

# Package ‘UPDhmm’

December 11, 2024

**Title** Detecting Uniparental Disomy through NGS trio data

**Version** 1.3.0

**BugReports** <https://github.com/martasevilla/UPDhmm/issues>

**Description** Uniparental disomy (UPD) is a genetic condition where an individual inherits both copies of a chromosome or part of it from one parent, rather than one copy from each parent. This package contains a HMM for detecting UPDs through HTS (High Throughput Sequencing) data from trio assays. By analyzing the genotypes in the trio, the model infers a hidden state (normal, father isodisomy, mother isodisomy, father heterodisomy and mother heterodisomy).

**biocViews** Software, HiddenMarkovModel, Genetics

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**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 7.3.1

**Depends** R (>= 4.3.0)

**Imports** HMM, utils, VariantAnnotation, GenomicRanges, S4Vectors, IRanges, stats

**Suggests** knitr, testthat (>= 2.1.0), BiocStyle, rmarkdown, markdown, karyoploteR, regioneR, dplyr

**VignetteBuilder** knitr

**Roxygen** list(markdown = TRUE)

**URL** <https://github.com/martasevilla/UPDhmm>

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UPDhmm-package	<i>UPDhmm: Detecting Uniparental Disomy through NGS trio data</i>
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## Description

Uniparental disomy (UPD) is a genetic condition where an individual inherits both copies of a chromosome or part of it from one parent, rather than one copy from each parent. This package contains a HMM for detecting UPDs through HTS (High Throughput Sequencing) data from trio assays. By analyzing the genotypes in the trio, the model infers a hidden state (normal, father isodisomy, mother isodisomy, father heterodisomy and mother heterodisomy).

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## See Also

Useful links:

- <https://github.com/martasevilla/UPDhmm>
- Report bugs at <https://github.com/martasevilla/UPDhmm/issues>

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addOr	<i>Function to transform a large collapsed VCF into a dataframe, incorporating predicted states along with the log-likelihood ratio and p-value.</i>
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**Description**

Function to transform a large collapsed VCF into a dataframe, incorporating predicted states along with the log-likelihood ratio and p-value.

**Usage**

```
addOr(filtered_def_blocks_states, largeCollapsedVcf, hmm, genotypes)
```

**Arguments**

filtered_def_blocks_states	data.frame object containing the blocks
largeCollapsedVcf	Input VCF file
hmm	Hidden Markov Model used to infer the events. The format should adhere to the general HMM format from HMM package with a series of elements: <ol style="list-style-type: none"> <li>1. The hidden states names in the "States" vector.</li> <li>2. All possible observations in the "Symbols" vector.</li> <li>3. Start probabilities of every hidden state in the "startProbs" vector.</li> <li>4. Transition probabilities matrix of the hidden states in "transProbs".</li> <li>5. Probabilities associated between every hidden state and all possible observations in the "emissionProbs" matrix.</li> </ol>
genotypes	Possible GT formats and its correspondence with the hmm

**Value**

data.frame containing the transformed information.

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applyViterbi	<i>Apply the hidden Markov model using the Viterbi algorithm.</i>
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**Description**

Apply the hidden Markov model using the Viterbi algorithm.

**Usage**

```
applyViterbi(largeCollapsedVcf, hmm, genotypes)
```

**Arguments**

largeCollapsedVcf	input vcf file
hmm	Hidden Markov Model used to infer the events
genotypes	Possible GT formats and its correspondence with the hmm

**Value**

largeCollapsedVcf

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asDfVcf	<i>Function to transform a large collapsed VCF into a dataframe with predicted states, including chromosome, start position, end position and metadata.</i>
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**Description**

Function to transform a large collapsed VCF into a dataframe with predicted states, including chromosome, start position, end position and metadata.

**Usage**

```
asDfVcf(largeCollapsedVcf, genotypes)
```

**Arguments**

largeCollapsedVcf	Name of the large collapsed VCF file.
genotypes	Possible GT formats and its correspondence with the hmm

**Value**

dataframe

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blocksVcf	<i>Function to simplify contiguous variants with the same state into blocks.</i>
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**Description**

Function to simplify contiguous variants with the same state into blocks.

**Usage**

```
blocksVcf(df)
```

**Arguments**

df                    data.frame resulting from the as\_df\_vcf function.

**Value**

data.frame containing information on the chromosome, start #' position of the block, end position of the block, and predicted state.

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calculateEvents	<i>Calculate UPD events in trio VCFs.</i>
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**Description**

This function predicts the hidden states by applying the Viterbi algorithm using the Hidden Markov Model (HMM) from the UPDhmm package. It takes the genotypes of the trio as input and includes a final step to simplify the results into blocks.

**Usage**

```
calculateEvents(largeCollapsedVcf, hmm = NULL)
```

**Arguments**

largeCollapsedVcf

The VCF file in the general format (largeCollapsedVcf) with VariantAnnotation package. Previously edited with vcfCheck() function from UPDhmm package

hmm

Default = NULL. If no arguments are added, the package will use the default HMM already implemented, based on Mendelian inheritance. If an optional HMM is desired, it should adhere to the general HMM format from HMM package with the following elements inside a list:

1. The hidden state names in the "States" vector.
2. All possible observations in the "Symbols" vector.

3. Start probabilities of every hidden state in the "startProbs" vector.
4. Transition probabilities matrix between states in "transProbs".
5. Probabilities associated between every hidden state and all possible observations in the "emissionProbs" matrix.

### Value

A data.frame object containing all detected events in the provided trio. If no events are found, the function will return an empty data.frame.

### Examples

```
file <- system.file(package = "UPDhmm", "extdata", "test_het_mat.vcf.gz")
vcf <- VariantAnnotation::readVcf(file)
processedVcf <- vcfCheck(vcf,
  proband = "NA19675", mother = "NA19678",
  father = "NA19679"
)
```

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hmm

*HMM data for predicting UPD events in trio genomic data*

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### Description

This dataset provides Hidden Markov Model (HMM) parameters for predicting uniparental disomy (UPD) events in trio genomic data.

**states** Five different possible states.

**symbols** Code symbols used for genotype combinations.

**startProbs** The initial probabilities of each state.

**transProbs** Probabilities of transitioning from one state to another.

**emissionProbs** Given a certain genotype combination, the odds of each possible state.

### Usage

```
data(hmm)
```

### Format

A list with 5 different elements

### Source

Created in-house based on basic Mendelian rules for calculating UPD events.

### Examples

```
data(hmm)
```

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vcfCheck	<i>Check quality parameters (optional) and change IDs.</i>
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### Description

This function takes a VCF file and converts it into a `largeCollapsedVcf` object using the `VariantAnnotation` package. It also rename the sample for subsequent steps needed in `UPDhmm` package. Additionally, it features an optional parameter, `quality_check`, which triggers warnings when variants lack sufficient quality based on RD and GQ parameters in the input VCF.

### Usage

```
vcfCheck(largeCollapsedVcf, father, mother, proband, check_quality = FALSE)
```

### Arguments

<code>largeCollapsedVcf</code>	The file in <code>largeCollapsedVcf</code> format.
<code>father</code>	Name of the father's sample.
<code>mother</code>	Name of the mother's sample.
<code>proband</code>	Name of the proband's sample.
<code>check_quality</code>	Optional argument. TRUE/FALSE. If quality parameters want to be measured. Default = FALSE

### Value

`largeCollapsedVcf` (VariantAnnotation VCF format).

### Examples

```
f1 <- system.file("extdata", "test_het_mat.vcf.gz", package = "UPDhmm")
vcf <- VariantAnnotation::readVcf(f1)
processedVcf <-
  vcfCheck(vcf, proband = "Sample1", mother = "Sample3", father = "Sample2")
```

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