

tugHall v 2.1: USER-GUIDE-Analysis

Requirements

R version 3.6
Libraries: `stringr`, `ape`, `ggplot2`, `ggtree`
Operation systems: Window, Mac. The code for analysis is not tested under Linux based systems.
Note that the program comprises two different procedures in general: the first is simulation and the second is the analysis of the simulation results. This User-Guide pertains to the analysis only.

The programs for the analysis can be run only after the simulation is completed, and the `cloneout.txt` file exists in the `tugHall_2.1/Output/` folder.

Table of Contents

1. Quick start guide
2. Inputs
3. Outputs
4. Figures
5. Relation to experimental measurements

1. Quick start guide

To perform the simulation, kindly see the [User-Guide-tugHall_v_2.1](#). After the simulation the file `tugHall_2.1/Output/cloneout.txt` is generated, which is used to analyze the evolution of cells. Also, since the functions and objects used after the simulation, the `RDatas` file saved after the simulation must be loaded, if required.

The simplest way to analyze the results after simulation:

- open R
- set `tugHall_2.1/` as the working directory
- load `RDatas`
- source(`"Code/Analysis_clones.R"`)

The code has initial input parameters and input files in the `/Input/` folder to define the names of the genes. In the dialogue box, the user can see the results of the simulation, which will be saved to the `/Output/` and `/Figures/` folders.

2. Inputs

To analyze the output data, the user has to obtain the results of the simulation in the `tugHall_2.1/Output/cloneout.txt` file and the functions and objects of simulations should be present in the R environment. That is why the `cloneout.txt` file is the input file for the analysis. For detailed information, kindly see the "Outputs" section in [User-Guide-tugHall](#).

3. Outputs

Output data contain several files and figures:

- `Order_of_dysfunction.txt` has information about the order of gene dysfunction during evolution.
- `VAF.txt` file has information about the variant allele frequencies (VAFs) for each gene and each site in the genes.
- the folder `tugHall_2.1/Figures/` has many plots (see [Figures](#)).

Order_of_dysfunction.txt file

`tugHall_2.1/Output/Order_of_dysfunction.txt` has information about the order of gene dysfunction during evolution in the next format (only first 10 lines are presented here):

Table 1. Order of gene dysfunction.

Order of gene dysfunction	Number of clones with same order	Number of cells with same order
PIK3CA	1	1

1. Order of gene dysfunction. Order of gene dysfunctions is the list of gene names in the order of mutations - from first to last by left to right. The blank line is related to the cells without dysfunction.
2. Number of clones with same order. This is the number of clones in the pool with the same order.
3. Number of cells with same order. This is the number of cells in the pool with the same order.

VAF.txt file

`tugHall_2.1/Output/VAF.txt` file has information about the VAFs for each gene and each site in the genes (first 10 lines):

Table 2. Variant allele frequencies.

DriverPasngr	Gene	Position	VAF_Primary	Ncells_Primary	Ncells_Primary_wMutation	Ncells_Primary	VAF_Metastatic	Ncells_Metastatic	Ncells_Metastatic_wMutation	Ncells_Metastatic	VAF_PriMet	Ncells_PriMet_wMutation	Ncells_PriMet
D	APC	5947	0.4867387	10277	10557	0	0	0	0	0	0.4867387	10277	10557
D	PIK3CA	379	0.4867387	10277	10557	0	0	0	0	0	0.4867387	10277	10557

1. **DriverPasngr** - D or P indicate the distinction between the Driver and Passenger genes.
2. **Gene** - name of gene, e.g. TP53, KRAS.
3. **Position** - position at mutated site in the gene, e.g. 123, 1028.
4. **VAF_Primary** - VAF for cells in the primary tumor = half of `Ncells_Primary_wMutation / Ncells_Primary`, e.g. 0.2.
5. `Ncells_Primary_wMutation` - number of primary-tumor cells, e.g., 40.
6. `Ncells_Primary` - number of primary-tumor cells, e.g., 100.
7. **VAF_Metastatic** VAF for metastatic cells = half of `Ncells_Metastatic_wMutation / Ncells_Metastatic`, e.g. 0.35.
8. `Ncells_Metastatic_wMutation` = number of metastatic cells with the mutation, e.g. 70.
9. `Ncells_Metastatic` = number of metastatic cells, e.g. 100.
10. **VAF_PriMet** VAF for all cells = half of `Ncells_PriMet_wMutation / Ncells_PriMet`, e.g. 0.275
11. `Ncells_PriMet_wMutation` number of all mutated cells, e.g. 110.
12. `Ncells_PriMet` number of all cells, e.g. 200.

4. Figures

The directory `Figures/` contains many output figures, generated during the analysis process of `cloneout.txt` file, including the evolution of the number of primary tumors and metastasis cells (Fig.1 left), hallmarks (Fig.1 right), and probabilities (Fig.2 left).

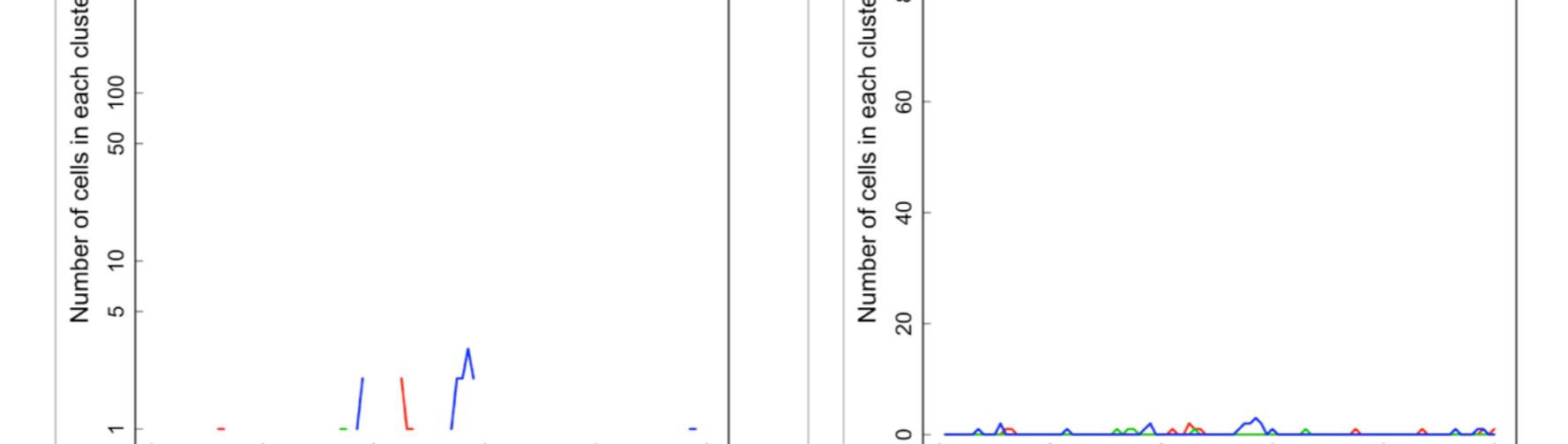


Fig.1. Results of the simulation: left - evolution of number of cells, right - evolution of hallmarks. Files are `tugHall_2.1/Figures/N_cells.jpg` and `tugHall_2.1/Figures/Hallmarks.jpg`.

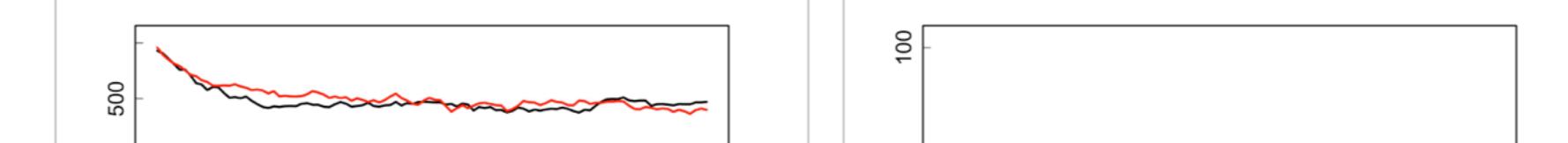


Fig.2. Results of the simulation: left - evolution of probabilities, right - evolution of number of clones and clusters. Files are `tugHall_2.1/Figures/Probabilities.jpg` and `tugHall_2.1/Figures/N_clones_clusters.jpg`.

The right side Fig.2 shows the evolution of the number of clones and clusters. Here, we have to define the cluster in the simulation, which is a pool of cells/clones with a same set of mutated driver genes **no matter which site in gene**. For this propose, we define the cluster ID as the binary number of mutated genes. Also, the analysis can calculate the evolution of number of cells in each cluster and clone:

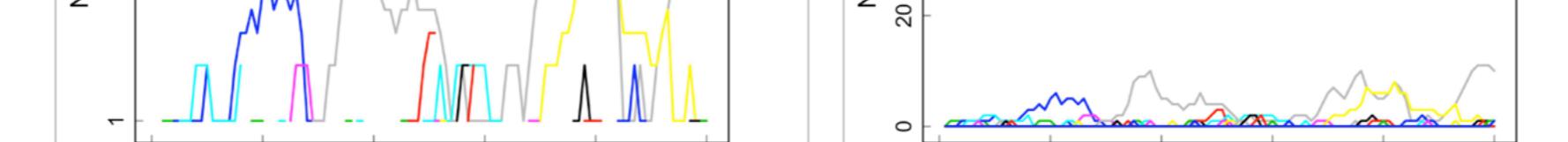


Fig.3. Results of the simulation: Upper left - evolution of number of cells in clusters (log scale). Upper right - evolution of the number of cells in clusters, magnified on linear scale. Lower left - evolution of the number of cells in clones (log scale). Lower right - evolution of number of cells in clones, magnified on linear scale. Files are `tugHall_2.1/Figures/N_cells_in_clusters_1.jpg` and `tugHall_2.1/Figures/N_cells_in_clusters_2.jpg` for clusters, `tugHall_2.1/Figures/N_cells_in_clones_1.jpg` and `tugHall_2.1/Figures/N_cells_in_clones_2.jpg` for clones.

Fig.4 shows the number of cells in each cluster and clone at the last time step to see which cluster/clone is dominant and prevails above the others:

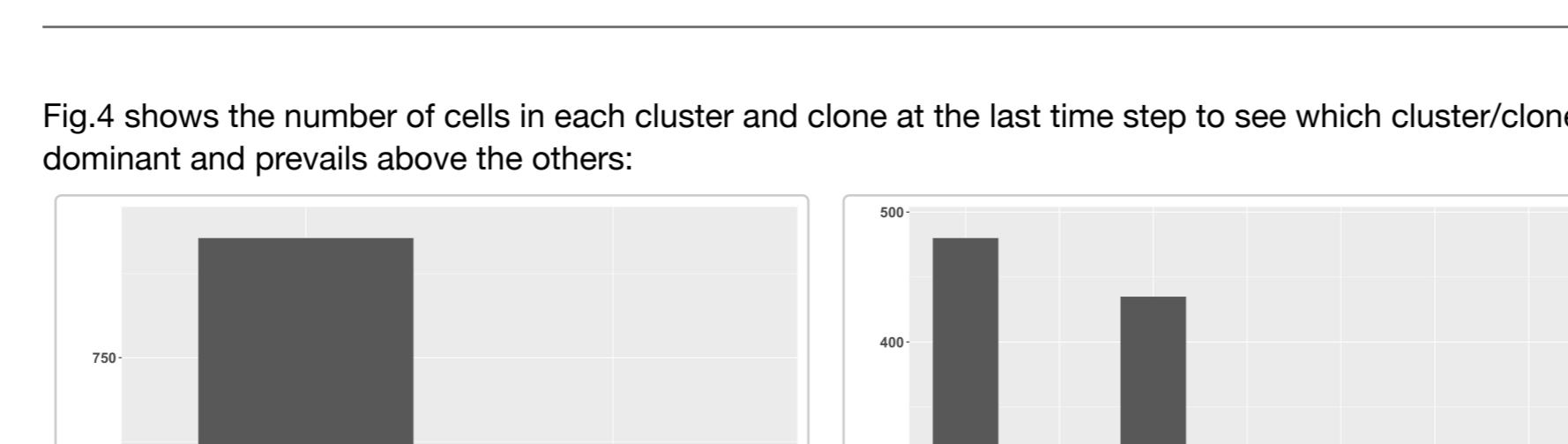


Fig.4. Results of the simulation: left - barplot for number of cells in clusters, right - same plot for clones. Files are `tugHall_2.1/Figures/Barplot_N_cells_clusters.jpg` and `tugHall_2.1/Figures/Barplot_N_cells_in_clones.jpg`.

During the simulation each clone has "clone ID" and number of cells in it. After simulation `Analysis_clones.R` executes clusters from the binary code of the mutated genes "Cluster ID". For example, if a gene is mutated, then its value in binary code is designated as 1, and if not, it is set to 0. For example, the clones have only 4 genes in simulation, and hence, the "Cluster ID" can have binary numbers from 0000 to 1111, which are the associated decimal numbers from 0 to 15. Each clone has information about the parent ID, and so, time of birth, so it is possible to find all clones having the same "Cluster ID". Subsequently, the cell with the earliest birth-day is found and its parent ID extracted. This parent ID can be used to find the "Cluster ID" for the parent, which is related to the parent of clone. Using this procedure, we can find all the relations between the parent and children for the clusters and for the clusters and also for clones, after that the tree for the clusters and clones at last time step are constructed (Fig.5).

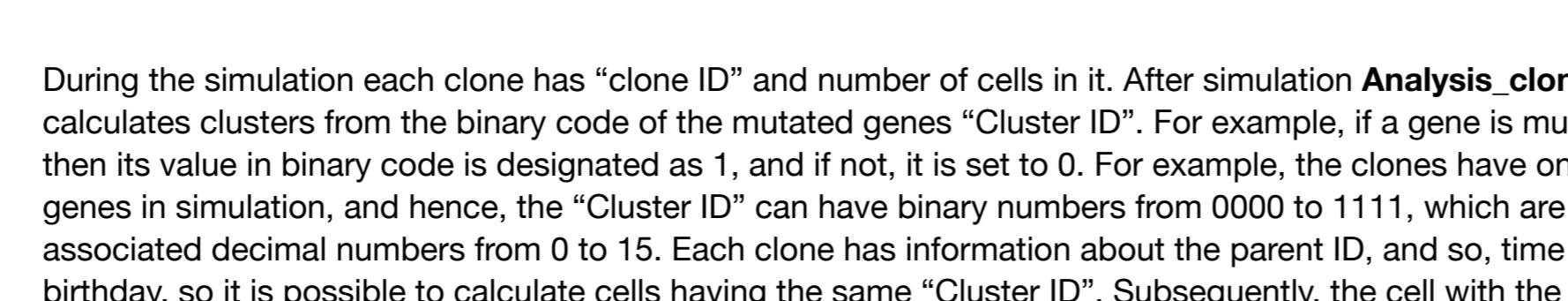


Fig.5. Tree of clusters and clones at the last time step. The numbers of the tree indicate the clusters IDs (for clones it is skipped) (upper) are the plots for clusters, and lower are the plots for clones, left plots are ggtree plots, right plots are time ggtree plots. The files are `tugHall_2.1/Figures/ggtree_clusters.jpg`, `tugHall_2.1/Figures/time_clusters.jpg` and `tugHall_2.1/Figures/ggtree_clones.jpg`, `tugHall_2.1/Figures/time_clones.jpg`.

Figs.6 and 7 show the inequality coefficients as a function of:

- time step;
- number of all cells;
- number of primary tumor cells;
- number of metastasis cells.



Fig.6. Results of simulation of inequality coefficient for driver mutated cells and for cells with any type of mutations: left - evolution of inequality coefficient, right - inequality coefficient as a function of all cells. Files are `tugHall_2.1/Figures/inequality.jpg` and `tugHall_2.1/Figures/inequality_all_cells.jpg`.

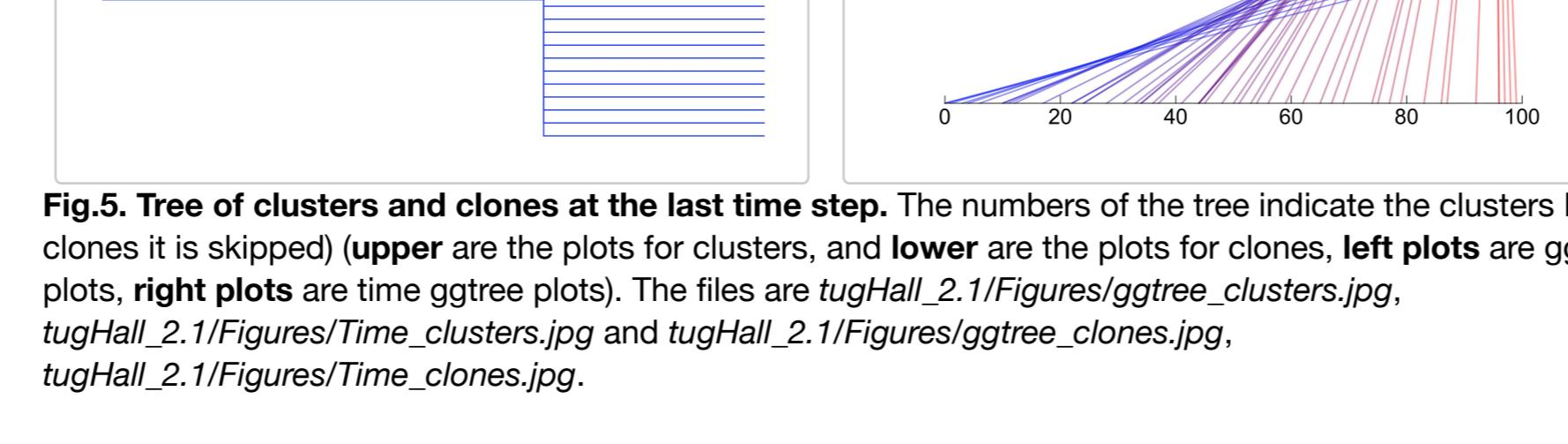


Fig.7. Results of simulation of inequality coefficient for driver mutated cells and for cells with any type of mutations: left - inequality coefficient as the function of primary tumor cells, right - inequality coefficient as the function of metastasis cells. Files are `tugHall_2.1/Figures/inequality_primary.jpg` and `tugHall_2.1/Figures/inequality_metastasis.jpg`.

5. Relation to experimental measurements

We here list variables processed from the tugHall outputs that are related to experimental measurements.

Variables processed from the simulator outputs	Relation to experimental measurements
--	---------------------------------------

Number of cells Observed tumor size. 10^6 cells correspond to the tumor tissue diameter of 1 cm. 10^9 cells correspond to that of 10 cm, $10^{12} - 10^{13}$ cells correspond to lethal burden. See Friberg and Mattson, Journal of Surgical Oncology, 1999.

VAF VAF calculated from sequence reads in the next-generation sequencer (NGS) under the assumption of 100% tumor purity.

Mutation number per base-pairs Tumor mutation burden calculated from NGS data.

Number of clones Number of clones estimated from NGS data by computational tools such as SciClone (Miller et al., PLOS Computational Biology, 2014) and SubcloneSelection (Williams et al., Nature Genetics, 2013).

Number of cells in clusters Number of cells in clusters estimated from NGS data by computational tools such as SciClone (Miller et al., PLOS Computational Biology, 2014) and SubcloneSelection (Williams et al., Nature Genetics, 2013).

Number of cells in clones Number of cells in clones estimated from NGS data by computational tools such as SciClone (Miller et al., PLOS Computational Biology, 2014) and SubcloneSelection (Williams et al., Nature Genetics, 2013).

Number of cells in each cluster and clone at the last time step Number of cells in each cluster and clone at the last time step to see which cluster/clone is dominant and prevails above the others:

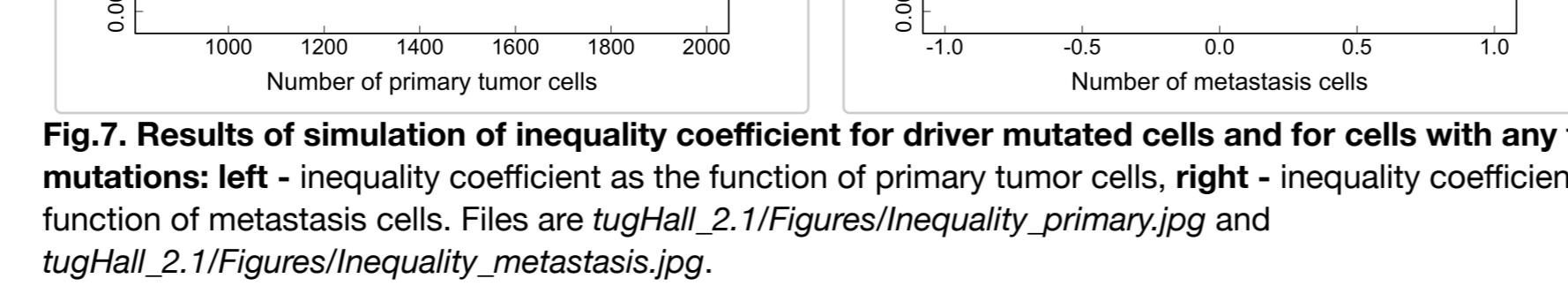


Fig.8. Results of the simulation: left - barplot for number of cells in clusters, right - same plot for clones. Files are `tugHall_2.1/Figures/Barplot_N_cells_clusters.jpg` and `tugHall_2.1/Figures/Barplot_N_cells_in_clones.jpg`.

Figs.6 and 7 show the inequality coefficients as a function of:

- time step;
- number of all cells;
- number of primary tumor cells;
- number of metastasis cells.

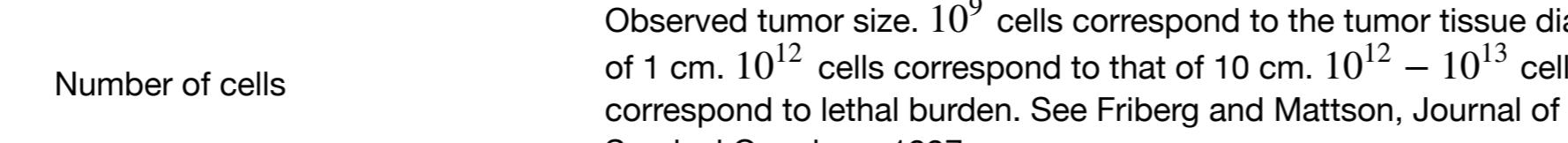


Fig.9. Results of simulation of inequality coefficient for driver mutated cells and for cells with any type of mutations: left - inequality coefficient as the function of primary tumor cells, right - inequality coefficient as the function of metastasis cells. Files are `tugHall_2.1/Figures/inequality_primary.jpg` and `tugHall_2.1/Figures/inequality_metastasis.jpg`.