

# Package ‘ASCAT’

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**Type** Package

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

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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

**RoxygenNote** 5.0.1

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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
```

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```

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**Description**

Function plotting the rounded ASCAT profiles over all chromosomes

**Usage**

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

**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
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

**Value**

plot showing the ASCAT profile of the sample

---

```
ascat.plotGenotypes
```

*ascat.plotGenotypes*

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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
```

*ascat.plotNonRounded*

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## Description

Function plotting the unrounded ASCAT copy number over all chromosomes

## Usage

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

## 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
bafsegmented	B Allele Frequency, segmented, in genomic sequence (only probes heterozygous in germline), with probe IDs
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

**Value**

plot showing the nonrounded copy number profile, using base plotting function

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`ascat.plotRawData`    *ascat.plotRawData*

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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`)

**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, minim = T)
```

## Arguments

d	distance matrix for a range of ploidy and tumour percentage values
psi_opt1	optimal ploidy
rho_opt1	optimal aberrant cell fraction
minim	when set to true, optimal regions in the sunrise plot are depicted in blue; if set to false, colours are inverted and red corresponds to optimal values (default: TRUE)

## Value

plot visualising range of ploidy and tumour percentage values

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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  
 HumanCNV370quad  
 HumanCore12  
 HumanCoreExome24  
 HumanOmniExpress12

## Value

predicted germline genotypes

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<code>ascat.runAscat</code>	<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,
  circos = NA, rho_manual = NA, psi_manual = NA)
```

## Arguments

<code>ASCATobj</code>	an ASCAT object from <code>ascat.aspcf</code>
<code>gamma</code>	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)
<code>pdfPlot</code>	Optional flag if nonrounded plots and ASCAT profile in pdf format are desired. Default=F
<code>y_limit</code>	Optional parameter determining the size of the y axis in the nonrounded plot and ASCAT profile. Default=5



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