

Sara Pidò

Expected PhD starting date: May 2020

Adv: Stefano Ceri



GeCo 5.0: User-Friendly Platform for supporting Genomic Computing

Other works

- Gaia Ceddia, Sara Pidò, Marco Masseroli: 'Computational analysis and comparison of gene networks from TCGA normal and cancer data'
Presented at CIBB 2019 and to be submitted at Lecture Notes in Bioinformatics.
- Sara Pidò, Gaia Ceddia, Marco Masseroli: 'Discovering relevant biomarkers by computational analysis on co-expression networks'
(Working on)



Motivation: Better Bioinformatics

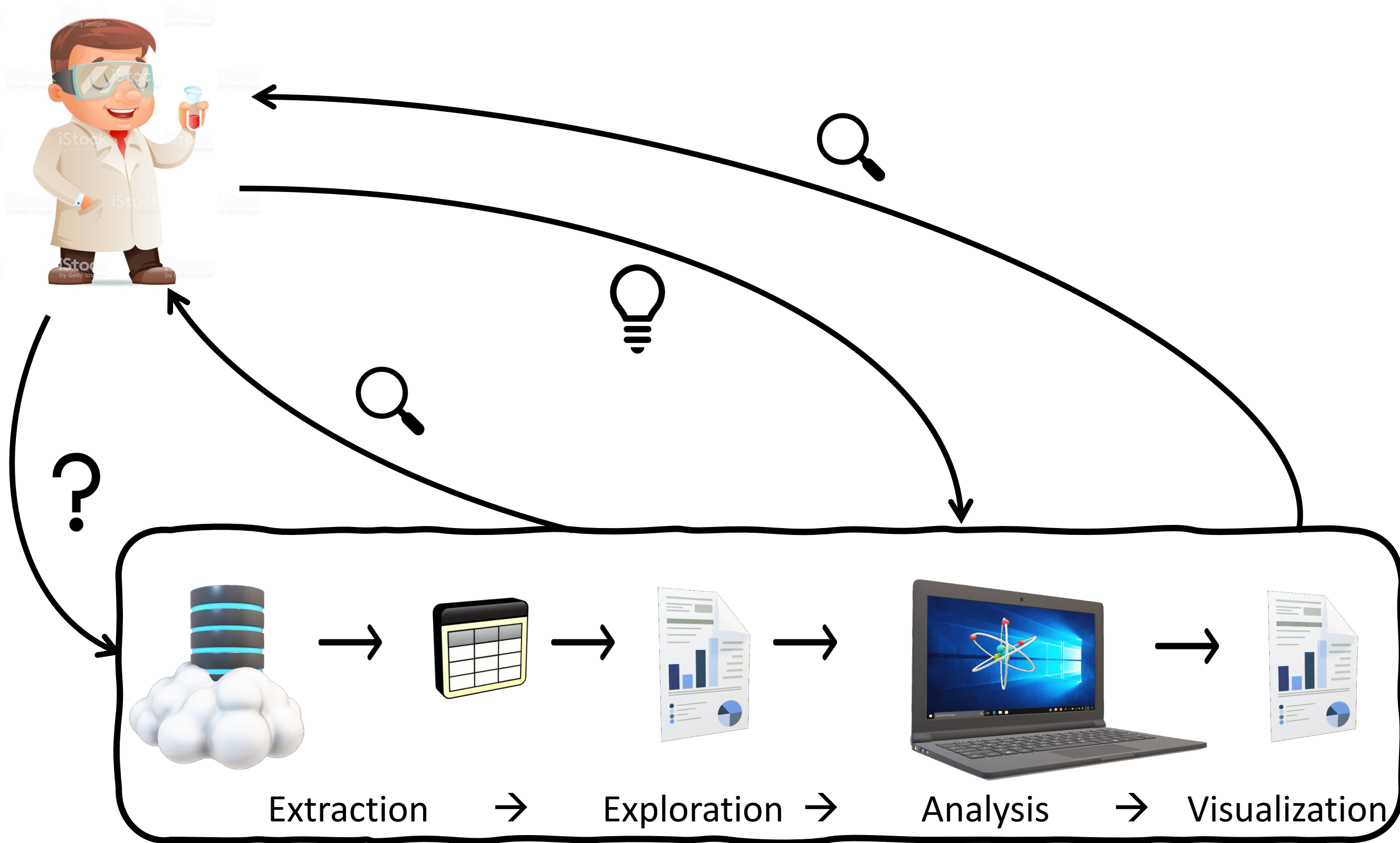
GOALS:

- Improving the accessibility to omics-data;
 - Improving the usability of bioinformatics tools and methods;
- Enable the biologist to perform complex computational biology studies.

CHALLENGES:

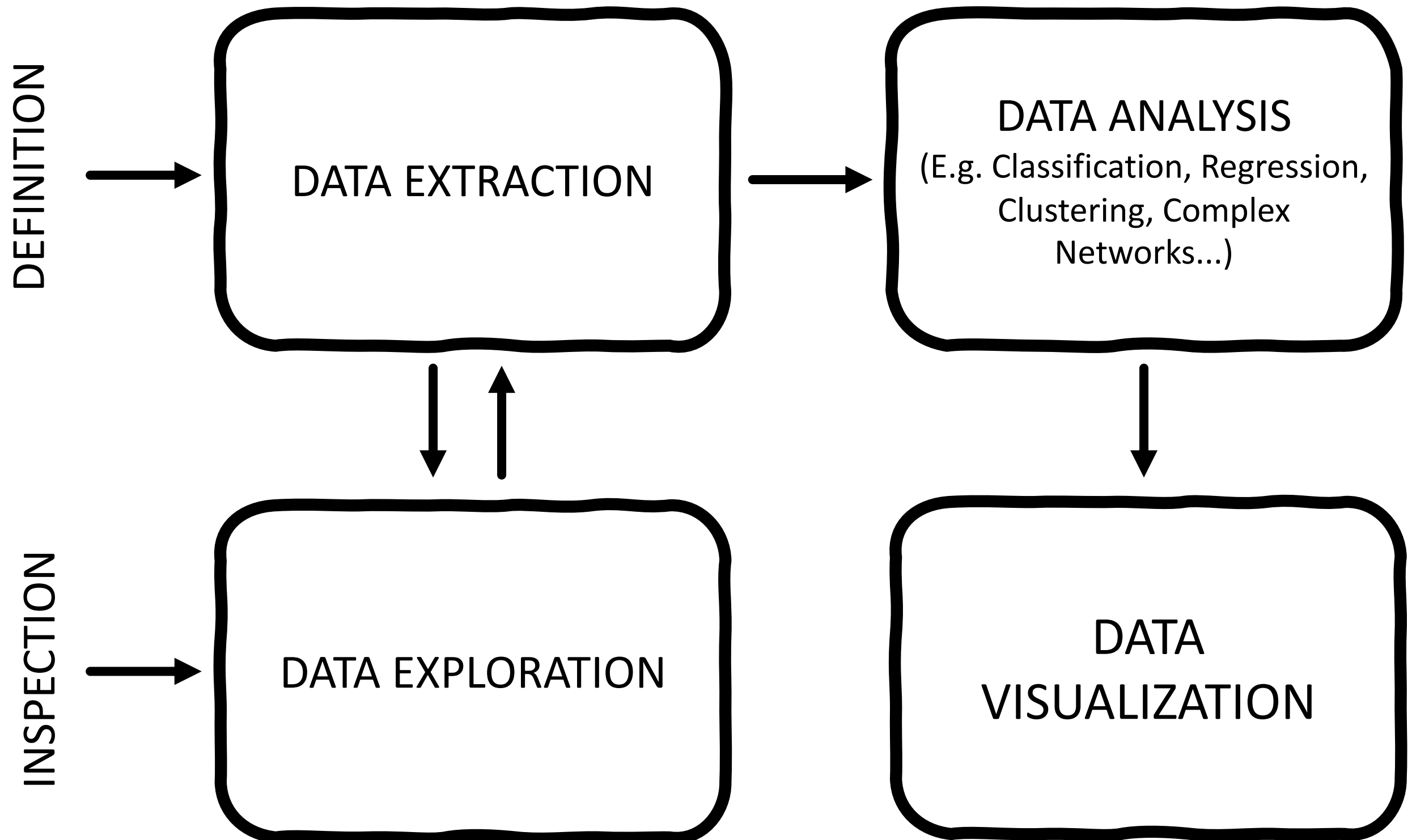
- The user is not required to have advanced computer science skills;
- The interface should be user-friendly;
- At the same time, guarantee the flexibility and complexity of the analysis;
- Enforce reproducibility.

Workflow

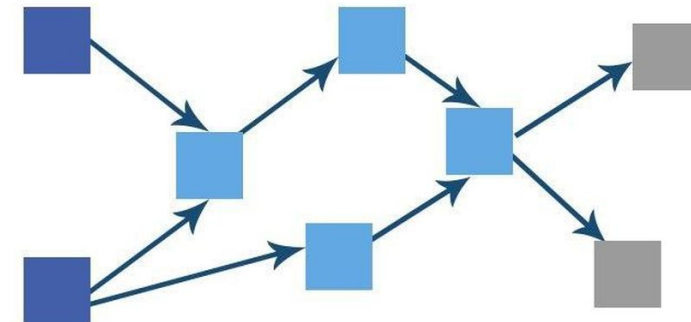
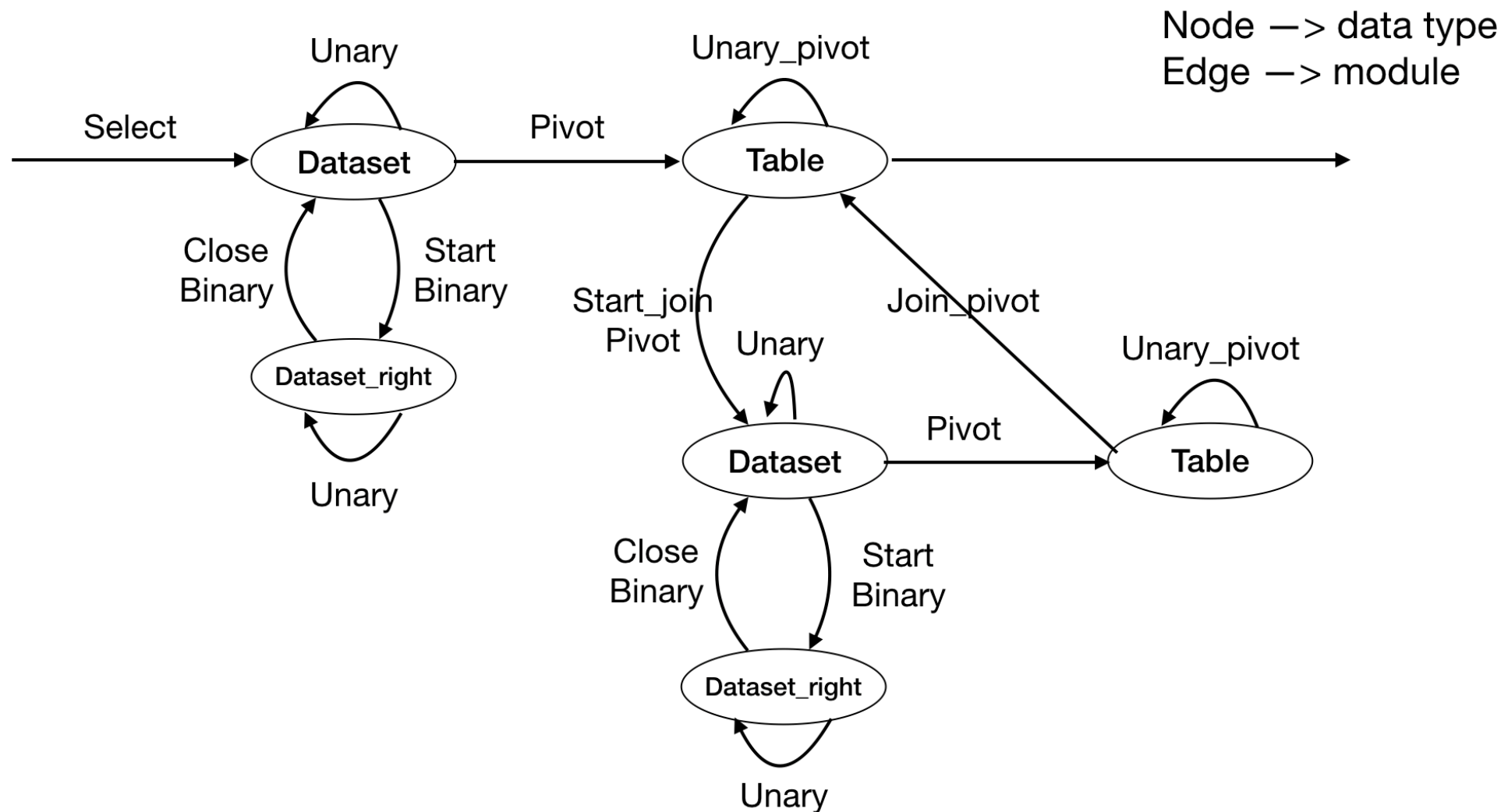


GECCO 5.0

Main Phases



Data Extraction



Data Analysis

3° LEVEL BLOCK → Parameter Tuning

2° LEVEL BLOCK → Validation

1° LEVEL BLOCKS

Clustering

Classification

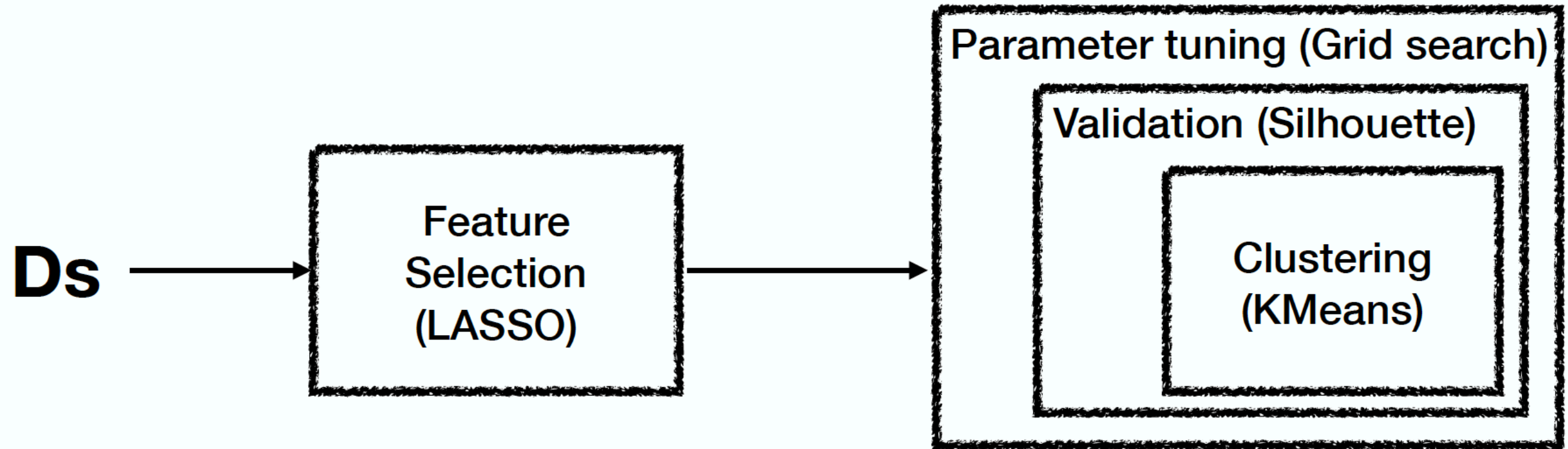
Regression

Complex
Networks

Dimensionality
Reduction

Hypotesis
Testing

An Example



```
Parameter_tuning (  
  Validation (  
    Clustering (  
      Feature_selection (Ds, method='lasso'),  
      method='KMeans', n_clusters=?),  
      method='silhouette'),  
      method='Grid search')
```