tugHall v 2.1: USER-GUIDE-TESTS

Requirements

R version **3.6**

Libraries: **stringr, actuar, MASS, RColorBrewer, ape, ggplot2, ggtree**

Operation systems: Window, Mac. The code for analysis is not tested under Linux based systems.

To perform the simulation, kindly see the **User-Guide-tugHall_v_2.1** file. After the simulation the file **tugHall_2.1/Output/cloneout.txt** is generated, which is used to analyze the evolution of cells.

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1. Environmental death

For tests we use directory *Enveronmental_death*:

- In the function **updateClone** of the class **hallmark** we have set **clone1$d = 1.0** to make devision for each time step.
- In the same function we have set **a = 0** to exclude apoptosis process.
- Set **k = 0.5** to check environmental death process.

Using these parameters, we should get constant number of cells in average. To check it, please, run the code and see results using **/Code/Average_tests.R** after finish of 100 trials for primary cells (Fig.1) and for metastasis cells (Fig.2).

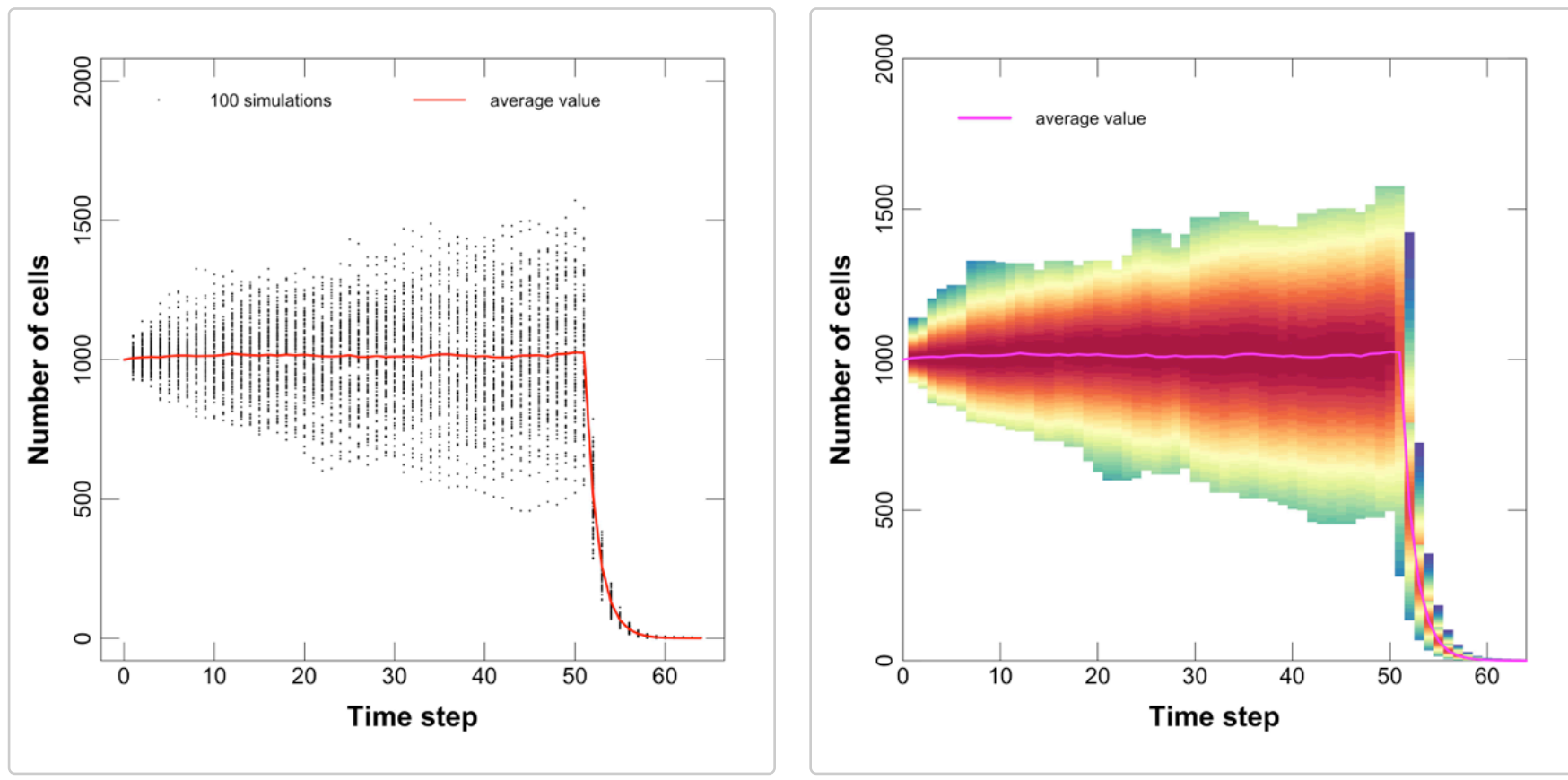

Fig.1. Evolution of number of primary cells for 100 trials: left - plot with dots, **right -** plot with distribution for each time step.

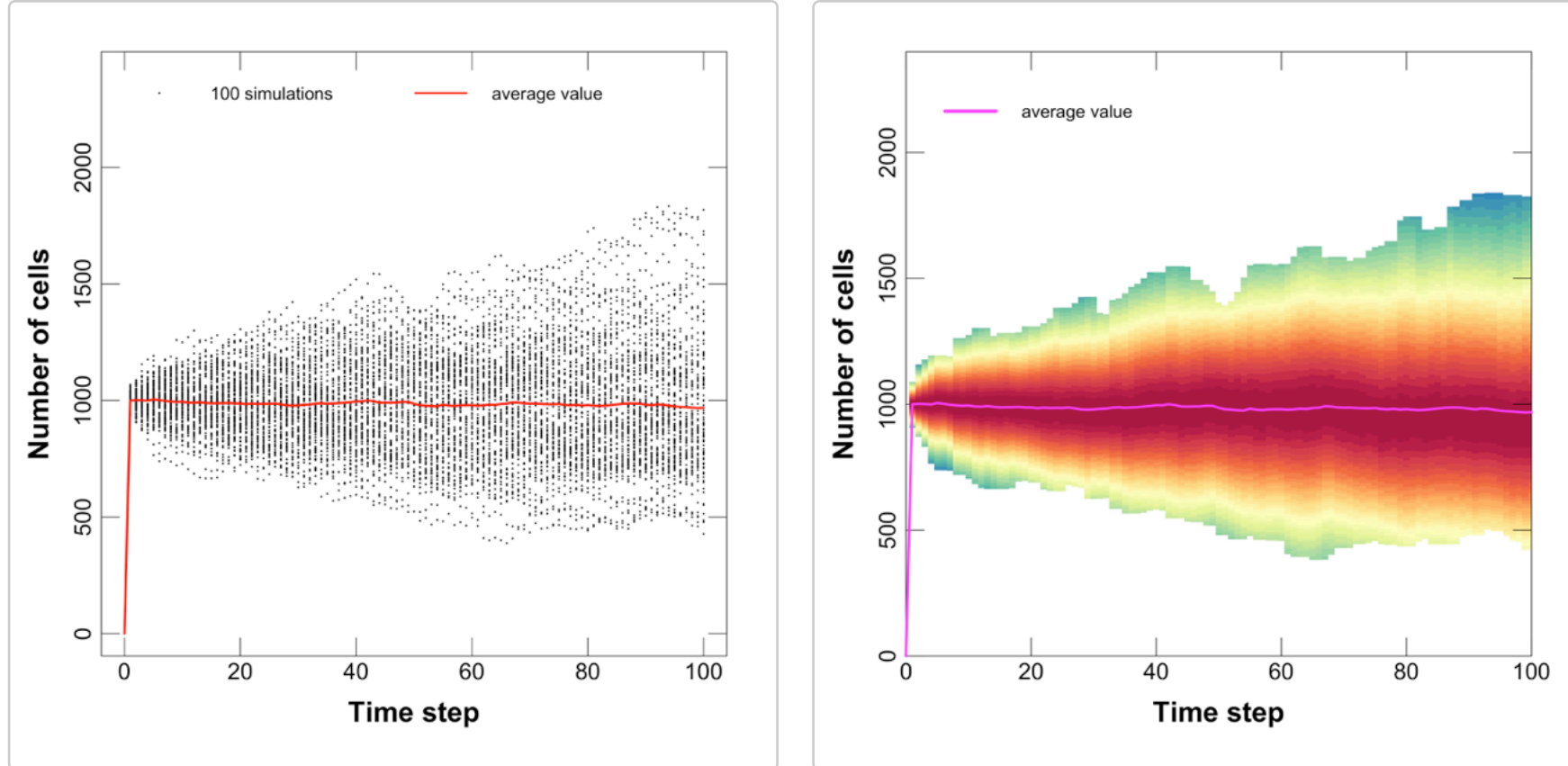

Fig.2. Evolution of number of metastasis cells for 100 trials: left - plot with dots, **right -** plot with distribution for each time step.

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2. Apoptosis death

For evolution tests we use directory *Apoptosis_death*:

- In the function **updateClone** of the class **hallmark** we have set **clone1$d = 1.0** to make devision for each time step.
- In the same function we have set **a = 0.5** to **fix probability of apoptosis death**.
- Set **k = 0** to **exclude** the environmental death.

Using these parameters, we should get constant number of cells in average. To check it, please, run the code and see results using **/Code/Average_tests.R** after finish of 100 trials for primary cells (Fig.3) and for metastasis cells (Fig.4).

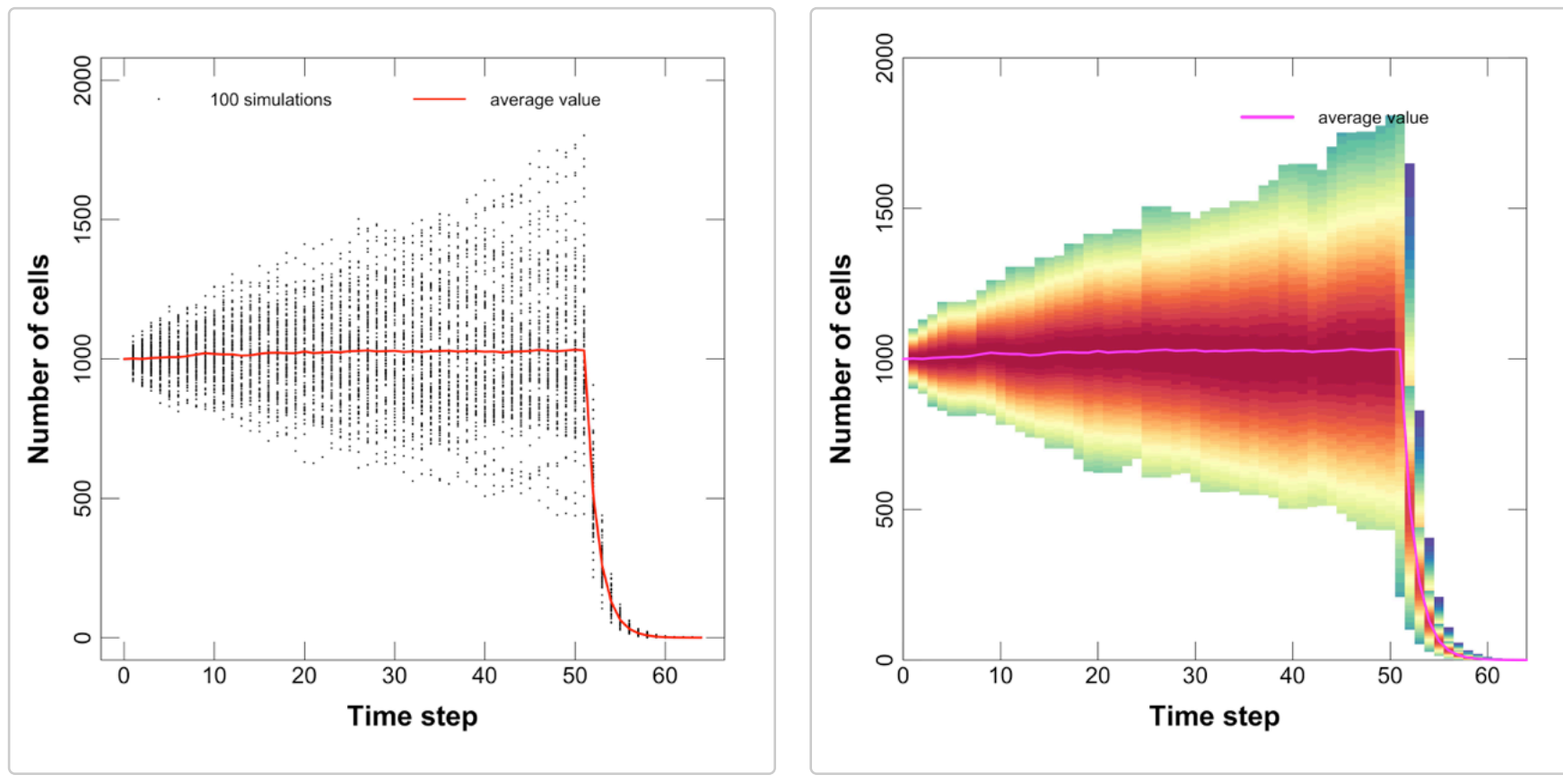

Fig.3. Evolution of number of primary cells for 100 trials: left - plot with dots, **right -** plot with distribution for each time step.

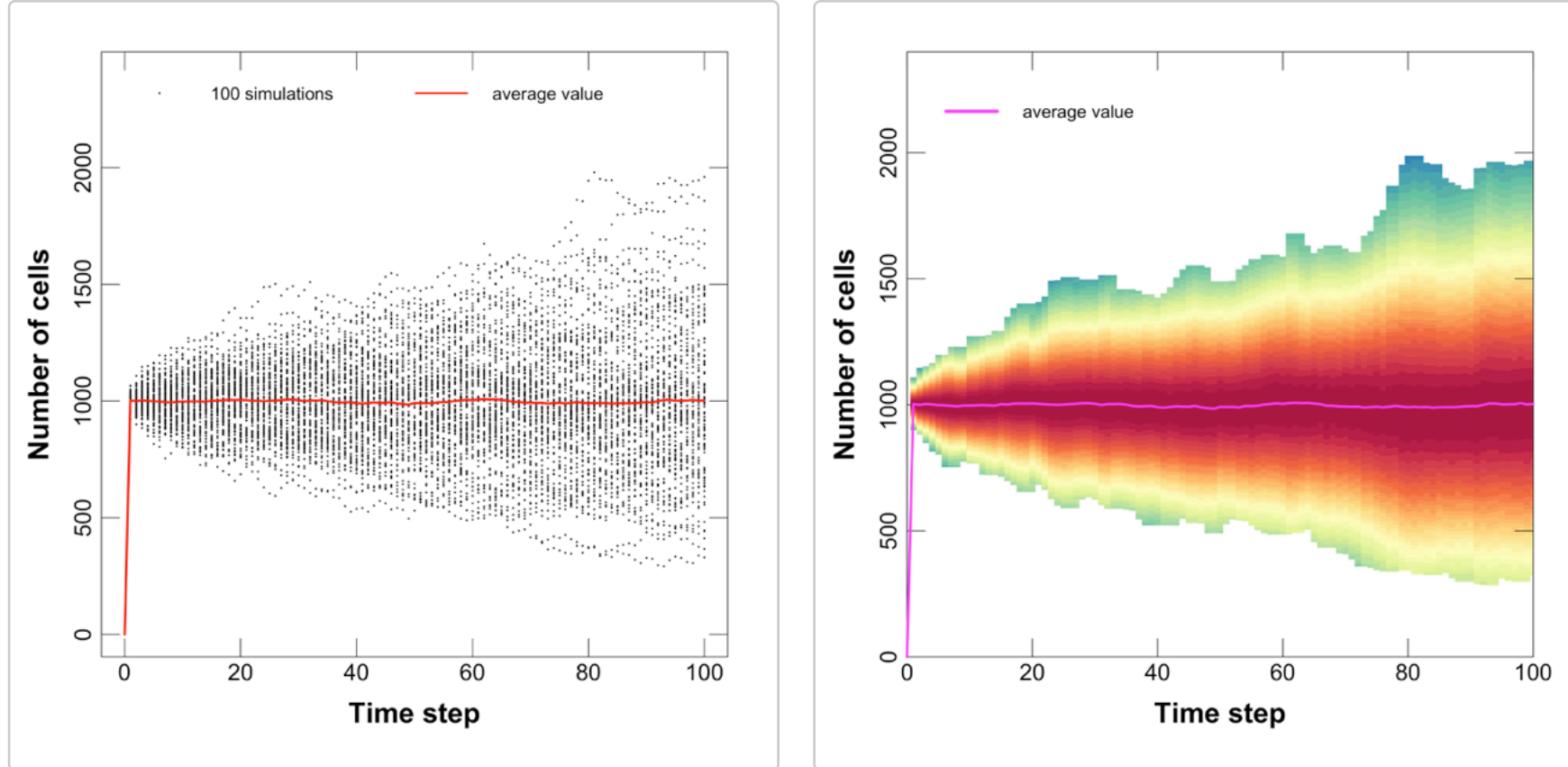

Fig.4. Evolution of number of metastasis cells for 100 trials: left - plot with dots, **right -** plot with distribution for each time step.

The test for correct calculation of apoptosis probability is in the folder **Apoptosis_function**. There is *cloninit.txt* file in the **/Input** folder, which has initial clones with a different combination of mutated genes. Apoptosis probability defines by not negative function:

$$a = \frac{1}{1+e^{-s\cdot(x-0.5)}} - H_a,$$

$$a = 0, \quad if \quad a < 0$$

where x is mutation density, s is parameter.

The file **/Output/clonout.txt** contents output data. There is no evolution, because in the **model** function we deleted this possibility. In the table below we can recalculate the mutation density and probability of apoptosis by hands (only data for first timestep are presented here):

Table 1. Subset of output data. The output data for all clones. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

Time	Index or Average	a	Apoptosis, H_a	mutation density, x
0	avg	0.2844715	0.15	0.3785714
0	1	0.0000000	1.00	0.1428571
0	2	0.0273468	0.00	0.1428571
0	3	0.0273468	0.00	0.1428571
0	4	0.0273468	0.00	0.1428571
0	5	0.0273468	0.00	0.1428571
0	6	0.0273468	0.00	0.1428571
0	7	0.0273468	0.00	0.1428571
0	8	0.0000000	1.00	0.2857143
0	9	0.1050006	0.00	0.2857143
0	10	0.1050006	0.00	0.2857143
0	11	0.0000000	1.00	0.7142857
0	12	0.6713475	0.00	0.5714286
0	13	0.1050006	0.00	0.2857143
0	14	0.9726532	0.00	0.8571429
0	15	0.6713475	0.00	0.5714286
0	16	0.8949994	0.00	0.7142857
0	17	0.3286525	0.00	0.4285714
0	18	0.6713475	0.00	0.5714286

0	19	0.6713475	0.00	0.5714286
0	20	0.3286525	0.00	0.4285714

To check calculation it is needed to pay attantion only on the a, H_a and **mutation density,** x columns. Also to check the calculation of the **mutation density,** x value, it is neccessary to see on the columns with driver genes in original file **Apoptosis_function/Output/cloneout.txt**. To see test “How hallmark apoptosis affects on a - apoptosis probability”, kindly see *Apoptosis* subsection in section Hallmarks tests.

3. Invasion/metastasis transformation

For evolution tests we use directory *Metastasis_transformation*:

- In the function **updateClone** of the class **hallmark** we have set **clone1$d = 1.0** to make devision for each time step.
- In the same function we have set **a = 0** to **exclude the apoptosis death**.
- In the same function we have set **im = 0.5** to **fix probability of invasion/transformation**.
- Set **k = 0** to **exclude** the environmental death.

Using these parameters, we should get constant number of cells in average. To check it, please, run the code and see results using **/Code/Average_tests.R** after finish of 100 trials for primary cells (Fig.5). For metastasis cells we have got transformation if $im' = 1$ that is easy to check by definition of all genes with mutations.

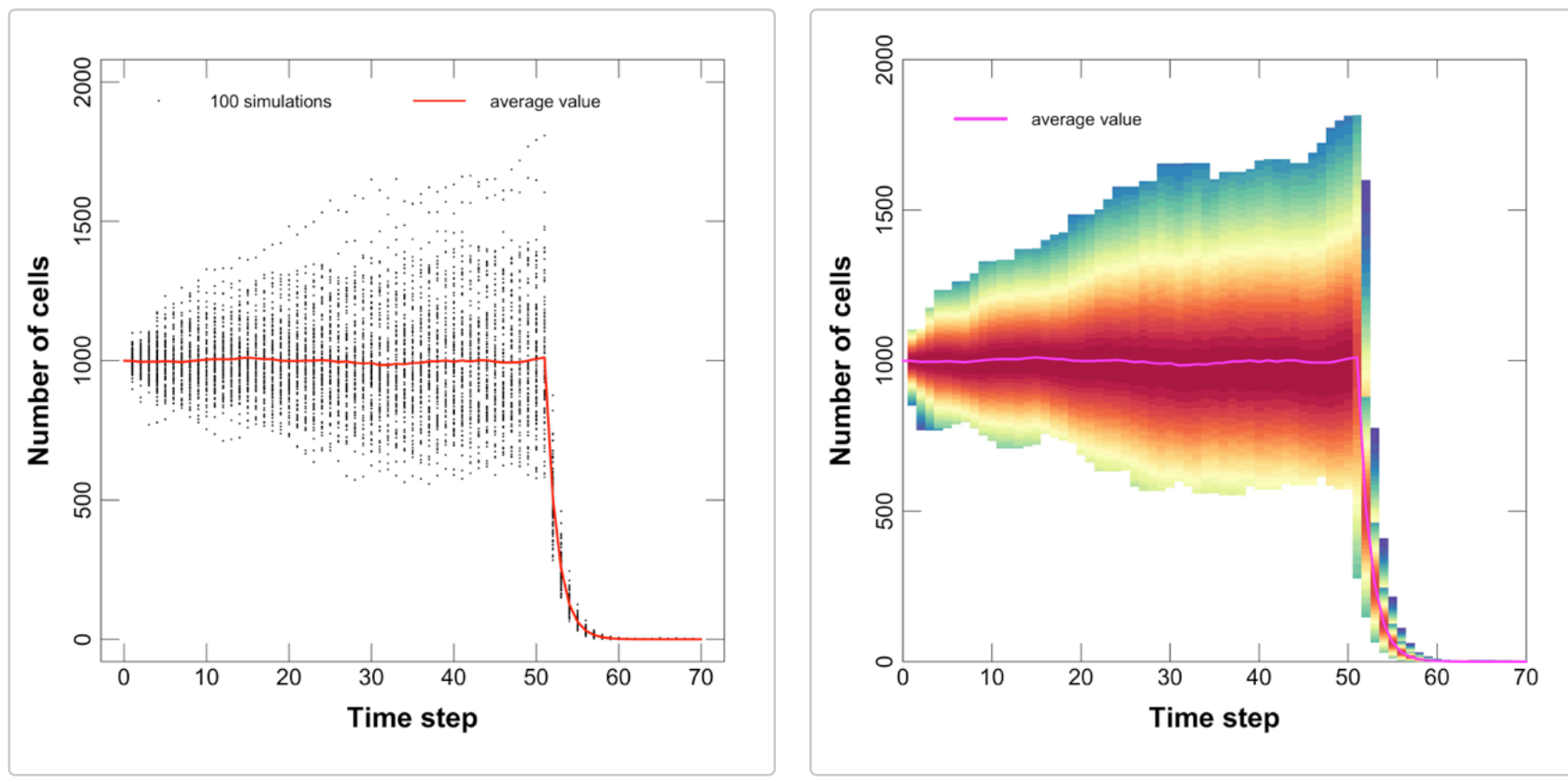

Fig.5. Evolution of number of primary cells for 100 trials: left - plot with dots, **right -** plot with distribution for each time step.

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4. Heyflick limit

Figures 1,3 and 5 show time evolution of number of primary cells. For primary cells, Heyflick limitations appears at 50 divisions. Because of division occurs at each time step, we can see sharp decrease of number of cell after Heyflick limitation (50 steps). For metastasis cells, Figs.2 and 4 show there is no Heyflick limitation, because of hallmark affect.

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5. Hallmarks tests

The hallmarks tests based on idea: we have to check the influence only of hallmarks variables on probabilities. In this way it does not matter that happens with the clones and how the clones depend on probabilities. ONLY one process we want to check - how the probabilities depend on Hallmarks variables. What is why we changed the code TO STOP processes of division and death of cells/clones (Please, kindly see **trial** function in the **Code/tugHall_2.1_functions.R** file). Please, check the **FIRST** and **SECOND** time steps, because the invasion/metastasis transformation occurs only after trial!

To check the results of tests, we need just to open **Output/cloneout.txt** file and check values of hallmarks and related probabilities for each clone. Here we can see the results of simlation for each hallmark variable separetly.

5.1. Apoptosis H_a

There are only genes GA1, GA2, GA3 and GA4 related to the apoptosis hallmark (Table 2). Table 3 shows subset of outdata after simulation. The apoptosis probability depends on apoptosis hallmark as a nonnegative linear function: $a = \frac{1}{1+e^{-s\cdot(x-0.5)}} - H_a$. To check this dependence we applied high mutation density to all clones, so $a = 0.7310586$ for primary tumor clones and $a = 0.6224593$ for metastasis clones. Table 3 allows to check dependences of apoptosis hallmark H_a on mutated genes $GA1, GA2, GA3, GA4$ as well as dependences of a on H_a. Empty cell in Table 3 means 0, full cell means 1 in the dependence of hallmark: $H_a = \sum w_i \cdot GA_i$, full cell has information about the mutated site and toime step when mutation happend, but it does not matter for calculation of a and H_a.

Table 2. Subset of gene's weights in definition of hallmarks 'Apoptosis'. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

Genes	Apoptosis, H_a
GA1	0.1
GA2	0.2
GA3	0.3
GA4	0.4

Table 3. Subset of output data. The output data for hallmark **Apoptosis**. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Time	AvgOrIndx	a.	Ha	type	mut_den	PosDriver.GA1	PosDriver.GA2	PosDriver.GA3	PosDrive
1	0	avg	0.1741084	0.0952381	0.0000000	0.302381				
2	0	1	0.7310586	0.0000000	0.0000000	0.600000				
3	0	2	0.6310586	0.1000000	0.0000000	0.600000	1:0			
4	0	3	0.4310586	0.3000000	0.0000000	0.600000	1:0	1:0		
5	0	4	0.1310586	0.6000000	0.0000000	0.600000	1:0	1:0	1:0	
6	0	5	0.0000000	1.0000000	0.0000000	0.600000	1:0	1:0	1:0	1:0
7	0	6	0.5224593	0.1000000	0.0000000	0.550000	1:0			
8	0	7	0.3224593	0.3000000	0.0000000	0.550000	1:0	1:0		
9	0	8	0.0224593	0.6000000	0.0000000	0.550000	1:0	1:0	1:0	
10	0	9	0.0000000	1.0000000	0.0000000	0.550000	1:0	1:0	1:0	1:0
44	1	avg	0.1741084	0.0952381	0.4047619	0.302381				
45	1	1	0.7310586	0.0000000	0.0000000	0.600000				
46	1	2	0.6310586	0.1000000	0.0000000	0.600000	1:0			
47	1	3	0.4310586	0.3000000	0.0000000	0.600000	1:0	1:0		
48	1	4	0.1310586	0.6000000	0.0000000	0.600000	1:0	1:0	1:0	
49	1	5	0.0000000	1.0000000	0.0000000	0.600000	1:0	1:0	1:0	1:0
50	1	6	0.5224593	0.1000000	1.0000000	0.550000	1:0			
51	1	7	0.3224593	0.3000000	1.0000000	0.550000	1:0	1:0		
52	1	8	0.0224593	0.6000000	1.0000000	0.550000	1:0	1:0	1:0	
53	1	9	0.0000000	1.0000000	1.0000000	0.550000	1:0	1:0	1:0	1:0

5.2. Angiogenesis H_b

There are only genes GB1, GB2, GB3 and GB4 related to the angiogenesis hallmark (Table 4). Table 5 shows subset of outdata after simulation. The division probability depends on angiogenesis hallmark as the function:

$d' = d - E' \cdot N$ for primary cells,

$d' = d$ for metastasis cells,

where N is a number of cells, $d = d_0 + H_d$. We define $H_d = 1$ by all mutated genes GD_i related to *growth/antigrowth* H_d hallmark. The E' is a friction coefficient, which equals:

$$E' = \frac{E_0}{1+F_0 \cdot H_b}$$

and $N_{max} = \frac{1}{E'}$ is a maximal number of primary cells, F_0 and E_0 are parameters defined by user, here $E_0 = 10^{-3}, F_0 = 2$. To check these dependences we applied different mutated genes related to angiogenesis hallmark. Table 5 allows to check dependences of angiogenesis hallmark H_b on mutated genes $GB1, GB2, GB3, GB4$ as well as dependences of N_{max} and E' on H_b. Empty cell with information of genes in Table 5 means 0, full cell means 1 in the dependence of hallmark: $H_b = \sum w_i \cdot GB_i$, full cell has information about the mutated site and time step when mutation happened, but it does not matter for calculation of H_b. Please, pay attantion that only for next time step we can check probabilities, because **trial** function is needed to change the state of cell to *metastasis*. That is why step 0 is skipped in the Table 5.

Table 4. Subset of gene's weights in definition of hallmarks 'Angiogenesis'. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Genes	Angiogenesis, H_b
5	GB1	0.1
6	GB2	0.2
7	GB3	0.3
8	GB4	0.4

Table 5. Subset of output data. The output data for hallmark **Angiogenesis**. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Time	AvgOrIndx	d.	E.	N	Nmax.	M	Hd	Hb	type	PosDriver.GB1	PosDriver.GB2	PosDriver.GB3	P
55	1	11	0.9791667	0.0008333	25	1200	17	1	0.1	0	1:0			
56	1	12	0.9843750	0.0006250	25	1600	17	1	0.3	0	1:0	1:0		
57	1	13	0.9886364	0.0004545	25	2200	17	1	0.6	0	1:0	1:0	1:0	
58	1	14	0.9916667	0.0003333	25	3000	17	1	1.0	0	1:0	1:0	1:0	
59	1	15	1.0000000	0.0003333	25	3000	17	1	1.0	1	1:0	1:0	1:0	
60	1	16	1.0000000	0.0004545	25	2200	17	1	0.6	1	1:0	1:0	1:0	
61	1	17	1.0000000	0.0006250	25	1600	17	1	0.3	1	1:0	1:0		
62	1	18	1.0000000	0.0008333	25	1200	17	1	0.1	1	1:0			

5.3. Growth/antigrowth H_d

There are only genes GD1, GD2, GD3 and GD4 related to the Growth/antigrowth hallmark (Table 6). Table 7 shows subset of outdata after simulation. The division probability depends on Growth/antigrowth hallmark as the linear function, restricted by 1:

$d = d_0 + H_d$,

$d = 1$, if $d > 1$.

And again the $d' = d - E' \cdot N$ for primary cells, and $d' = d$ for metastasis cells, where N is a number of cells, $d = d_0 + H_d$. We define $H_b = 0$ and $E' = \frac{E_0}{1+F_0 \cdot H_b} = 10^{-3}$ for all cells.

To check these dependences we applied different mutated genes related to Growth/antigrowth hallmark. Table 7 allows to check dependences of Growth/antigrowth hallmark H_d on mutated genes $GD1, GBD, GD3, GD4$ as well as dependences of d on H_d for primary and metastasis cells. Empty cell with information of genes in Table 7 means 0, full cell means 1 in the dependence of hallmark: $H_d = \sum w_i \cdot GD_i$, full cell has information about the mutated site and time step when mutation happened, but it does not matter for calculation of H_d. Please, pay attantion that only for next time step we can check probabilities, because **trial** function is needed to change the state of cell to *metastasis*. That is why step 0 is skipped in the Table 7.

Table 6. Subset of gene's weights in definition of hallmarks 'Growth/antigrowth'. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Genes	Growth/antigrowth, H_d
17	GD1	0.1
18	GD2	0.2
19	GD3	0.3
20	GD4	0.4

Table 7. Subset of output data. The output data for hallmark **Growth/antigrowth**. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Time	AvgOrIndx	d.	E.	N	Nmax.	M	Hd	Hb	type	PosDriver.GD1	PosDriver.GD2	PosDriver.GD3	PosDriver
77	1	33	0.000	0.001	25	1000	17	0.0	0	0				
78	1	34	0.075	0.001	25	1000	17	0.1	0	0	1:0			
79	1	35	0.275	0.001	25	1000	17	0.3	0	0	1:0	1:0		
80	1	36	0.575	0.001	25	1000	17	0.6	0	0	1:0	1:0	1:0	
81	1	37	0.975	0.001	25	1000	17	1.0	0	0	1:0	1:0	1:0	1:0
82	1	38	1.000	0.001	25	1000	17	1.0	0	1	1:0	1:0	1:0	1:0
83	1	39	0.600	0.001	25	1000	17	0.6	0	1	1:0	1:0	1:0	
84	1	40	0.300	0.001	25	1000	17	0.3	0	1	1:0	1:0		
85	1	41	0.100	0.001	25	1000	17	0.1	0	1	1:0			
86	1	42	0.000	0.001	25	1000	17	0.0	0	0				

5.4. Immortalization H_i

There are only genes GI1, GI2, GI3 and GI4 related to the Immortalization hallmark (Table 8). Table 9 shows subset of outdata after simulation. The immortalization probability i depends on immortalization hallmark H_i as a nonnegative linear function: $i' = 1 - H_i$. To check this dependence we applied different mutated rate for genes GI1, GI2, GI3 and GI4.

Table 9 allows to check the dependence for H_i of immortalization hallmark on mutated genes $GI1, GI2, GI3, GI4$ as well as dependences of i on H_i for primary and metastasis cells. Empty cell in Table 9 means 0, full cell means 1 in the dependence of hallmark: $H_i = \sum w_i \cdot GI_i$, full cell has information about the mutated site and toime step when mutation happend, but it does not matter for calculation of i and H_i.

Table 8. Subset of gene's weights in definition of hallmarks 'Immortalization'. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Genes	Immortalization, H_i
13	GI1	0.1
14	GI2	0.2
15	GI3	0.3
16	GI4	0.4

Table 9. Subset of output data. The output data for hallmark **Immortalization**. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Time	AvgOrIndx	i.	Hi	type	PosDriver.GI1	PosDriver.GI2	PosDriver.GI3	PosDriver.GI4

68	1	24	1.0	0.0	0					
69	1	25	0.9	0.1	0	1:0				
70	1	26	0.7	0.3	0	1:0	1:0			
71	1	27	0.4	0.6	0	1:0	1:0	1:0		
72	1	28	0.0	1.0	0	1:0	1:0	1:0	1:0	
73	1	29	0.0	1.0	1	1:0	1:0	1:0	1:0	
74	1	30	0.4	0.6	1	1:0	1:0	1:0		
75	1	31	0.7	0.3	1	1:0	1:0			
76	1	32	0.9	0.1	1	1:0				
77	1	33	1.0	0.0	0					

5.4. Invasion/metastasis H_{im}

There are only genes GIM1, GIM2, GIM3 and GIM4 related to the Invasion/metastasis hallmark (Table 10). Table 11 shows subset of outdata after simulation. The invasion/metastasis probability im' depends on invasion/metastasis hallmark H_{im} as a linear function:

$$im' = H_{im}.$$

To check this dependence we applied different mutated rate for genes GIM1, GIM2, GIM3 and GIM4.

Table 11 allows to check the dependence for H_{im} of Invasion/metastasis hallmark on mutated genes $GIM1, GIM2, GIM3, GIM4$ as well as dependences of im' on H_{im} for primary and metastasis cells. Empty cell in Table 11 means 0, full cell means 1 in the dependence of hallmark: $H_{im} = \sum w_i \cdot GIM_i$, full cell has information about the mutated site and toime step when mutation happend, but it does not matter for calculation of im' and H_{im}.
Please, pay attantion that only for next time step we can check status of cells, because **trial** function is needed to change the state of cell to *metastasis*. The status dependes on im' probability, if $im' = 1$ then $type = 1 \ \ or \ \ 'metastasis'$, for other cases $type = 0 \ \ or \ \ 'primary'$.

Table 10. Subset of gene's weights in definition of hallmarks 'Invasion/metastasis'. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Genes	Invasion / Metastasis, H_{im}
9	GIM1	0.1
10	GIM2	0.2
11	GIM3	0.3
12	GIM4	0.4

Table 11. Subset of output data. The output data for hallmark **Invasion/metastasis**. The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*.

	Time	AvgOrIndx	im.	Him	type	PosDriver.GIM1	PosDriver.GIM2	PosDriver.GIM3	PosDriver.GIM4
20	0	19	0.0	0.0	0				
21	0	20	0.1	0.1	0	1:0			
22	0	21	0.3	0.3	0	1:0	1:0		
23	0	22	0.6	0.6	0	1:0	1:0	1:0	
24	0	23	1.0	1.0	0	1:0	1:0	1:0	1:0
63	1	19	0.0	0.0	0				
64	1	20	0.1	0.1	0	1:0			
65	1	21	0.3	0.3	0	1:0	1:0		
66	1	22	0.6	0.6	0	1:0	1:0	1:0	

67	1	23	1.0	1.0	1	1:0	1:0	1:0	1:0	

6. Tests for mutations

In this tests, we check the only **mutation** process and how it affects on hallmark variables. So, the normal reaction for test is the random changes in the genes with formula:

$$m' = m_0 \cdot l_{CDS},$$

where m_0 is the initial rate of mutation defined by user, l_{CDS} is the CDS length of a gene. If a gene is changed then the related hallmark also has to be changed. The mutation process depends on several parameters: m_0, u_s, u_o and the CDS lengths of the genes. the variables m_0, u_s, u_o are defined by user, the CDS lengths of the genes are defined in the **Gene_cds2** files (Table 12). The parameters u_s, u_o define the mutatopn processes in the suppressors and oncogenes respectively. Mutation of driver genes depends on probabilities u_s and u_o . Mutation of passenger genes depends on probabilities $(1 - u_s)$ and $(1 - u_o)$ without changes in the hallmarks variables.

Mutation occurs only during division process, so the mutation must occur for parents and daughter cells independently. FOR TEST we changed the code and **switch off** the death of cell in order to check the mutation process. The *cloneinit.txt* file is permanent for all tests (Table 13), it has the cells with all combinations of 4 genes + GD. The GD gene is needed, because the mutation occurs **ONLY** during the division process, that is why we need GD (GD switch on the division process with the probability 1).

In this tests we change only the **Gene_cds2** and u_s, u_o, m_0 to check the calculations of hallmarks variables. The results of simulations are in Table 14.

Table 12. Gene_cds_2 files: Different files for test simulations. (The names of columns are related to the description in the *USER-GUIDE-tugHall_v_2.1*).

Table 12. A) Files for oncogenes (**gene_cds2_o.txt** - left) and supressors (**gene_cds2_s.txt** - right).

Gene	Length of CDS	Hallmark	o/s	Weight
GA	1	apoptosis	o	1
GB	1	angiogenesis	o	1
GIM	1	invasion	o	1
GI	1	immortalization	o	1
GD	1	growth	o	1

Gene	Length of CDS	Hallmark	o/s	Weight
GA	1	apoptosis	s	1
GB	1	angiogenesis	s	1
GIM	1	invasion	s	1
GI	1	immortalization	s	1
GD	1	growth	s	1

Table 12. B) Files for oncogenes (**gene_cds2_o_100.txt** - left) and supressors (**gene_cds2_s_100.txt** - right).

Gene	Length of CDS	Hallmark	o/s	Weight
GA	100	apoptosis	o	1
GB	100	angiogenesis	o	1
GIM	100	invasion	o	1
GI	100	immortalization	o	1
GD	100	growth	o	1

Gene	Length of CDS	Hallmark	o/s	Weight
GA	100	apoptosis	s	1
GB	100	angiogenesis	s	1
GIM	100	invasion	s	1
GI	100	immortalization	s	1
GD	100	growth	s	1

Table 12. C) Files for oncogenes (**gene_cds2_o_1000_1.txt** - left) and supressors (**gene_cds2_s_1000_1.txt** - right).

Gene	Length of CDS	Hallmark	o/s	Weight
GA	1000	apoptosis	o	1
GB	1	angiogenesis	o	1

Gene	Length of CDS	Hallmark	o/s	Weight
GA	1	apoptosis	s	1
GB	1000	angiogenesis	s	1

GIM	1	invasion	o	1	GIM	1	invasion	s	1
GI	1	immortalization	o	1	GI	1	immortalization	s	1
GD	1	growth	o	1	GD	1	growth	s	1

Table 13. Input file **cloneinit.txt** with initial clones, which have mutated genes

ID	Mutated genes	Number of cells
1	GA	1
2	GI	1
3	GD	1
4	GB	1
5	GIM	1
6		1
7	GD,GA	1
8	GD,GA,GI	1
9	GD,GA,GI,GB	1
10	GD,GA,GI,GB,GIM	1
11	GD,GA,GB	1
12	GD,GA,GB,GIM	1
13	GD,GA,GIM	1
14	GD,GI	1
15	GD,GI,GB	1
16	GD,GI,GB,GIM	1
17	GD,GB	1
18	GD,GB,GIM	1
19	GD,GIM	1
20	GD,GA,GI,GIM	1
21	GD,GI,GIM	1
22	GD,GA	1
23	GD,GI	1
24	GD,GB	1
25	GD,GIM	1

Table 14. Results of test's simulations from the file **Results.txt**

Genefile	u_s	u_o	m_0	Results	Conclusion
gene_cds2_o.txt	0.0	0.0	0.000	The cell divisions with the HD Hallmarks without mutations. Please, check the mutation rate	For oncogenes without mutation - correct
gene_cds2_s.txt	0.0	0.0	0.000	Same as previous	For suppressors same - correct
gene_cds2_o_100.txt	0.0	0.0	1.000	The mutation occurs only in the passenger part of genes	Correct
gene_cds2_s_100.txt	0.0	0.0	1.000	The mutation occurs only in the passenger part of genes	Correct
gene_cds2_o_100.txt	0.0	1.0	1.000	The mutation occurs only in the driver part of genes	Correct
gene_cds2_s_100.txt	0.0	1.0	1.000	The mutation occurs only in the passenger part of genes, because of $u_s = 0$	Correct
				The mutation occurs only in the passenger	

gene_cds2_o_100.txt	1.0	0.0	1.000	part of genes, because of $u_o = 0$	Correct
gene_cds2_s_100.txt	1.0	0.0	1.000	The mutation occurs only in the driver part of genes	Correct
gene_cds2_o_100.txt	1.0	1.0	1.000	The mutation occurs only in the driver part of genes	Correct
gene_cds2_s_100.txt	1.0	1.0	1.000	The mutation occurs only in the driver part of genes	Correct
gene_cds2_o_100.txt	0.5	0.5	1.000	The mutation occurs in the driver and passenger parts of genes	Correct
gene_cds2_s_100.txt	0.5	0.5	1.000	The mutation occurs in the driver and passenger parts of genes	Correct
gene_cds2_o_1000_1.txt	0.5	0.5	0.001	The mutation occurs only in the driver and passenger parts of gene with a **longest CDS**	Correct
gene_cds2_s_1000_1.txt	0.5	0.5	0.001	The mutation occurs only in the driver and passenger parts of gene with a **longest** CDS	Correct