R documentation

of 'MethylTransition/man/MethylCalculation.Rd'

December 20, 2018

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Description

Calculate the ratio of each methylation class after n cell cycle(s).

Usage

```
MethylCalculation(original_classes, u, d, p, cell_cycle = 1)
```

Arguments

original_classes

The original methylation classes

u The paramater that describing the methylation probablity on CpG site

d The paramater that describing the de-methylation probablity on 5mCpG site

The paramater that describing the methylation probablity on semi-CpG site

cell_cycle The cell cycle times

total The total genes when do the calculation loops The loop times for the calculation

Details

The transition matrix of this model describes the changes of DNA methylation during one cell cycle in three steps: passive demethylation by DNA replication, active DNA methylation changes affected by DNA methylation-modifying enzymes and DNA methylation combinations during homologous recombination. For each CpG site in a chromsome, the methylation states are one of these four types: 0-0, 0-1, 1-0, 1-1. The transition matrix after DNA replication would be:

	original(0-0)	original(0-1)	original(1-0)	original(1-1)
after_replication(0-0)	1	a	1-a	0
after_replication(0-1)	0	1-a	0	1-a
after_replication(1-0)	0	0	0	a
after_replication(1-1)	0	0	0	0

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among this matrix ,a is the methylation change probability with DNA replication and equal to 0.5. Then the transition matrix after active DNA methylation changes would be:

	after_replication(0-0)	after_replication(0-1)	after_replication(1-0)
after_enzymemodifying(0-0)	$(1-u)\times(1-u)$	$(1 - u - p + u \times p) \times d$	$d \times (1 - u - p + u \times p)$
after_enzymemodifying(0-1)	$u \times (1-u)$	$(1 - u - p + u \times p) \times (1 - d)$	$d \times (u + p - u \times p)$
after_enzymemodifying(1-0)	$u \times (1-u)$	$(u+p-u\times p)\times d$	$(1-d)\times(1-u-p+u\times p)$
after_enzymemodifying(1-1)	$u \times u$	$(u+p-u\times p)\times (1-d)$	$(1-d)\times(u+p-u\times p)$

The paramater u described the methylation probablity on CpG site. The paramater d described the de-methylation probablity on 5mCpG site. The paramater p described the methylation probablity on semi-CpG site. Thus the mathlation state change is $P = Penzymemodifying \cdot Preplication \cdot original_classes$ We using $t_{i,j}$ represent the i and j vector of the matrix $Penzymemodifying \cdot Preplication$. Then two chromsomes are combined during homologous recombination. The observed DNA methylation of each CpG site is the combination of the methylation types in both chromsomes. The observed transition matrix would be:

	original_class1(0)	original_class2(1/4)	original_class3(1/2)	original_class4(3/4)	ori
terminational_class1(0)	$x_{1,1}$	$x_{1,2}$	$x_{1,3}$	$x_{1,4}$	
terminational_class2(1/4)	$x_{2,1}$	$x_{2,2}$	$x_{2,3}$	$x_{2,4}$	
terminational_class3(1/2)	$x_{3,1}$	$x_{3,2}$	$x_{3,3}$	$x_{3,4}$	
terminational_class4(3/4)	$x_{4,1}$	$x_{4,2}$	$x_{4,3}$	$x_{4,4}$	
terminational_class5(1)	$x_{5,1}$	$x_{5,2}$	$x_{5,3}$	$x_{5,4}$	

and

$$x_{1,1} = t_{1,1} \times t_{1,1}$$

$$x_{1,2} = 1/4 \times (t_{1,1} \times t_{1,2} + t_{1,1} \times t_{1,3} + t_{1,2} \times t_{1,1} + t_{1,3} \times t_{1,1})$$

$$x_{1,3} = 1/6 \times (t_{1,1} \times t_{1,4} + t_{1,2} \times t_{1,2} + t_{1,2} \times t_{1,3} + t_{1,3} \times t_{1,2} + t_{1,3} \times t_{1,3} + t_{1,4} \times t_{1,1})$$

$$x_{1,4} = 1/4 \times (t_{1,2} \times t_{1,4} + t_{1,3} \times t_{1,4} + t_{1,4} \times t_{1,2} + t_{1,4} \times t_{1,3})$$

$$x_{1,5} = t_{1,4} \times t_{1,4}$$

$$x_{2,1} = t_{1,1} \times t_{2,1} + t_{1,1} \times t_{3,1} + t_{2,1} \times t_{1,1} + t_{3,1} \times t_{1,1}$$

$$x_{2,2} = 1/4 \times (t_{1,1} \times t_{2,2} + t_{1,1} \times t_{2,3} + t_{1,2} \times t_{2,1} + t_{1,3} \times t_{2,1} + t_{1,1} \times t_{3,3} + t_{1,2} \times t_{3,1} + t_{1,3} \times t_{3,1} + t_{2,1} \times t_{1,2} + t_{2,1} \times t_{2,3}$$

$$x_{2,3} = 1/6 \times (t_{1,1} \times t_{2,4} + t_{1,2} \times t_{2,2} + t_{1,2} \times t_{2,3} + t_{1,3} \times t_{2,2} + t_{1,3} \times t_{2,3} + t_{1,4} \times t_{2,3} + t_{1,4} \times t_{3,4} + t_{1,4} \times t_{3,4} + t_{1,2} \times t_{3,3} + t_{1,4} \times t_{3,4} + t_{4,4} \times t_{4,4} + t_{4,4$$

 $x_{4,1} = t_{2,1} \times t_{4,1} + t_{3,1} \times t_{4,1} + t_{4,1} \times t_{2,1} + t_{4,1} \times t_{3,1}$

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$$x_{4,2} = 1/4 \times (t_{2,1} \times t_{4,2} + t_{2,1} \times t_{4,3} + t_{2,2} \times t_{4,1} + t_{2,3} \times t_{4,1} + t_{3,1} \times t_{4,2} + t_{3,1} \times t_{4,3} + t_{3,2} \times t_{4,1} + t_{3,3} \times t_{4,1} + t_{4,1} \times t_{2,2} + t_{4,1} \times t_{4,3} = 1/6 \times (t_{2,1} \times t_{4,4} + t_{2,2} \times t_{4,2} + t_{2,3} \times t_{4,2} + t_{2,3} \times t_{4,3} + t_{2,4} \times t_{4,1} + t_{3,1} \times t_{4,4} + t_{3,2} \times t_{4,2} + t_{3,2} \times t_{4,3} + t_{3,3} \times t_{4,4} + t_{3,4} \times t_{4,4} + t_{2,3} \times t_{4,4} + t_{2,4} \times t_{4,3} + t_{3,2} \times t_{4,4} + t_{3,3} \times t_{4,4} + t_{3,4} \times t_{4,3} + t_{4,2} \times t_{2,4} + t_{4,3} \times t_{4,4} + t_{3,4} \times t_{4,4} + t_{3,4} \times t_{4,4} + t_{4,4} \times t_{2,4} + t_{4,4} \times t_{3,4} \times t_{4,4} + t_{4,4} \times t_{4,4} \times$$

Value

terminational_classes The terminational methylation classes average_methylation_level The average methylation level after [n] cell cycle(s).

References

Zhao, C. et.al.(2018). A DNA methylation state transition model reveals the programmed epigenetic heterogeneity in pre-implantation embryos. Under revision.

Examples

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 ${\it MethylCalculation}, {\it 1}$