



Karolinska  
Institutet

SciLifeLab

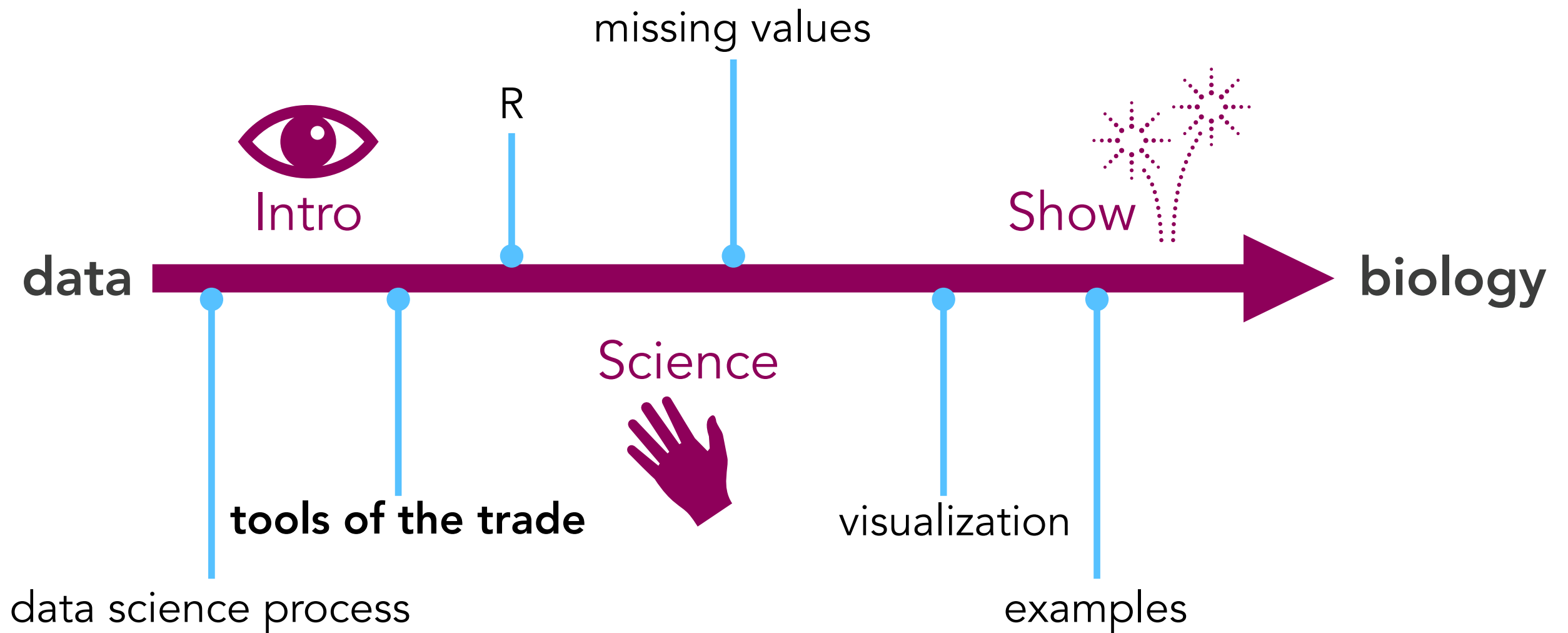


# Tools of the trade

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# We need tools for each step

Data sourcing

Data value chain

Data acquisition

Data storage

Data analysis

Data visualization

# We need tools for each step

Data sourcing

Data value chain

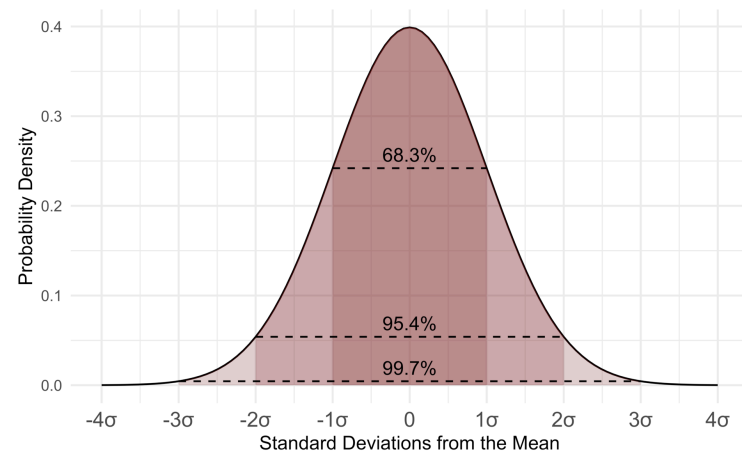
Data acquisition

Data storage

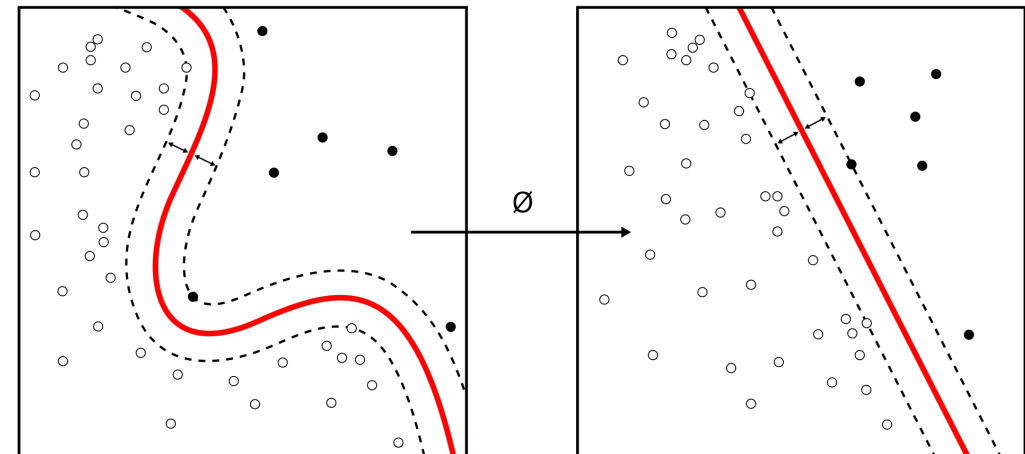
Data analysis

Data visualization

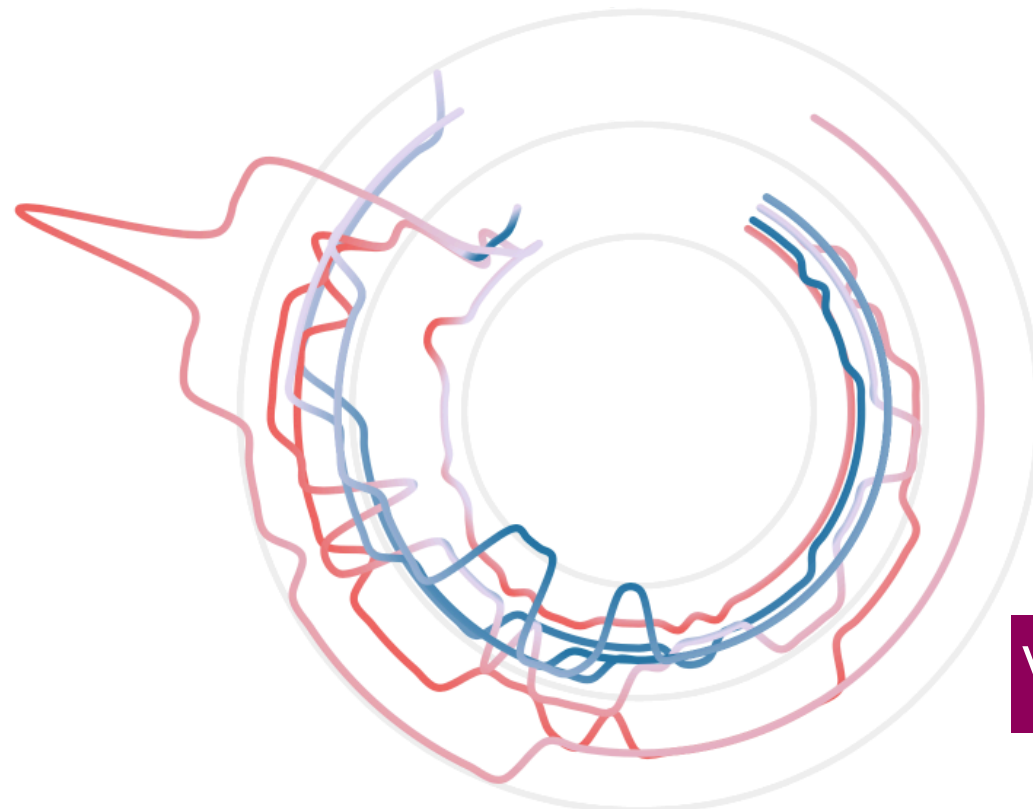
# Multiple faces



Statistics



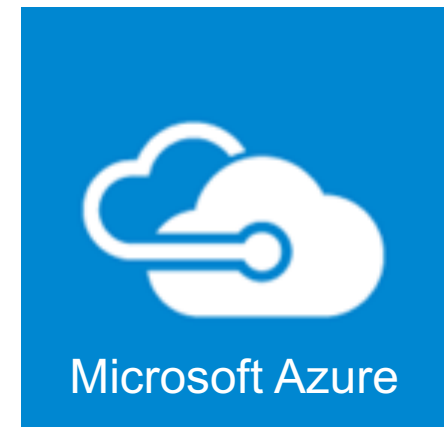
Machine Learning



Visualization

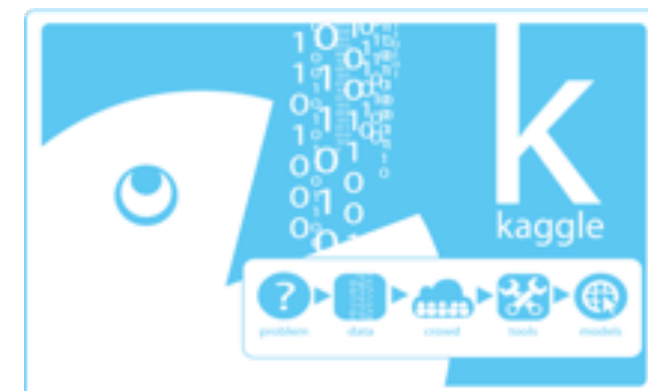
# Multiple tools

Perseus = Interface for R



Google Cloud Platform

IBM Watson



**Why *R***  
**rather than *Perseus*?**

# Limitations

You find what is allowed to find.



You find \*



```
41 # determine protein overlap to cell line panel
42 proteins.meltome <- row.names(meltome.avg)
43 panel <- removeNAsFromESet(eSet = panel.raw, na_ratio = 0)
44 proteins.panel <- fData(panel)$gene_symbol
45 intersection <- intersect(proteins.meltome, proteins.panel)
```

Damn \*\*\*\*, isn't that hard to learn?



# How I learned R

1. Find a problem.
2. Divide it in smaller pieces.
3. Google solutions for them or ask seniors.
4. Implement!

That's exactly what we do now!

# Quick R crash course

# Goals

Try, try, try, ...

get a feeling of R's power

preparation to missing value imputation

Please start up RStudio on your machine.

Find all the code here:

**<https://github.com/higsch/bioinfo-workshop>**