

# tugHall version 1.1

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**tugHall** (*tumor gene-Hallmark*) is cancer-cell evolution model simulator, wherein gene mutations are linked to the tumor cell behaviors, which are influenced by the hallmarks of cancer.

This is an **R**-based script to simulate the cancer cell evolution in the framework of the model proposed by **Prof. Mamoru Kato**, Head of Bioinformatics Department, Research Institute, National Cancer Center, Tokyo, JAPAN.

## Authors and contributor list:

**Iurii Nagornov**

**Mamoru Kato**

*Department of Bioinformatics, Research Institute, National Cancer Center Japan, Tokyo, Japan*

All questions and requests can be sent to inagonov@ncc.go.jp

## Project source can be downloaded from websites

[https://github.com/nagornovys/Cancer\\_cell\\_evolution](https://github.com/nagornovys/Cancer_cell_evolution) - the developing resource

## Short description

The wide availability of recent cancer genomic data requires a coherent model that can sort out the relevant findings to systematically explain the clonal evolution and resultant intra-tumor heterogeneity (ITH). Here, we present a new mathematical model designed to computationally simulate the evolution of cancer cells. The model connects well-known cancer hallmarks with the specific mutational states of tumor-related genes. The cell behavior phenotypes are stochastically determined and the hallmarks interfere probabilistically with the phenotypic probabilities. In turn, the hallmark variables depend on the mutational states of tumor-related genes. Thus, it is expected our software can be used to deepen our understanding of cancer-cell evolution and generation of ITH.

## Content of package

- **User-Guide-tugHall.Rmd** and **User-Guide-tugHall.html** are the user guides to install, run, and use tugHall simulator in R Markdown and html formats.
- **User-Guide-Analysis.Rmd** and **User-Guide-Analysis.html** are the user guide to analyze the results of a single simulation in R Markdown and html formats.
- **/tugHall/** is a directory with the program code, input, and output data.
- **/FOR\_DEVELOPMENT/** is a directory for development.