

# Package ‘ClonalSim’

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**Type** Package

**Title** Simulation of Tumor Clonal Evolution with Realistic Sequencing Noise

**Version** 1.0.0

**Description** ClonalSim generates realistic mutational profiles of tumor samples with hierarchical clonal structure. It simulates founder, shared, and private mutations with biologically realistic noise models including intra-tumor heterogeneity (Beta distribution) and technical sequencing noise (negative binomial depth variation, binomial read sampling, base errors). The package is designed for benchmarking variant callers, testing clonal deconvolution algorithms, and teaching tumor heterogeneity concepts.

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ClonalSim-package	<i>ClonalSim: Simulation of Tumor Clonal Evolution with Realistic Sequencing Noise</i>
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## Description

ClonalSim generates realistic mutational profiles of tumor samples with hierarchical clonal structure. It simulates founder, shared, and private mutations with biologically realistic noise models including intra-tumor heterogeneity (Beta distribution) and technical sequencing noise (negative binomial depth variation, binomial read sampling, base errors). The package is designed for benchmarking variant callers, testing clonal deconvolution algorithms, and teaching tumor heterogeneity concepts.

ClonalSim generates realistic mutational profiles of tumor samples with hierarchical clonal structure. It simulates founder, shared, and private mutations with biologically realistic noise models.

## Details

The package implements a two-stage noise model:

### 1. Biological Noise (Intra-Tumor Heterogeneity):

- Uses Beta distribution (more realistic than Gaussian for frequencies)
- Models spatial/temporal heterogeneity within tumor
- Configurable concentration parameter controls variability

### 2. Technical Sequencing Noise:

- **Depth overdispersion:** Negative binomial distribution (models GC bias, mappability, PCR artifacts)
- **Stochastic read sampling:** Binomial distribution (each read independently sampled)
- **Base calling errors:** Illumina-like error rates

## Main Functions

- `simulateTumor`: Main simulation function
- `ClonalSimData`: S4 class for results
- `toGRanges`: Export to GenomicRanges
- `toVCF`: Export to VCF format
- `toPyClone`: Export for PyClone analysis
- `toSciClone`: Export for SciClone analysis

## Use Cases

- **Benchmarking:** Test variant callers and mutation detection pipelines
- **Algorithm Development:** Test clonal deconvolution algorithms
- **Education:** Teach tumor heterogeneity concepts
- **Method Validation:** Positive controls for analysis pipelines

## Author(s)

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## References

- McGranahan N, Swanton C. Clonal Heterogeneity and Tumor Evolution: Past, Present, and the Future. *Cell*. 2017.
- Dentro SC, Wedge DC, Van Loo P. Principles of Reconstructing the Subclonal Architecture of Cancers. *Cold Spring Harb Perspect Med*. 2017.
- Roth A, et al. PyClone: statistical inference of clonal population structure in cancer. *Nat Methods*. 2014.
- Miller CA, et al. SciClone: inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution. *PLoS Comput Biol*. 2014.

## See Also

Useful links:

- <https://github.com/gbucci/ClonalSim>
- Report bugs at <https://github.com/gbucci/ClonalSim/issues>

## Examples

```
# Basic simulation
sim <- simulateTumor()
sim

# Access results
mutations <- getMutations(sim)
head(mutations)

# Visualize
plot(sim, type = "vaf_density")

# Export to Bioconductor
gr <- toGRanges(sim)

# Custom simulation: low purity tumor
sim_low_purity <- simulateTumor(
  subclone_freqs = c(0.1, 0.15, 0.15), # 40% purity
  n_mut_per_clone = c(20, 25, 30)
)

# High coverage sequencing
sim_deep <- simulateTumor(
  subclone_freqs = c(0.3, 0.4, 0.3),
  n_mut_per_clone = c(30, 40, 30),
  sequencing_noise = list(mean_depth = 500, depth_dispersion = 100)
)
```

---

applyBiologicalNoise *Apply biological noise using Beta distribution*

---

## Description

Simulates intra-tumor heterogeneity using a Beta distribution. The Beta distribution is more realistic than Gaussian for frequency data as it is naturally bounded between 0 and 1.

## Usage

```
applyBiologicalNoise(true_freq, n_mutations, concentration = 50)
```

**Arguments**

true\_freq        numeric, the true allele frequency (0-1)  
n\_mutations      integer, number of mutations to generate  
concentration    numeric, concentration parameter for Beta distribution (alpha + beta). Higher values = less variability. Default: 50

**Details**

For a clone with true frequency  $f$ , VAF values are sampled from  $\text{Beta}(\alpha, \beta)$  where:

- $\alpha = f * \text{concentration}$
- $\beta = (1-f) * \text{concentration}$

Higher concentration values result in VAF closer to the expected frequency, while lower values increase spread, simulating spatial/temporal heterogeneity.

**Value**

numeric vector of VAF values with biological noise

**Examples**

```
# Generate 100 mutations with true frequency 0.3 and moderate heterogeneity
vaf <- applyBiologicalNoise(0.3, 100, concentration = 50)
hist(vaf, main = "VAF with biological noise", xlab = "VAF")

# High heterogeneity (low concentration)
vaf_high_het <- applyBiologicalNoise(0.3, 100, concentration = 20)

# Low heterogeneity (high concentration)
vaf_low_het <- applyBiologicalNoise(0.3, 100, concentration = 100)
```

---

ClonalSimData

*Constructor for ClonalSimData*

---

**Description**

Constructor for ClonalSimData

**Usage**

```
ClonalSimData(  
  mutations = data.frame(),  
  params = list(),  
  clonal_structure = data.frame(),  
  metadata = list()  
)
```

**Arguments**

mutations	data.frame with mutation data
params	list with simulation parameters
clonal_structure	data.frame with clone hierarchy
metadata	list with additional metadata

**Value**

ClonalSimData object

**Examples**

```
# Typically created by simulateTumor(), but can be constructed manually
mutations <- data.frame(
  Mutation = "mut1",
  Chromosome = "chr1",
  Position = 1000000,
  Ref = "A",
  Alt = "T",
  True_VAF = 0.5,
  VAF = 0.48,
  Depth = 100,
  Alt_reads = 48,
  Clone = "Clone1",
  Type = "private"
)
params <- list(subclone_freqs = c(0.5))
sim_data <- ClonalSimData(mutations = mutations, params = params)
```

---

ClonalSimData-class    *ClonalSimData Class*

---

**Description**

S4 class to store results from tumor clonal evolution simulation

**Arguments**

object	ClonalSimData object
--------	----------------------

**Value**

TRUE if valid, otherwise error message

**Slots**

mutations data.frame containing mutation information with columns: Mutation, Chromosome, Position, Ref, Alt, True\_VAF, VAF, Depth, Alt\_reads, Clone, Type, Clone\_IDs  
params list containing simulation parameters: subclone\_freqs, n\_mut\_per\_clone, n\_mut\_founder, n\_mut\_shared, biological\_noise, sequencing\_noise  
clonal\_structure data.frame defining hierarchical clone relationships  
metadata list containing additional metadata (date, version, seed)

**Examples**

```
# Create a simple simulation
sim <- simulateTumor(
  subclone_freqs = c(0.3, 0.4, 0.3),
  n_mut_per_clone = c(30, 40, 30)
)

# Access mutations
head(getMutations(sim))

# Access parameters
getSimParams(sim)
```

---

getClonalStructure	<i>Get clonal structure</i>
--------------------	-----------------------------

---

**Description**

Get clonal structure

**Usage**

```
getClonalStructure(object)
```

**Arguments**

object            ClonalSimData object

**Value**

data.frame defining clone hierarchy

**Examples**

```
sim <- simulateTumor()
structure <- getClonalStructure(sim)
print(structure)
```

---

`getMetadata`*Get metadata*

---

**Description**

Get metadata

**Usage**

```
getMetadata(object)
```

**Arguments**

`object` ClonalSimData object

**Value**

list with metadata

**Examples**

```
sim <- simulateTumor()
metadata <- getMetadata(sim)
metadata$date
```

---

`getMutations`*Get mutations data frame*

---

**Description**

Get mutations data frame

**Usage**

```
getMutations(object)
```

**Arguments**

`object` ClonalSimData object

**Value**

data.frame with mutation information

**Examples**

```
sim <- simulateTumor()  
mutations <- getMutations(sim)  
head(mutations)
```

---

*getObservedVAF*                      *Get observed VAF values (with sequencing noise)*

---

**Description**

Get observed VAF values (with sequencing noise)

**Usage**

```
getObservedVAF(object)
```

**Arguments**

object                      ClonalSimData object

**Value**

numeric vector of observed VAF values

**Examples**

```
sim <- simulateTumor()  
obs_vaf <- getObservedVAF(sim)  
summary(obs_vaf)
```

---

*getSimParams*                      *Get simulation parameters*

---

**Description**

Get simulation parameters

**Usage**

```
getSimParams(object)
```

**Arguments**

object                      ClonalSimData object

**Value**

list with simulation parameters

**Examples**

```
sim <- simulateTumor()
params <- getSimParams(sim)
params$subclone_freqs
```

---

getTrueVAF

*Get true VAF values (biological, without sequencing noise)*

---

**Description**

Get true VAF values (biological, without sequencing noise)

**Usage**

```
getTrueVAF(object)
```

**Arguments**

object            ClonalSimData object

**Value**

numeric vector of true VAF values

**Examples**

```
sim <- simulateTumor()
true_vaf <- getTrueVAF(sim)
summary(true_vaf)
```

---

plot, ClonalSimData, missing-method  
*Plot method for ClonalSimData*

---

## Description

Plot method for ClonalSimData

## Usage

```
## S4 method for signature 'ClonalSimData,missing'  
plot(x, y, type = "vaf_density", ...)
```

## Arguments

x	ClonalSimData object
y	unused (for S4 compatibility)
type	character indicating plot type: "vaf_density", "vaf_scatter", "depth_histogram", "clone_matrix". Default is "vaf_density"
...	additional arguments passed to plotting functions

## Details

Note: You need to load ggplot2 explicitly before using plot(): `library(ggplot2)`

## Value

ggplot2 object

## Examples

```
library(ggplot2)  
sim <- simulateTumor()  
plot(sim, type = "vaf_density")  
plot(sim, type = "vaf_scatter")
```

---

```
print.summary.ClonalSimData
```

*Print summary method*

---

**Description**

Print summary method

**Usage**

```
## S3 method for class 'summary.ClonalSimData'  
print(x, ...)
```

**Arguments**

x	summary.ClonalSimData object
...	additional arguments (unused)

**Value**

NULL (prints to console)

---

```
show.ClonalSimData-method
```

*Show method for ClonalSimData*

---

**Description**

Show method for ClonalSimData

**Usage**

```
## S4 method for signature 'ClonalSimData'  
show(object)
```

**Arguments**

object	ClonalSimData object
--------	----------------------

**Value**

NULL (prints to console)

**Examples**

```
sim <- simulateTumor()  
show(sim)
```

---

simulateDepth	<i>Simulate realistic sequencing depth</i>
---------------	--

---

### Description

Simulates sequencing coverage with realistic overdispersion using negative binomial distribution, which better captures real NGS variability compared to Poisson.

### Usage

```
simulateDepth(  
  n_mutations,  
  mean_depth = 100,  
  distribution = "negative_binomial",  
  dispersion = 20  
)
```

### Arguments

n_mutations	integer, number of mutations
mean_depth	numeric, mean sequencing coverage. Default: 100
distribution	character, distribution type: "negative_binomial" (realistic, default), "poisson" (simpler), or "uniform" (for testing)
dispersion	numeric, size parameter for negative binomial. Lower values = more variable coverage. Default: 20

### Details

The negative binomial distribution allows overdispersion (variance > mean), which occurs in real sequencing due to:

- GC content bias
- Mappability differences
- PCR amplification artifacts

The dispersion parameter controls variability: lower values produce more variable coverage across positions.

### Value

integer vector of depth values

## Examples

```
# Realistic depth with overdispersion
depth_realistic <- simulateDepth(1000, mean_depth = 100, dispersion = 20)
hist(depth_realistic, main = "Realistic depth", xlab = "Depth")

# More variable coverage (low dispersion)
depth_variable <- simulateDepth(1000, mean_depth = 100, dispersion = 10)

# Uniform coverage (for testing)
depth_uniform <- simulateDepth(1000, mean_depth = 100, distribution = "uniform")
```

---

simulateSequencingReads

*Simulate sequencing reads with binomial sampling*

---

## Description

Simulates stochastic read counts using binomial distribution, which models the independent sampling of each sequencing read.

## Usage

```
simulateSequencingReads(true_vaf, depth, error_rate = 0.001)
```

## Arguments

true_vaf	numeric vector, true variant allele frequencies
depth	integer vector, sequencing depth at each position
error_rate	numeric, base miscall rate (0-1). Default: 0.001 (0.1 typical for Illumina)

## Details

Each sequencing read is independently sampled from the DNA pool. Given a true VAF and depth  $D$ , the number of alternative reads follows a binomial distribution:  $\text{alt\_reads} \sim \text{Binomial}(D, \text{VAF})$ .

This introduces natural sampling variation, with higher uncertainty at:

- Low sequencing depth
- Low variant frequency

The `error_rate` parameter simulates base miscalls from sequencer optical/ chemistry errors.

## Value

list with three components:

- `vaf`: observed VAF values
- `alt_reads`: alternative allele read counts
- `ref_reads`: reference allele read counts

**Examples**

```
# Simulate reads for mutations at VAF 0.3 with depth 100
true_vaf <- rep(0.3, 100)
depth <- rep(100, 100)
reads <- simulateSequencingReads(true_vaf, depth)

# Observed VAF varies due to sampling
hist(reads$vaf, main = "Observed VAF", xlab = "VAF")
abline(v = 0.3, col = "red", lty = 2)

# Check alt_reads distribution
hist(reads$alt_reads, main = "Alt read counts", xlab = "Alt reads")
```

---

simulateTumor

*Simulate tumor clonal evolution with realistic noise*


---

**Description**

Main function to simulate a heterogeneous tumor sample with hierarchical clonal structure, including realistic biological and technical sequencing noise.

**Usage**

```
simulateTumor(
  subclone_freqs = c(0.15, 0.25, 0.3, 0.3),
  n_mut_per_clone = c(20, 25, 30, 15),
  n_mut_founder = 10,
  n_mut_shared = list(`2 3 4` = 15, `3 4` = 12, `1 2` = 8),
  biological_noise = list(enabled = TRUE, concentration = 50),
  sequencing_noise = list(enabled = TRUE, mean_depth = 100, depth_variation =
    "negative_binomial", depth_dispersion = 20, error_rate = 0.001, binomial_sampling =
    TRUE),
  germline_variants = list(enabled = FALSE, n_variants = 50, vaf_expected = 0.5)
)
```

**Arguments**

**subclone\_freqs** numeric vector, frequencies of each subclone (must sum to  $\leq 1$ ). Default: c(0.15, 0.25, 0.30, 0.30)

**n\_mut\_per\_clone** integer vector, number of private mutations per clone. Default: c(20, 25, 30, 15)

**n\_mut\_founder** integer, number of founder mutations (present in all clones). Default: 10

**n\_mut\_shared** named list, shared mutations between clone groups. Names indicate which clones (e.g., "2 3 4"), values are mutation counts. Default: list("2 3 4" = 15, "3 4" = 12, "1 2" = 8)

**biological\_noise**

list with biological noise parameters:

- enabled: logical, enable biological noise (default: TRUE)
- concentration: numeric, Beta distribution concentration (default: 50)

**sequencing\_noise**

list with sequencing noise parameters:

- enabled: logical, enable sequencing noise (default: TRUE)
- mean\_depth: numeric, average coverage (default: 100)
- depth\_variation: character, distribution type (default: "negative\_binomial")
- depth\_dispersion: numeric, dispersion parameter (default: 20)
- error\_rate: numeric, base miscall rate (default: 0.001)
- binomial\_sampling: logical, use binomial sampling (default: TRUE)

**germline\_variants**

list with germline variant parameters:

- enabled: logical, include germline variants (default: FALSE)
- n\_variants: integer, number of germline variants to simulate (default: 50)
- vaf\_expected: numeric, expected VAF for heterozygous germline (default: 0.5)

Germline variants will have VAF adjusted by tumor purity:  $\text{observed\_VAF} = \text{germline\_vaf} * \text{tumor\_purity} + 0.5 * (1 - \text{tumor\_purity})$

**Value**

ClonalSimData object containing mutations, parameters, and metadata

**Examples**

```
# Basic simulation with default parameters
sim <- simulateTumor()
show(sim)
plot(sim)

# Custom clonal structure
sim <- simulateTumor(
  subclone_freqs = c(0.2, 0.3, 0.5),
  n_mut_per_clone = c(30, 40, 30)
)

# Low purity tumor (40% purity)
sim <- simulateTumor(
  subclone_freqs = c(0.1, 0.15, 0.15),
  n_mut_per_clone = c(20, 25, 30)
)

# High coverage sequencing
sim <- simulateTumor(
  sequencing_noise = list(
    enabled = TRUE,
```

```
    mean_depth = 500,  
    depth_dispersion = 100  
  )  
)  
  
# No noise (ideal data for testing)  
sim <- simulateTumor(  
  biological_noise = list(enabled = FALSE),  
  sequencing_noise = list(enabled = FALSE)  
)  
  
# Include germline variants  
sim <- simulateTumor(  
  subclone_freqs = c(0.3, 0.4), # 70% purity  
  n_mut_per_clone = c(40, 50),  
  germline_variants = list(enabled = TRUE, n_variants = 100)  
)
```

---

summary,ClonalSimData-method

*Summary method for ClonalSimData*

---

## Description

Summary method for ClonalSimData

## Usage

```
## S4 method for signature 'ClonalSimData'  
summary(object)
```

## Arguments

object            ClonalSimData object

## Value

list with summary statistics

## Examples

```
sim <- simulateTumor()  
summary(sim)
```

toDataFrame

*Export mutation data to data frame*

---

**Description**

Simple export to data.frame (useful for compatibility with other tools like PyClone, SciClone)

**Usage**

```
toDataFrame(object, file = NULL, include_true_vaf = TRUE)
```

**Arguments**

object            ClonalSimData object  
file              character, optional file path to write CSV. Default: NULL  
include\_true\_vaf   logical, include True\_VAF column. Default: TRUE

**Value**

data.frame with mutation data

**Examples**

```
sim <- simulateTumor()
df <- toDataFrame(sim)
head(df)

# Export to CSV (use tempdir to avoid writing to user's filesystem)
csv_file <- tempfile(fileext = ".csv")
toDataFrame(sim, file = csv_file)
```

---

toGRanges*Convert ClonalSimData to GRanges object*

---

**Description**

Converts mutation data to a GenomicRanges::GRanges object, the standard Bioconductor data structure for genomic intervals.

**Usage**

```
toGRanges(object, include_metadata = TRUE)
```

**Arguments**

object            ClonalSimData object  
 include\_metadata       logical, include all metadata columns. Default: TRUE

**Value**

GRanges object with mutation information

**Examples**

```
sim <- simulateTumor()
gr <- toGRanges(sim)
print(gr)

# Access metadata columns
GenomicRanges::mcols(gr)

# Subset by chromosome
gr_chr1 <- gr[GenomicRanges::seqnames(gr) == "chr1"]
```

---

toPyClone	<i>Convert to PyClone input format</i>
-----------	--

---

**Description**

Exports data in format suitable for PyClone clonal deconvolution analysis.

**Usage**

```
toPyClone(object, file, sample_id = "sample1")
```

**Arguments**

object            ClonalSimData object  
 file             character, file path to write TSV  
 sample\_id        character, sample identifier. Default: "sample1"

**Value**

data.frame formatted for PyClone (invisibly)

**Examples**

```
sim <- simulateTumor()
pyclone_file <- tempfile(fileext = ".tsv")
toPyClone(sim, file = pyclone_file)
```

---

toSciClone	<i>Convert to SciClone input format</i>
------------	---

---

**Description**

Exports data in format suitable for SciClone clonal analysis.

**Usage**

```
toSciClone(object, file)
```

**Arguments**

object	ClonalSimData object
file	character, file path to write TSV

**Value**

data.frame formatted for SciClone (invisibly)

**Examples**

```
sim <- simulateTumor()
sciclone_file <- tempfile(fileext = ".tsv")
toSciClone(sim, file = sciclone_file)
```

---

toVCF	<i>Convert ClonalSimData to VCF format</i>
-------	--

---

**Description**

Exports mutation data to Variant Call Format (VCF), the standard format for variant data. Returns a VariantAnnotation::VRanges object which can be written to VCF file.

**Usage**

```
toVCF(object, sample_name = "TumorSample", output_file = NULL)
```

**Arguments**

object	ClonalSimData object
sample_name	character, sample name for VCF. Default: "TumorSample"
output_file	character, optional file path to write VCF. If NULL, returns VRanges object without writing. Default: NULL

**Value**

VRanges object (invisibly if `output_file` is specified)

**Examples**

```
sim <- simulateTumor()

# Get VRanges object
vr <- suppressWarnings(toVCF(sim))
print(vr)

# Write to VCF file (use tempdir to avoid writing to user's filesystem)
vcf_file <- tempfile(fileext = ".vcf")
suppressWarnings(toVCF(sim, output_file = vcf_file))
```

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