

# Introduction to statistical analysis with R software for cancer scientists

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# **Introduction to statistical analysis with R software for Cancer Scientists**

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# Outline

1. R overview
2. Mastering R...no thanks. Let's use it
3. *Changing paradigm*: From plots to LATTICES  
(Tumor growth is inherently a three-dimensional process).
5. How can R help us (PRACTICALLY)
  - 5A Neural Network with cancer data with R
  - 5B R and the power of simulation for cancer data  
(Creating and visualizing spatial simulations of tumor growth)

## R overview but, before we start, some Q&As

As an MD **and** Researcher do I need to know R?

**YES**

As an MD **and** Researcher can I learn R?

**YES**

**How?**

Tutorials AND other *ad hoc* resources;  
learning by doing (COPY AND PASTE!)  
interdisciplinary links among different depts.;

As an MD **and** Researcher should I know Statistics?

Being a good practitioner is  
usually enough  
Again interdisciplinary links  
(statisticians,  
mathematicians, physicists)  
are vital

# Download R and RStudio

- Download R :

<http://cran.r-project.org/bin/>

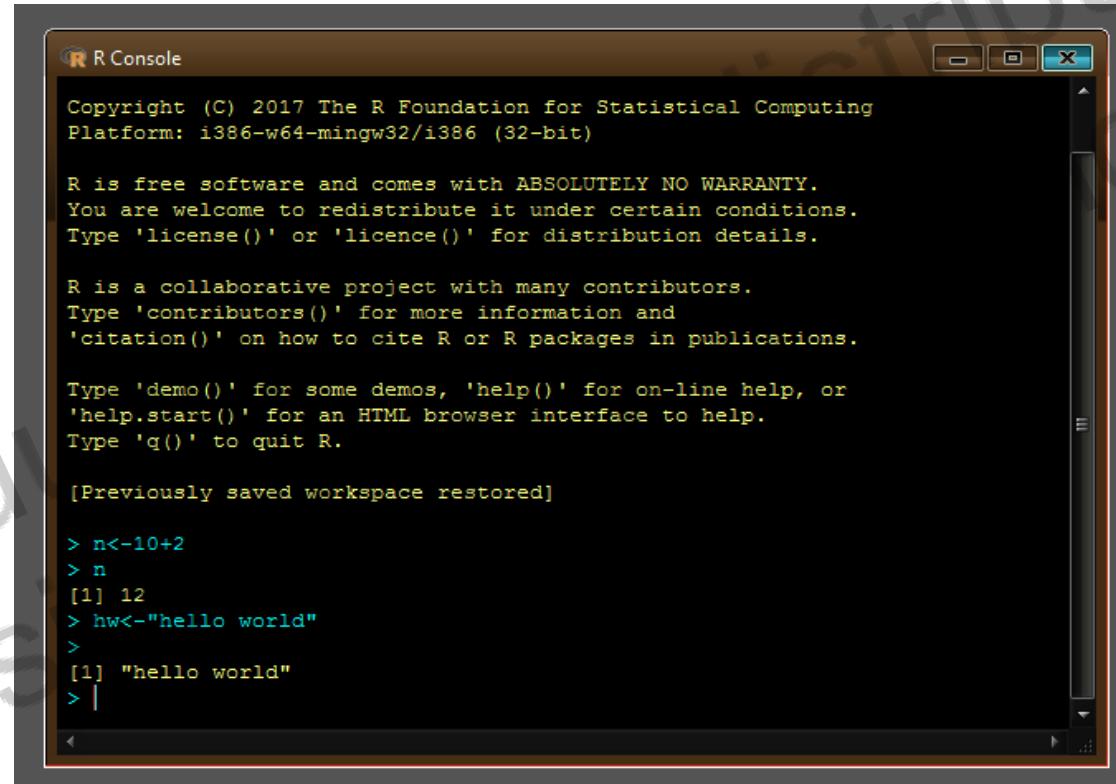
# Installation

## Installing R on windows PC :

- Use internet browser to point to : <http://mirror.aarnet.edu.au/pub/CRAN>
- Under the heading Precompiled Binary Distributions, choose the link Windows.
- Next heading is R for Windows; choose the link base.
- Click on download option(R xxxxx for windows).
- Save this to the folder C:\R on your PC.
- When downloading is complete, close or minimize the Internet browser.
- Double click on R 3.4.1-win32.exe in C:\R to install.

# R is Relatively Easy

- Double click the R icon on the Desktop and the R Console will open.
- Wait while the program loads. You observe something like this.



The image shows a screenshot of the R Console window. The window title is "R Console". The text area displays the standard R startup message, including copyright information, a warranty notice, and instructions for redistribution. Below this, the R environment is shown as a workspace. The user has entered the following commands:

```
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: i386-w64-mingw32/i386 (32-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

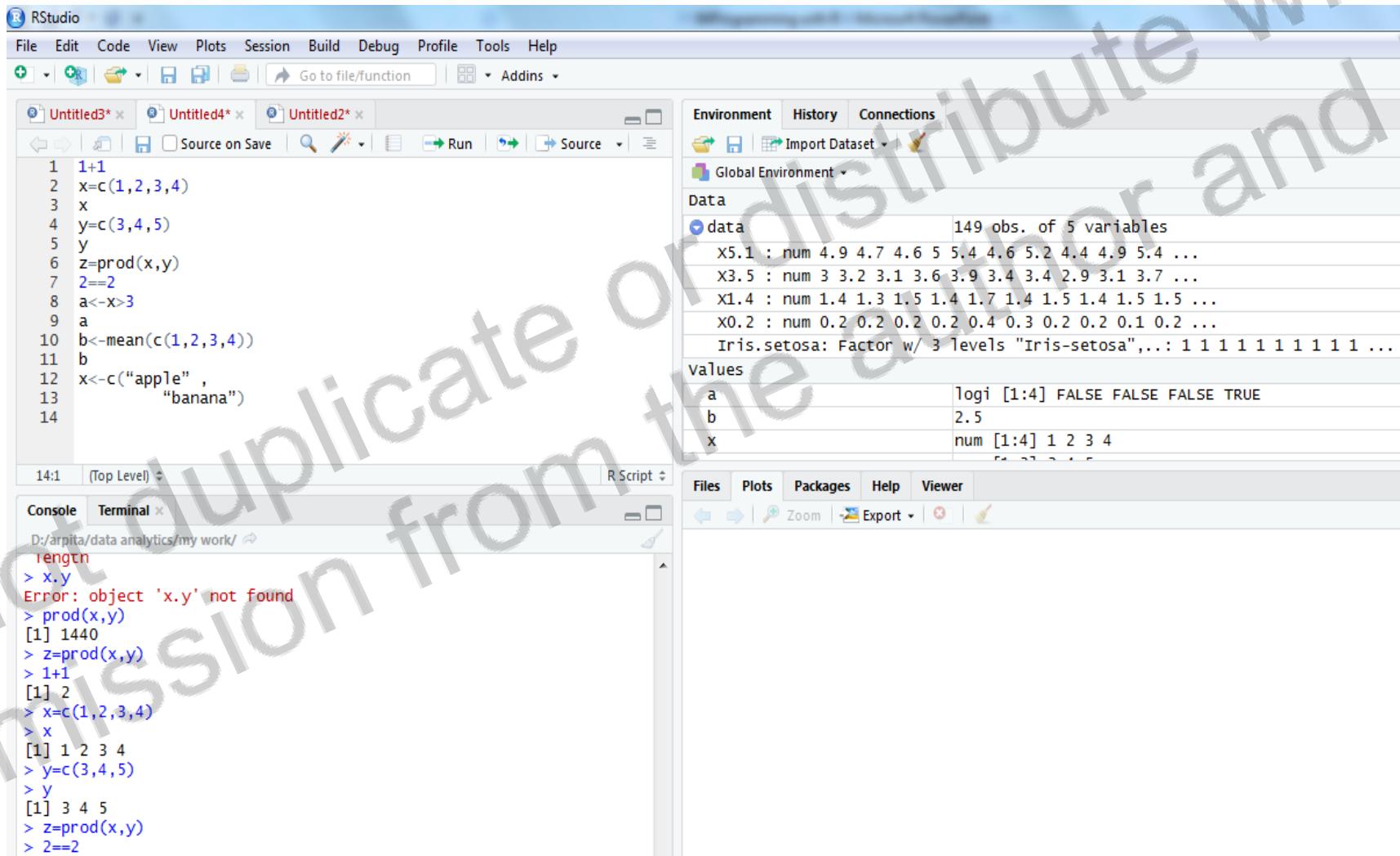
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Previously saved workspace restored]

> n<-10+2
> n
[1] 12
> hw<-"hello world"
>
[1] "hello world"
> |
```

- You can type your own program at the prompt line >.

# R command in integrated environment



The screenshot shows the RStudio interface with the following components:

- Script Editor:** Contains the following R code:

```
1 1+1
2 x=c(1,2,3,4)
3 x
4 y=c(3,4,5)
5 y
6 z=prod(x,y)
7 2==2
8 a<-x>3
9 a
10 b<-mean(c(1,2,3,4))
11 b
12 x<-c("apple",
13 "banana")
14
```

- Console:** Displays the following R session output:

```
D:/arpita/data analytics/my work/
> length
> x.y
Error: object 'x.y' not found
> prod(x,y)
[1] 1440
> z=prod(x,y)
> 1+1
[1] 2
> x=c(1,2,3,4)
> x
[1] 1 2 3 4
> y=c(3,4,5)
> y
[1] 3 4 5
> z=prod(x,y)
> 2==2
```

- Global Environment:** Shows the following data:

Object	Type	Value
data	149 obs. of 5 variables	X5.1 : num 4.9 4.7 4.6 5 5.4 4.6 5.2 4.4 4.9 5.4 ... X3.5 : num 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 3.7 ... X1.4 : num 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 1.5 ... X0.2 : num 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 0.2 ... Iris.setosa: Factor w/ 3 levels "Iris-setosa",...: 1 1 1 1 1 1 1 1 1 1 ...
a	logi [1:4]	FALSE FALSE FALSE TRUE
b	2.5	
x	num [1:4]	1 2 3 4

# How to use R for simple maths

- `> 3+5`
- `> 12 + 3 / 4 - 5 + 3*8`
- `> (12 + 3 / 4 - 5) + 3*8`
- `> pi * 2^3 - sqrt(4)`
- `>factorial(4)`
- `>log(2,10)`
- `>log(2, base=10)`
- `>log10(2)`
- `>log(2)`

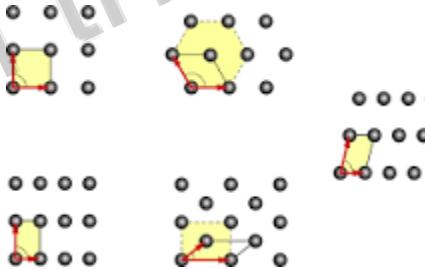
**Note**

- R ignores spaces

# Lattice

Lattice data are **observations from a random process observed over a countable collection of spatial regions, and supplemented by a neighborhood structure.**

The observation locations can be regular (equally spaced grid) or irregular, and data at a particular location typically represent the entire region.



a regular geometrical arrangement of points or objects over an area or in space  
*specifically* : the arrangement of atoms in a crystal

# HOW R PRACTICALLY HELP US

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## canceR

platforms all rank 1021 / 2140 support 1 / 4 in BioC 7 years  
build ok updated < 3 months dependencies 155

DOI: [10.18129/B9.bioc.canceR](https://doi.org/10.18129/B9.bioc.canceR) [f](#) [t](#)

A Graphical User Interface for accessing and modeling the Cancer Genomics Data of MSKCC

Bioconductor version: Release (3.15)

The package is user friendly interface based on the `cgdsr` and other modeling packages to explore, compare, and analyse all available Cancer Data (Clinical data, Gene Mutation, Gene Methylation, Gene Expression, Protein Phosphorylation, Copy Number Alteration) hosted by the Computational Biology Center at Memorial-Sloan-Kettering Cancer Center (MSKCC).

Author: Karim Mezhoud, Nuclear Safety & Security Department, Nuclear Science Center of Tunisia.

Maintainer: Karim Mezhoud <[kmezhoud@gmail.com](mailto:kmezhoud@gmail.com)>

Citation (from within R, enter `citation("canceR")`):

Tunisia, KMNS&SDNSCo (2022), *canceR: A Graphical User Interface for accessing and modeling the Cancer Genomics Data of MSKCC*, R package version 1.30.01.

### Installation

To install this package, start R (version "4.2") and enter:

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install("canceR")
```

For older versions of R, please refer to the appropriate [Bioconductor release](#).

### Documentation

To view documentation for the version of this package installed in your system, start R and enter:

```
browseVignettes("canceR")
```

### Documentation »

#### Bioconductor

- Package [vignettes](#) and manuals.
- [Workflows](#) for learning and use.
- Several [online books](#) for comprehensive coverage of a particular research field, biological question, or technology.
- [Course and conference](#) material.
- [Videos](#).
- Community [resources](#) and [tutorials](#).

[R / CRAN](#) packages and [documentation](#)

### Support »

Please read the [posting guide](#). Post questions about Bioconductor to one of the following locations:

- [Support site](#) - for questions about Bioconductor packages
- [Bioc-devel](#) mailing list - for package developers

**1. Neural network for cancer research**

**2. simulations of tumor growth**

Practical sessions – share screen mode

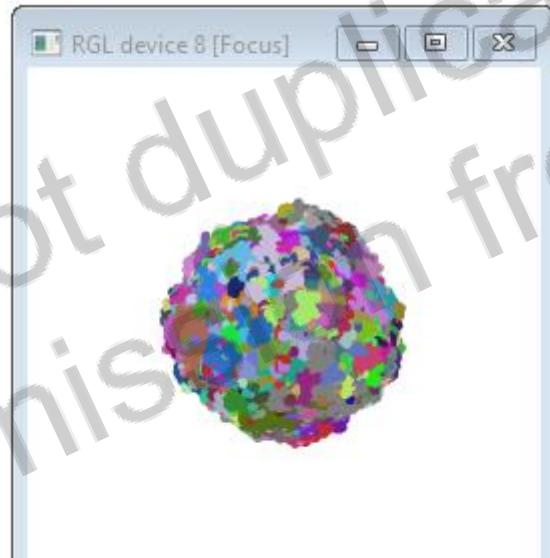
## Creating and visualizing spatial simulations of tumor growth using SITH

The cells within a cancerous tumor are usually highly diverse. An average tumor contains **hundreds of thousands of mutations** spread throughout billions of cancer cells, although it is thought that only a **small** percentage of these mutations are “drivers” which facilitate the progression of cancer into later stages (Greaves and Maley [2012](#)). A lack of understanding about the **evolutionary** process which results in the observed intratumor heterogeneity is a major obstacle preventing the development of effective cancer therapies (Stanta and Bonin [2018](#)).

```

> out <- simulateTumor(max_pop = 250000, verbose = FALSE)
> visualizeTumor(out, background = "white")
>
> names(out)
[1] "cell_ids"      "genotypes"      "muts"          "phylo_tree"    "color_scheme"  "drivers"
[7] "time"          "params"
> head(out$cell_ids)
   x  y  z genotype nmut distance
1 15 -16 17   6358   2 27.74887
2  1 -23 32    16   2 39.42081
3 -11 19 28   1665   3 35.58089
4 13 -5 34   27691   2 36.74235
5 32 17 -3   64270   7 36.35932
6 43  1 -9   34824   4 43.94315
> head(out$muts)  ## mutation allele frequency (MAF)
  id count MAF
1 0 250000  1
2 1 0 0
3 2 0 0
4 3 0 0
5 4 0 0
6 5 0 0
>
>
> visualizeTumor(out, background = "white")          ## 3D plot of the simulated tumor
> visualizeTumor(out, background = "white")
>
>
> par(mfrow = c(1,2))
> plotSlice(tumor = out)
> plotSlice(tumor = out, plot.type = "heat")
> plotSlice(tumor = out)
> visualizeTumor(out, background = "white")
> sp <- spatialDistribution(tumor = out)

```



```

library(tumr)
set.seed(1126490984)

out <- simulateTumor(max_pop = 250000, verbose = FALSE)
visualizeTumor(out, background = "white")

names(out)
head(out$cell_ids)
head(out$muts)  ## mutation allele frequency (MAF)

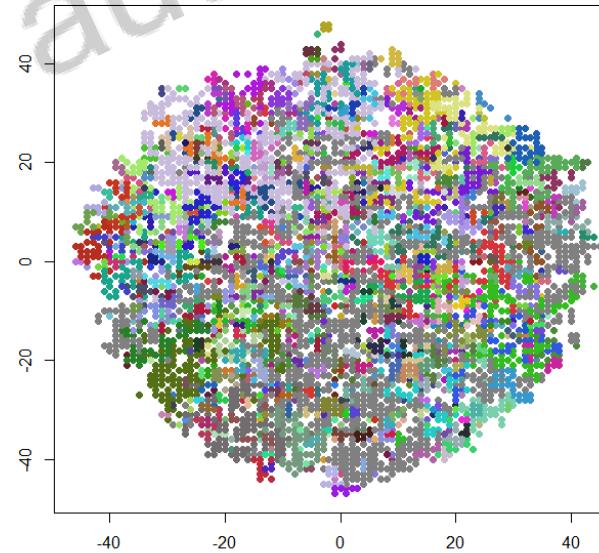
visualizeTumor(out, background = "white")          ## 3D plot of the simulated tumor
visualizeTumor(out, background = "white", plot.type = "heat") ## which colors cells on a scale from blue to red,
                                                               ## depending on the number of mutations within the cell.

par(mfrow = c(1,2))
plotSlice(tumor = out)
plotSlice(tumor = out, plot.type = "heat")

sp <- spatialDistribution(tumor = out)

# Spatial distribution of mutants

```



## Take home concepts

### Use R knowing that it is not your core business

Interdisciplinary approach!  
Alone we are the  
“nothing” proceeding in the  
“Nihil”

Use grants, collaborations, students exchanges to establish a statistical R-based community within your research groups

R is free and the information/help Available on the net can solve most of the issues

Questions? Comments?

THANK YOU!!

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