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BioHPC

Machine Learning using R

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2021-08-18

Outline

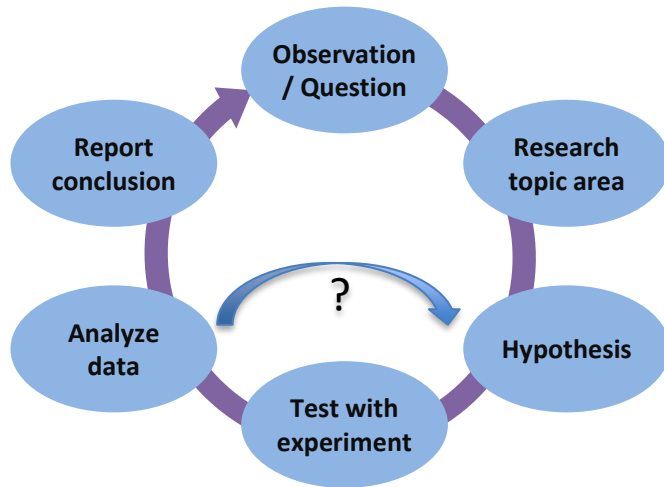
A primer on ML

- ML for hypothesis search & discovery

Hand-on in R

- Assessing available data
- Picking algorithms/model types
 - Descriptive / Predictive models
- Pre-processing of data
- Cross validation
- Assessing results

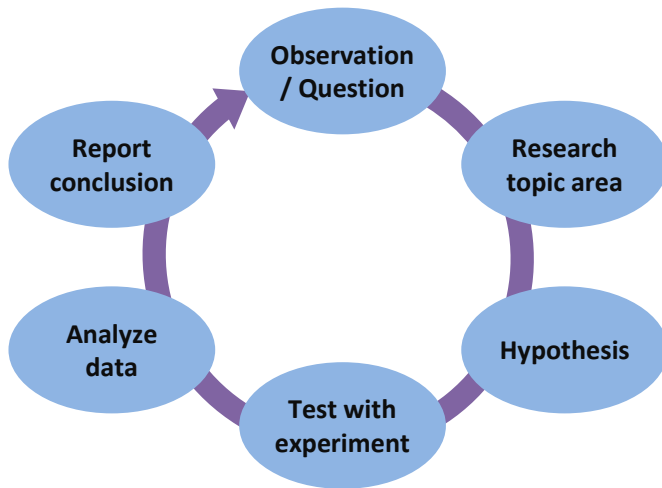
ML for hypothesis search & discovery



The Scientific Method

- **Universal-Orthodox**
all sciences, all scientists
- **Hypothesis-centric**
Focus on accepting/dismissing hypothesis
- **Cyclic-open**
Fail test > re-pose question: inner cycle

ML for hypothesis search & discovery



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Learning

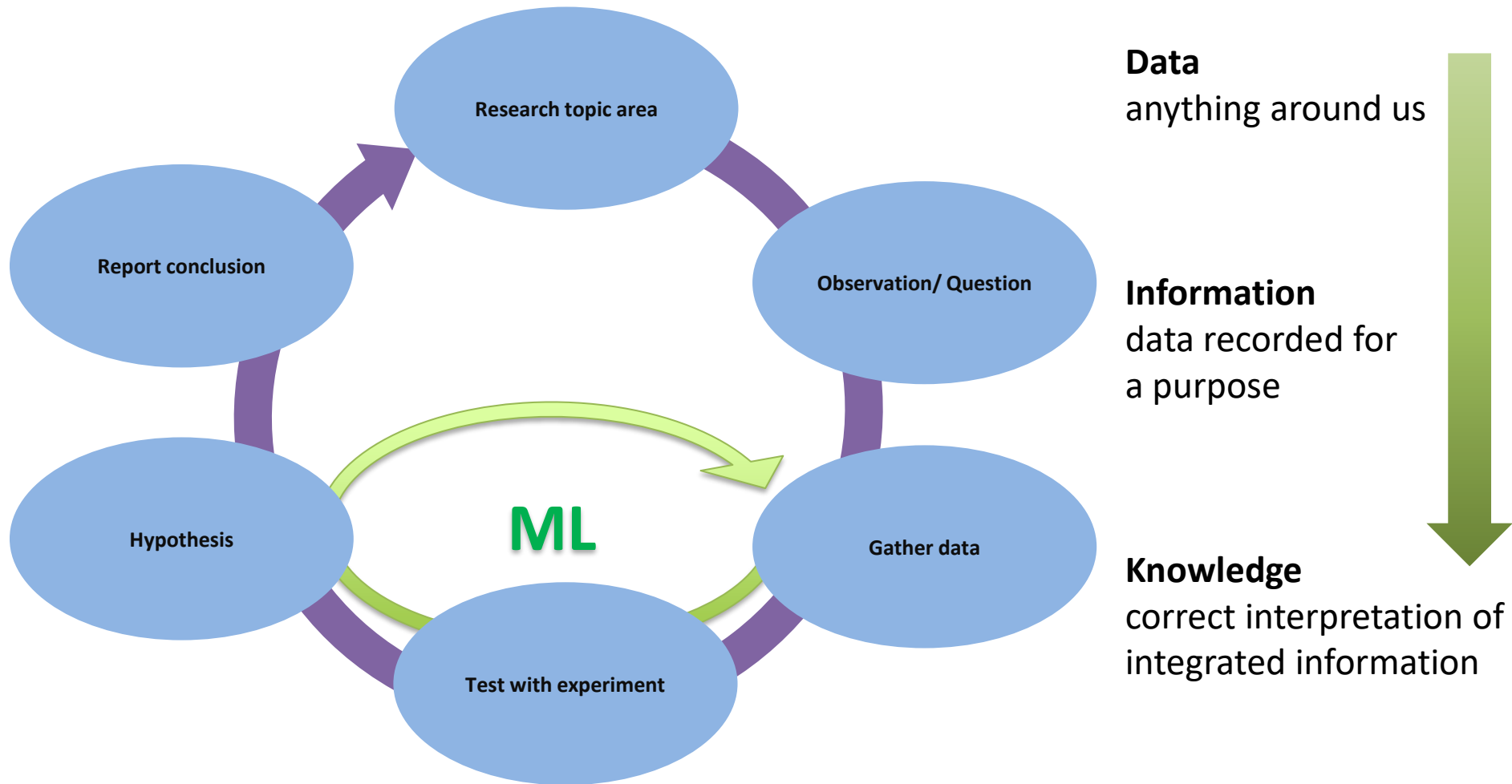
Inference



The ML Method

- **Domain-Unorthodox**
Results outweigh Method
- **Data-centric**
Improve data rather than question the observation
- **Causality/Predictability**
correct prediction ?= accept hypothesis

ML for hypothesis search & discovery



Hands-on in R

In this tutorial we will:

- Explore some unknown dataset
- Establish a few questions we can learn the answer from the data
- Preprocess/sample/reshape data if necessary
- Run a few different ML models to answer our questions
- Assess the model results
- Present our findings in a compact format

You will need the following:

RStudio:

- Personal computer
- BioHPC workstation
- Nucleus node

Sample data:

<https://archive.ics.uci.edu/ml/datasets/wine+quality>

Accessing available data

Data properties

The data provided contains measurements of Portuguese vino verde. Each row represents measurements of a specific wine label. Measurements are values of physio-chemical properties of the wine. Each row contains a 'quality' indicator as scored by tasters. Data is available for Red and White whines.

Possible questions:

- Can we determine if wine is Red or White depending on physiochemical attributes?
- Can we determine perceived quality of the wine based on physiochemical attributes?
 - Quality as label (classification)
 - Quality as value (regression)

RStudio demo

Q&A time

Thank you