# Building meaningful machine learning models for disease prediction

#### Dr Shirin Glander

Dep. of Genetic Epidemiology Institute of Human Genetics University of Münster

shirin.glander@wwu.de

https://shiring.github.io https://github.com/ShirinG

31.03.2017

1/19

#### Table of contents

- What makes a model meaningful?
- Machine Learning (ML) in disease modeling
- A quick recap of ML basics
- 4 How to build ML models in R
- 5 Evaluating ML model performance

#### About me

2005 - 2011 BSc and MSc of Science in Biology Evolutionary genetics, immune memory in Drosophila



2011 - 2015 PhD in Biology
Is the immune system of plants required to adapt to flowering time change?

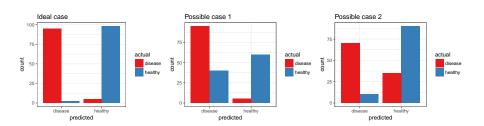
since 2015 Bioinformatics Postdoc
Autoinflammatory diseases & innate immunity
Next Generation Sequencing

# What makes a model meaningful?

# Meaningful models

- answer the question(s) posed...
- ... with sufficient accuracy to be trustworthy

# Accuracy depends on the problem!



5/19

# Machine Learning (ML) in disease modeling

\*"Machine Learning for Detection and Diagnosis of Disease" (2006). In: Annual Review of Biomedical Engineering 8.1. PMID: 16834566, S. 537-565.

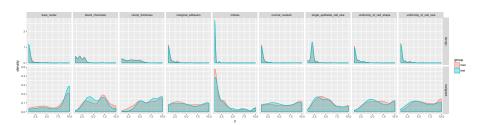
# A quick recap of ML basics

## How to build ML models in R

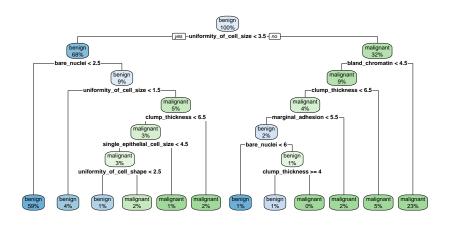
## Session setup

Code will be available on my website and on Github Breast cancer Wisconsin dataset caret package h2o package

# Distribution

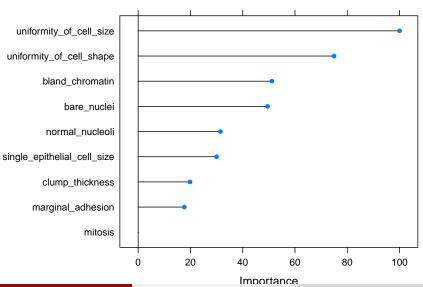


#### **Decision trees**

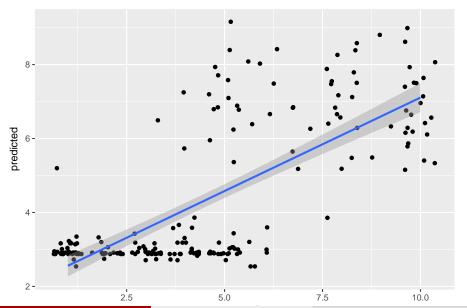


# Random Forest

# Feature importance

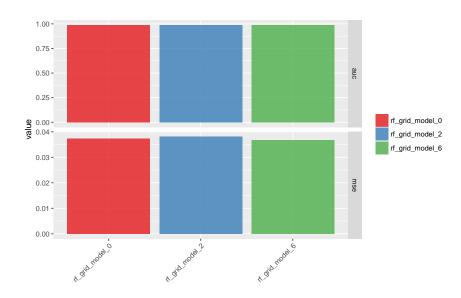


# (Generalized) Linear Models



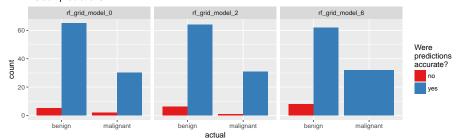
# Evaluating ML model performance

### **AUC and MSE**

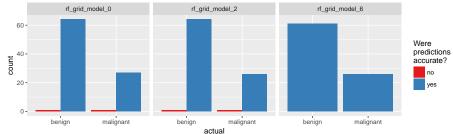


### Predictions on test data

#### Default predictions



#### Stringent predictions



# Thank you for your attention!

# Questions?

Slides and code will be available on Github: https://github.com/ShirinG/Webinar\_ML\_for\_disease

Code will also be on my website: https://shiring.github.io

shirin.glander@wwu.de