-copynumber-onco-som-ssa: A program to implement the somatic mutation analysis pipeline for OncoScan arrays
  - ps-metrics: A program to generate various QC metrics for SNPs for Axiom arrays.
  - ps-classification: A program which reads a metrics table generated by ps-metrics and classifies SNPs based on a number of customizable criteria.
  - otv-caller: A program for identifying *off-target variants*.
  - apt-genotype-eureka: A program for performing recommended genotype calling analysis on Eureka binning files.
  - nibls: A program for converting sequence data from the Eureka platform into binning files to be used in genotyping or visualization.
  - apt-probeset-summarize: A program for analyzing expression arrays including 3' IVT and exon arrays. Supports background correction (MAS5,RMA), normalization (linear scaling, quantile, sketch), and summarization (PLIER, RMA, MAS5) methods.
- Utility Programs:
  - ps-call-adjust:Rewrites any genotype call to "No Call" where the call's confidence score fails a user-specified threshold, and outputs a calls file with the adjusted calls. To adjust only a given set of probesets, use a probeset list file with probeset_id as the first line. More details describing the use of `ps-call-adjust`.
  - ps-extract:extracts data from calls, confidences, summary, references, posteriors (biallelic and multiallelic), and priors (biallelic and multiallelic) files for a supplied set of probesets and/or samples. Every input file has a matching output file.
  - ps-bac:Tests for batch effects when samples were genotyped in batches.
  - apt2-summary-file-util:Application that converts summary.a5 to .txt file format and summary.txt to summary.a5 format.
  - apt-sample-util: A program that splits samples by plate barcode from report, summary, confidence and calls

files.
    - apt-cel-transformer: A program for applying arbitrary chipstream methods (ie quantile normalization, RMA background correction) to a set of cel files, resulting in a new set of cel files.
    - apt-cel-extract: A program for extracting feature level intensities from CEL files.
    - apt-cel-convert: A program for converting CEL files to different formats.
    - apt-chp-to-txt: A program to dump AGCC and XDA chp files as text.
    - apt-file5-util: A program to convert between a5 and text formats.
    - apt-engine-wrapper: A program to directly call analysis engines. The main use is to run it with the help option in order to find out what options various sub-engines will except.
    - apt-annotation-converter: A program to create custom SQLite format annotation files from csv files.
    - apt2-dset-util: A program for converting between the file formats supported by the APT2 framework, including OSCHP and text files (Supports up to 500 samples).
    - apt-param-convert: A program for converting XML parameter files used in legacy applications to those used in newer APT2 applications (e.g. from apt-probeset-genotype to apt-genotype-axiom).
    - apt-package-util: A program for creating batch folder used by Axiom Analysis Suite from output produced by APT or GTC.
    - apt-format-result: A program for creating VCF or PLINK file formats from Axiom Analysis Suite output files.
    - apt-copynumber-format-igv: A program for exporting probe and segment level data into a format compatible with the Integrative Genome Viewer (IGV).
    - apt-suitcase-extract: A program for converting .suitcase files generated by Axiom Analysis Suite version 1 to folder format required by version 1.1.
- Legacy Programs (likely to be removed in later APT releases):
    - apt-midas: A program to compute MiDAS (alternative splice detection) scores from exon array results.
    - apt-summary-genotype: A program to run BRLMM-P family of algorithms on allele summaries.
    - apt-copynumber-workflow: A program to run the copy number analysis workflow on SNP6 arrays.

More Detailed Documentation

For specific details see:

- Index.html: This document
- Install.html: Notes on how to install APT
- Change.html: Specific changes associated with each release version
- Vignette.html: List of vignettes available for APT. Vignettes are brief and concise documents on specific topics.
- FAQ.html: List of FAQs pertaining to the whole of APT. Program and application FAQ items are listed in program manuals and application vignettes.
- File-Formats.html: Information about file formats used by APT.

History and Changes

The APT code provides the back end analysis engine for Expression Console and Genotype Console. The APT packaged evolved out of an early exon array analysis package called ExACT. **All users should review the** Change Log **for details on changes made to APT.** Changes to algorithm behavior and the addition of new features will be itemized in the Change Log. The latest information and downloads for APT are available on the APT DevNet website.

Compute Platforms

See the Platforms page for more information.

Support

Support for APT is handled through the Affymetrix Developer Network. Specifically, questions, problems, feature requests, and other inquiries should be made through the Developer Network email address, devnet@affymetrix.com. To get emails updates about APT or to view previous APT announcements see the APT User Form.

APT is not supported through the Affymetrix call center, Field Application Specialists, or other standard Affymetrix Technical Support channels.

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