

# Package ‘ASCAT’

October 22, 2015

**Type** Package

**Title** Allele-Specific Copy Number Analysis of Tumours

**Version** 3.0

**Date** 2015-09-22

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**Description** R package of ASCAT as published in <http://www.ncbi.nlm.nih.gov/pubmed/20837533>

**Depends** R (>= 2.13.0),  
RColorBrewer

**License** GPL-3

**LazyLoad** yes

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ascat.aspcf	<i>ascat.aspcf</i>
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## Description

run ASPCF segmentation

## Usage

```
ascat.aspcf(ASCATobj, selectsamples = 1:length(ASCATobj$samples),
  ascat.gg = NULL, penalty = 25)
```

## Arguments

ASCATobj	an ASCAT object
selectsamples	a vector containing the sample number(s) to PCF. Default = all
ascat.gg	germline genotypes (NULL if germline data is available)
penalty	penalty of introducing an additional ASPCF breakpoint (expert parameter, don't adapt unless you know what you're doing)

## Details

This function can be easily parallelised by controlling the selectsamples parameter it saves the results in LogR\_PCFed[sample]\_[segment].txt and BAF\_PCFed[sample]\_[segment].txt; if these files exist, the results are read from them. Hence, after parallelisation, copy all the files into the current directory, and run this function to read in the results

## Value

output: ascat data structure containing:

1. Tumor\_LogR data matrix
2. Tumor\_BAF data matrix
3. Tumor\_LogR\_segmented: matrix of LogR segmented values
4. Tumor\_BAF\_segmented: list of BAF segmented values; each element in the list is a matrix containing the segmented values for one sample (only for probes that are germline homozygous)
5. Germline\_LogR data matrix
6. Germline\_BAF data matrix
7. SNPpos: position of all SNPs
8. ch: a list containing vectors with the indices for each chromosome (e.g. Tumor\_LogR[ch[[13]],] will output the Tumor\_LogR data of chromosome 13)
9. chr: a list containing vectors with the indices for each distinct part that can be segmented separately (e.g. chromosome arm, stretch of DNA between gaps in the array design)

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ascat.GCcorrect	<i>ascat.GCcorrect</i>
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### Description

Corrects logR of the tumour sample(s) with genomic GC content

### Usage

```
ascat.GCcorrect(ASCATobj, GCcontentfile = NULL)
```

### Arguments

ASCATobj            an ASCAT object  
 GCcontentfile    File containing the GC content around every SNP for increasing window sizes

### Details

Note that probes not present in the GCcontentfile will be lost from the results

### Value

ASCAT object with corrected tumour logR

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ascat.loadData	<i>ascat.loadData</i>
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### Description

Function to read in SNP array data

### Usage

```
ascat.loadData(Tumor_LogR_file, Tumor_BAF_file, Germline_LogR_file = NULL,
  Germline_BAF_file = NULL, chrs = c(1:22, "X", "Y"), gender = NULL,
  sexchromosomes = c("X", "Y"))
```

### Arguments

Tumor\_LogR\_file            file containing logR of tumour sample(s)  
 Tumor\_BAF\_file    file containing BAF of tumour sample(s)  
 Germline\_LogR\_file            file containing logR of germline sample(s), NULL  
 Germline\_BAF\_file            file containing BAF of germline sample(s), NULL  
 chrs            a vector containing the names for the chromosomes (e.g. c(1:22,"X"))  
 gender            a vector of gender for each cases ("XX" or "XY"). Default = all female ("XX")  
 sexchromosomes    a vector containing the names for the sex chromosomes

## Details

germline data files can be NULL - in that case these are not read in

## Value

ascat data structure containing:

1. Tumor\_LogR data matrix
2. Tumor\_BAF data matrix
3. Tumor\_LogR\_segmented: placeholder, NULL
4. Tumor\_BAF\_segmented: placeholder, NULL
5. Germline\_LogR data matrix
6. Germline\_BAF data matrix
7. SNPpos: position of all SNPs
8. ch: a list containing vectors with the indices for each chromosome (e.g. Tumor\_LogR[ch[[13]],] will output the Tumor\_LogR data of chromosome 13)
9. chr: a list containing vectors with the indices for each distinct part that can be segmented separately (e.g. chromosome arm, stretch of DNA between gaps in the array design)
10. gender: a vector of gender for each cases ("XX" or "XY"). Default = NULL: all female ("XX")

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ascat.plotAscatProfile

*ascat.plotAscatProfile*

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## Description

ascat.plotAscatProfile

## Usage

```
ascat.plotAscatProfile(n1all, n2all, heteroprobes, ploidy, rho, goodnessOfFit,
  nonaberrant, y_limit = 5, nAfull, ch, lrr, bafsegmented, chrs,
  textFlag = FALSE)
```

## Arguments

n1all	copy number major allele
n2all	copy number minor allele
heteroprobes	probes with heterozygous germline
ploidy	ploidy of the sample
rho	purity of the sample
goodnessOfFit	estimated goodness of fit
nonaberrant	boolean flag denoting non-aberrated samples
y_limit	Optional parameter determining the size of the y axis in the nonrounded plot and ASCAT profile. Default=5
nAfull	copy number major allele
ch	a list containing c vectors, where c is the number of chromosomes and every vector contains all probe numbers per chromosome

lrr	(unsegmented) log R, in genomic sequence (all probes), with probe IDs
bafsegmented	B Allele Frequency, segmented, in genomic sequence (only probes heterozygous in germline), with probe IDs
chrs	a vector containing the names for the chromosomes (e.g. c(1:22,"X"))
textFlag	Optional flag to add the positions of fragments located outside of the plotting area to the plots. Default=F

### Value

plot showing the ASCAT profile of the sample

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ascat.plotGenotypes	<i>ascat.plotGenotypes</i>
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### Description

ascat.plotGenotypes

### Usage

```
ascat.plotGenotypes(ASCATobj, title, Tumor_BAF_noNA, Hom, ch_noNA)
```

### Arguments

ASCATobj	an ASCAT object
title	main title of the plot
Tumor_BAF_noNA	B-allele frequencies of the tumour sample with removed NA values
Hom	Boolean vector denoting homozygous SNPs
ch_noNA	vector of probes per chromosome (NA values excluded)

### Value

plot showing classified BAF per sample, with unused SNPs in green, germline homozygous SNPs in blue and all others in red

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ascat.plotNonRounded	<i>ascat.plotNonRounded</i>
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### Description

ascat.plotNonRounded

### Usage

```
ascat.plotNonRounded(ploidy, rho, goodnessOfFit, nonaberrant, nAfull, nBfull,
  y_limit = 5, ch, bafsegmented, lrr, chrs, textFlag = FALSE)
```

**Arguments**

ploidy	ploidy of the sample
rho	purity of the sample
goodnessOfFit	estimated goodness of fit
nonaberrant	boolean flag denoting non-aberrated samples
nAfull	copy number major allele
nBfull	copy number minor allele
y_limit	Optional parameter determining the size of the y axis in the nonrounded plot and ASCAT profile. Default=5
ch	a list containing c vectors, where c is the number of chromosomes and every vector contains all probe numbers per chromosome
bafsegmented	B Allele Frequency, segmented, in genomic sequence (only probes heterozygous in germline), with probe IDs
lrr	(unsegmented) log R, in genomic sequence (all probes), with probe IDs
chrs	a vector containing the names for the chromosomes (e.g. c(1:22,"X"))
textFlag	Optional flag to add the positions of fragments located outside of the plotting area to the plots. Default=F

**Value**

plot showing the nonrounded copy number profile

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ascat.plotRawData	<i>ascat.plotRawData</i>
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**Description**

Plots SNP array data

**Usage**

```
ascat.plotRawData(ASCATobj)
```

**Arguments**

ASCATobj	an ASCAT object (e.g. data structure from ascat.loadData)
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**Value**

Produces png files showing the logR and BAF values for tumour and germline samples

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`ascat.plotSegmentedData`  
*ascat.plotSegmentedData*

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### Description

plots the SNP array data before and after segmentation

### Usage

```
ascat.plotSegmentedData(ASCATobj)
```

### Arguments

ASCATobj            an ASCAT object (e.g. from `ascat.aspcf`)

### Value

png files showing raw and segmented tumour logR and BAF

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`ascat.plotSunrise`        *ascat.plotSunrise*

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### Description

`ascat.plotSunrise`

### Usage

```
ascat.plotSunrise(d, psi_opt1, rho_opt1)
```

### Arguments

d                    distance matrix for a range of ploidy and tumour percentage values  
 psi\_opt1           optimal ploidy  
 rho\_opt1           optimal aberrant cell fraction

### Value

plot visualising range of ploidy and tumour percentage values

`ascat.predictGermlineGenotypes`*ascat.predictGermlineGenotypes*

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**Description**

predicts the germline genotypes of samples for which no matched germline sample is available

**Usage**

```
ascat.predictGermlineGenotypes(ASCATobj, platform = "AffySNP6")
```

**Arguments**

ASCATobj	an ASCAT object
platform	used array platform

**Details**

Currently possible values for platform:

AffySNP6 (default)  
Custom10k  
Illumina109k  
IlluminaCytoSNP  
Illumina610k  
Illumina660k  
Illumina700k  
Illumina1M  
Illumina2.5M  
IlluminaOmni5  
Affy10k  
Affy100k  
Affy250k\_sty  
Affy250k\_nsp  
AffyOncoScan  
AffyCytoScanHD

**Value**

predicted germline genotypes



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ascat.runAscat	<i>ascat.runAscat</i>
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## Description

ASCAT main function, calculating the allele-specific copy numbers

## Usage

```
ascat.runAscat(ASCATobj, gamma = 0.55, pdfPlot = F, y_limit = 5,
  textFlag = F, circos = NA, rho_manual = NA, psi_manual = NA)
```

## Arguments

ASCATobj	an ASCAT object from ascat.aspcf
gamma	technology parameter, compaction of Log R profiles (expected decrease in case of deletion in diploid sample, 100% aberrant cells; 1 in ideal case, 0.55 of Illumina 109K arrays)
pdfPlot	Optional flag if nonrounded plots and ASCAT profile in pdf format are desired. Default=F
y_limit	Optional parameter determining the size of the y axis in the nonrounded plot and ASCAT profile. Default=5
textFlag	Optional flag to add the positions of fragments located outside of the plotting area to the plots. Default=F
circos	Optional file to output the non-rounded values in Circos track format. Default=NA
rho_manual	optional argument to override ASCAT optimization and supply rho parameter (not recommended)
psi_manual	optional argument to override ASCAT optimization and supply psi parameter (not recommended)

## Details

Note: for copy number only probes, nA contains the copy number value and nB = 0.

## Value

an ASCAT output object, containing:

1. nA: copy number of the A allele
2. nB: copy number of the B allele
3. aberrantcellfraction: the aberrant cell fraction of all arrays
4. ploidy: the ploidy of all arrays
5. failedarrays: arrays on which ASCAT analysis failed
6. nonaberrantarrays: arrays on which ASCAT analysis indicates that they show virtually no aberrations
7. segments: an array containing the copy number segments of each sample (not including failed arrays)
8. segments\_raw: an array containing the copy number segments of each sample without any rounding applied

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runASCAT	<i>runASCAT</i>
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## Description

the ASCAT main function

## Usage

```
runASCAT(lrr, baf, lrrsegmented, bafsegmented, gender, SNPpos, chromosomes,
  chrnames, sexchromosomes, failedqualitycheck = F, distancepng = NA,
  copynumberprofilespng = NA, nonroundedprofilepng = NA,
  aberrationreliabilitypng = NA, gamma = 0.55, rho_manual = NA,
  psi_manual = NA, pdfPlot = F, y_limit = 5, textFlag = F,
  circos = NA)
```

## Arguments

lrr	(unsegmented) log R, in genomic sequence (all probes), with probe IDs
baf	(unsegmented) B Allele Frequency, in genomic sequence (all probes), with probe IDs
lrrsegmented	log R, segmented, in genomic sequence (all probes), with probe IDs
bafsegmented	B Allele Frequency, segmented, in genomic sequence (only probes heterozygous in germline), with probe IDs
gender	a vector of gender for each cases ("XX" or "XY"). Default = NULL: all female ("XX")
SNPpos	position of all SNPs
chromosomes	a list containing c vectors, where c is the number of chromosomes and every vector contains all probe numbers per chromosome
chrnames	a vector containing the names for the chromosomes (e.g. c(1:22,"X"))
sexchromosomes	a vector containing the names for the sex chromosomes
failedqualitycheck	did the sample fail any previous quality check or not?
distancepng	if NA: distance is plotted, if filename is given, the plot is written to a .png file
copynumberprofilespng	if NA: possible copy number profiles are plotted, if filename is given, the plot is written to a .png file
nonroundedprofilepng	if NA: copy number profile before rounding is plotted (total copy number as well as the copy number of the minor allele), if filename is given, the plot is written to a .png file
aberrationreliabilitypng	if NA: aberration reliability score is plotted, if filename is given, the plot is written to a .png file
gamma	technology parameter, compaction of Log R profiles (expected decrease in case of deletion in diploid sample, 100% aberrant cells; 1 in ideal case, 0.55 of Illumina 109K arrays)

rho_manual	optional argument to override ASCAT optimization and supply rho parameter (not recommended)
psi_manual	optional argument to override ASCAT optimization and supply psi parameter (not recommended)
pdfPlot	Optional flag if nonrounded plots and ASCAT profile in pdf format are desired. Default=F
y_limit	Optional parameter determining the size of the y axis in the nonrounded plot and ASCAT profile. Default=5
textFlag	Optional flag to add the positions of fragments located outside of the plotting area to the plots. Default=F
circos	Optional file to output the non-rounded values in Circos track format. Default=NA

**Value**

a list containing optimal purity and ploidy

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