

# OncoRay – National Center for Radiation Research in Oncology, Dresden

## **Radiomics** opportunities and challenges

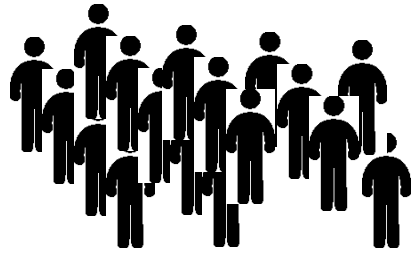
Alex Zwanenburg



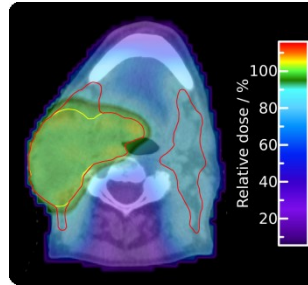
Universitätsklinikum  
Carl Gustav Carus



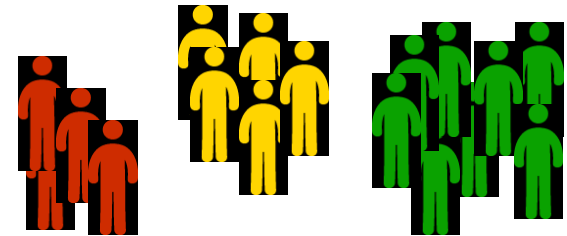
# Radiomics for personalised medicine



same cancer diagnosis

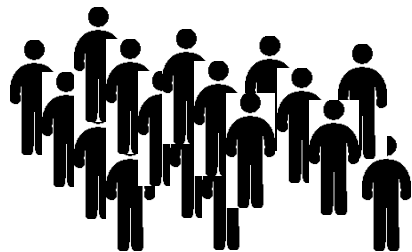


same treatment

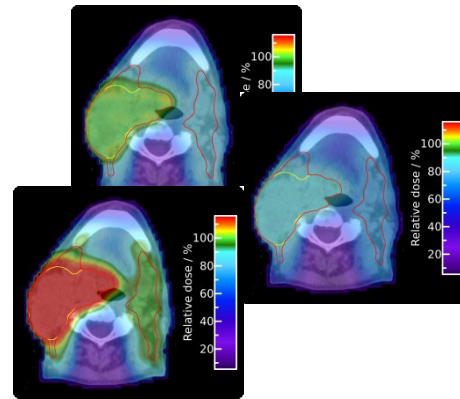


treatment result

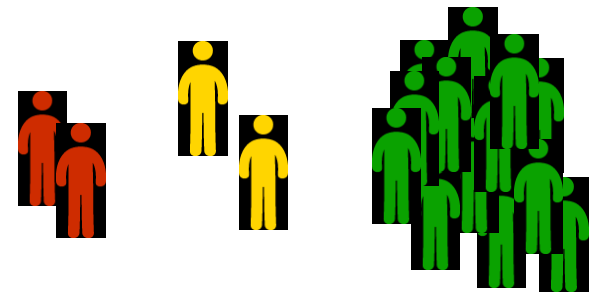
inter-patient heterogeneity



same cancer diagnosis

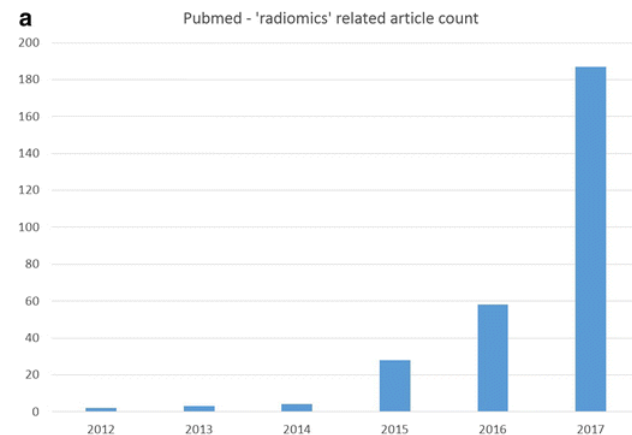
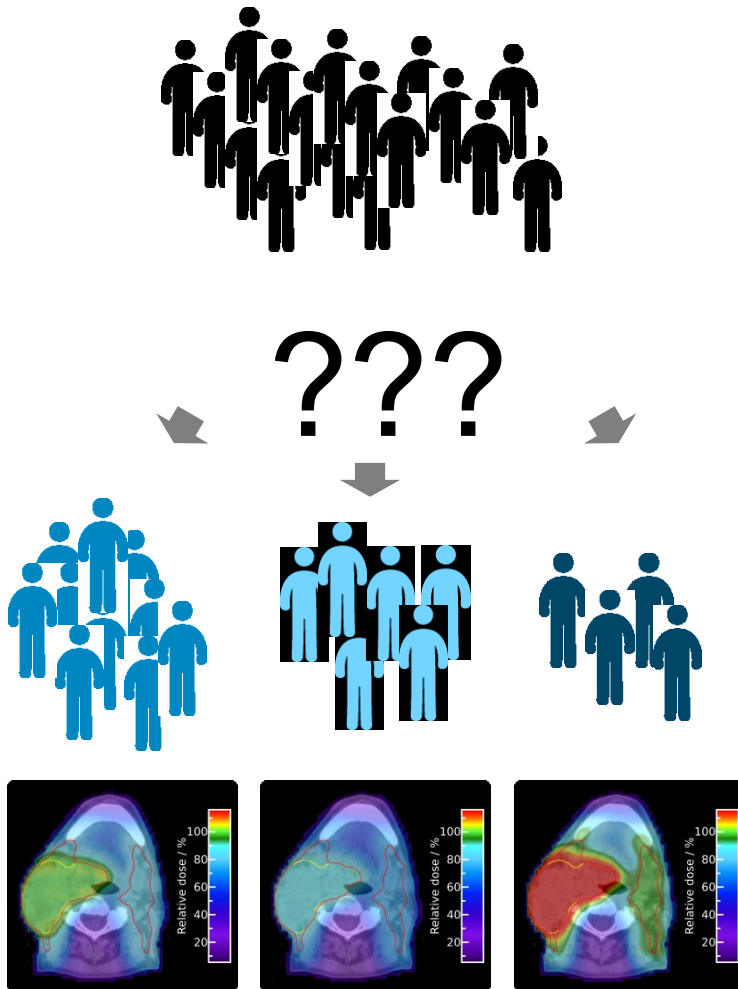


personalised  
treatment



improved treatment result

- **Treatment personalisation based on:**
  - Clinical data (staging)
  - Demographic data (smoking, age)
  - Tumour genetics (gene mutations, RNA expressions)
  - Imaging
- **Radiomics:** High-throughput analysis of medical imaging



Choi, J.Y. Nucl Med Mol Imaging (2018).

# A spectrum of imaging

*amount of quantified information →*

## **Visual assessment**

no quantification

*lung nodule detection,  
tumor localization,  
nodal involvement*

## **Quantitative analysis**

quantification of simple  
features

*tumor staging, RT dose  
planning, treatment  
individualization*

## **Conventional radiomics**

quantification using  
handcrafted features

*treatment  
individualization,  
differentiation of  
histological subtypes*

## **Deep learning radiomics**

convolutional neural  
networks

*lung nodule detection,  
tumor localization &  
segmentation,  
treatment  
individualization*

“*It depends ...*”

- Most radiomic studies are difficult to reproduce:
  - Important details are not reported
  - Bias in development and validation of radiomic models
  - Data may not provide the required heterogeneity:
    - Small data sets
    - Single center cohorts
- Addressing heterogeneity:
  - Use more data from different sources (*study-centric solution*)
  - Reduce sources of variability (*field-wide solution*)

## *Visual assessment*

acquisition  
and  
reconstruction

## **Sources of variability**

- inter-observer variability

## *Visual assessment*

acquisition  
and  
reconstruction

## *Quantitative analysis*

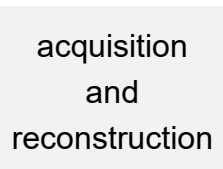
acquisition  
and  
reconstruction

segmentation

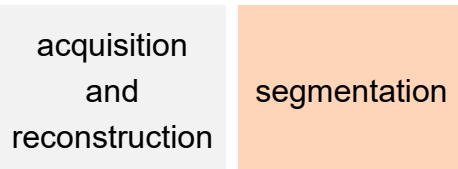
## **Sources of variability**

- inter-observer variability
- image acquisition
- image reconstruction
- segmentation
- software errors

## *Visual assessment*



## *Quantitative analysis*



## *Conventional radiomics*

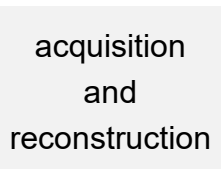


## **Sources of variability**

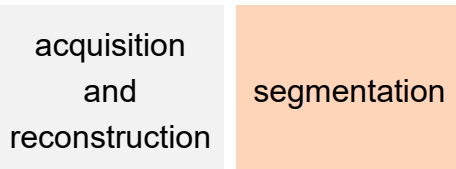
- inter-observer variability
- image acquisition
- image reconstruction
- segmentation
- software errors
- image processing
- feature computation
- modelling approaches
- modelling errors



## *Visual assessment*



## *Quantitative analysis*



## *Conventional radiomics*



## *Deep learning radiomics*



## **Sources of variability**

- inter-observer variability
- image acquisition
- image reconstruction
- segmentation
- software errors
- image processing
- feature computation
- modelling approaches
- modelling errors
- deep learning architecture

# Can we reduce variability?



## Sources of variability

- image acquisition
- image reconstruction
- segmentation
- image processing
- feature computation
- software errors
- modelling approaches
- modelling errors

## Reducing variability

- calibration, standard protocols
- standard protocols & algorithms
- standard protocols, (semi-)automated contouring
- standard workflow, benchmarks
- standard definitions, benchmarks
- benchmarks
- guidelines
- guidelines, benchmarks

# Can we reduce variability?



## Sources of variability

- image acquisition
- image reconstruction
- segmentation
- image processing
- feature computation
- software errors
- modelling approaches
- modelling errors

## Reducing variability

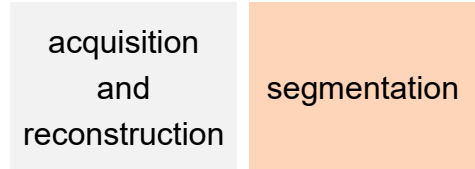
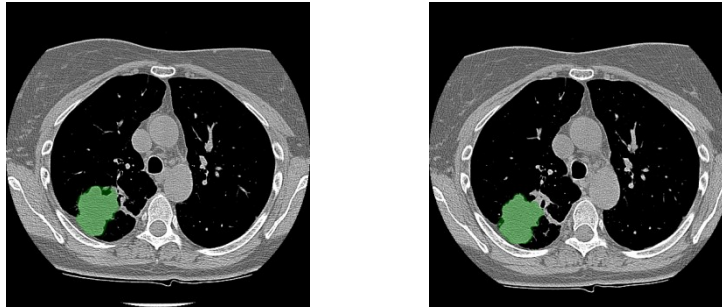
identifying robust features

Image Biomarker Standardisation Initiative

TRIPOD

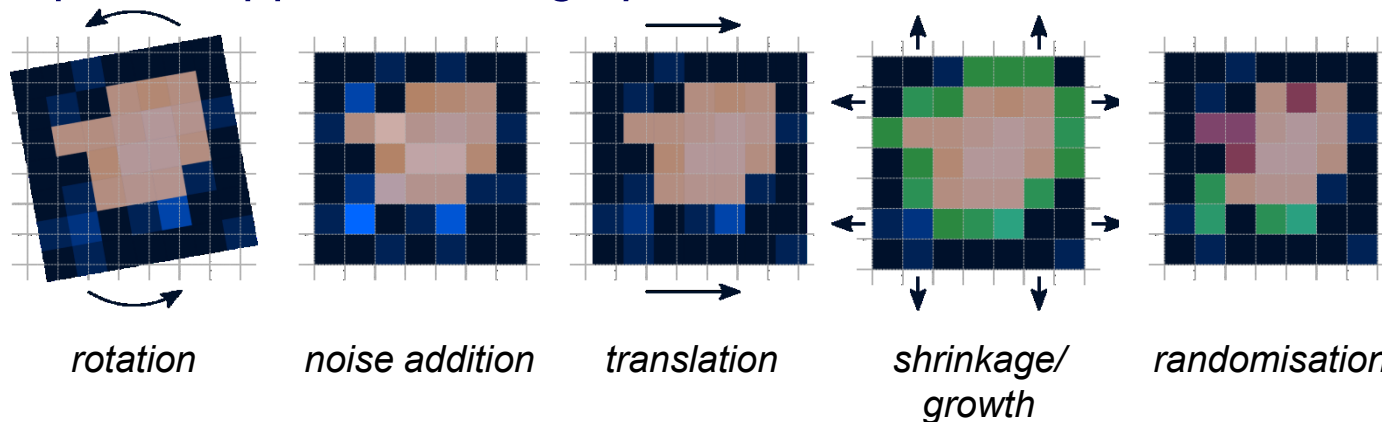
# Finding robust features

- Conventional approach: *test-retest imaging*



Tumour-phenotype specific!

- Proposed approach: *image perturbations*



Perturbations can identify robust features if no test-retest set is available.

# Image biomarker standardisation initiative



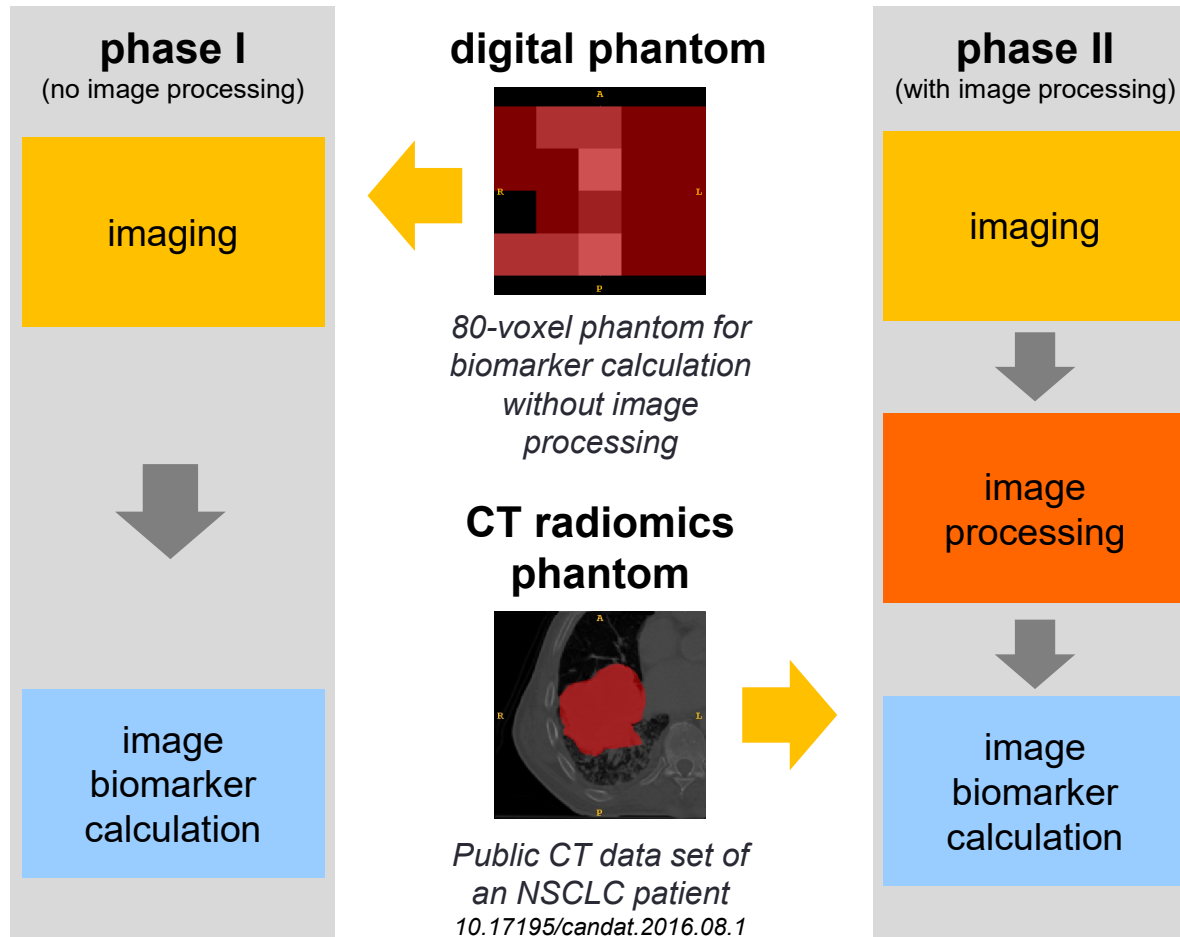
- Aims:
  - Establish **nomenclature** and **definitions** for 172 commonly used image biomarkers
  - Establish an **image processing scheme** for feature computation
  - Provide **benchmark data sets** and associated values for software verification
  - Provide a set of **reporting guidelines**

image  
processing

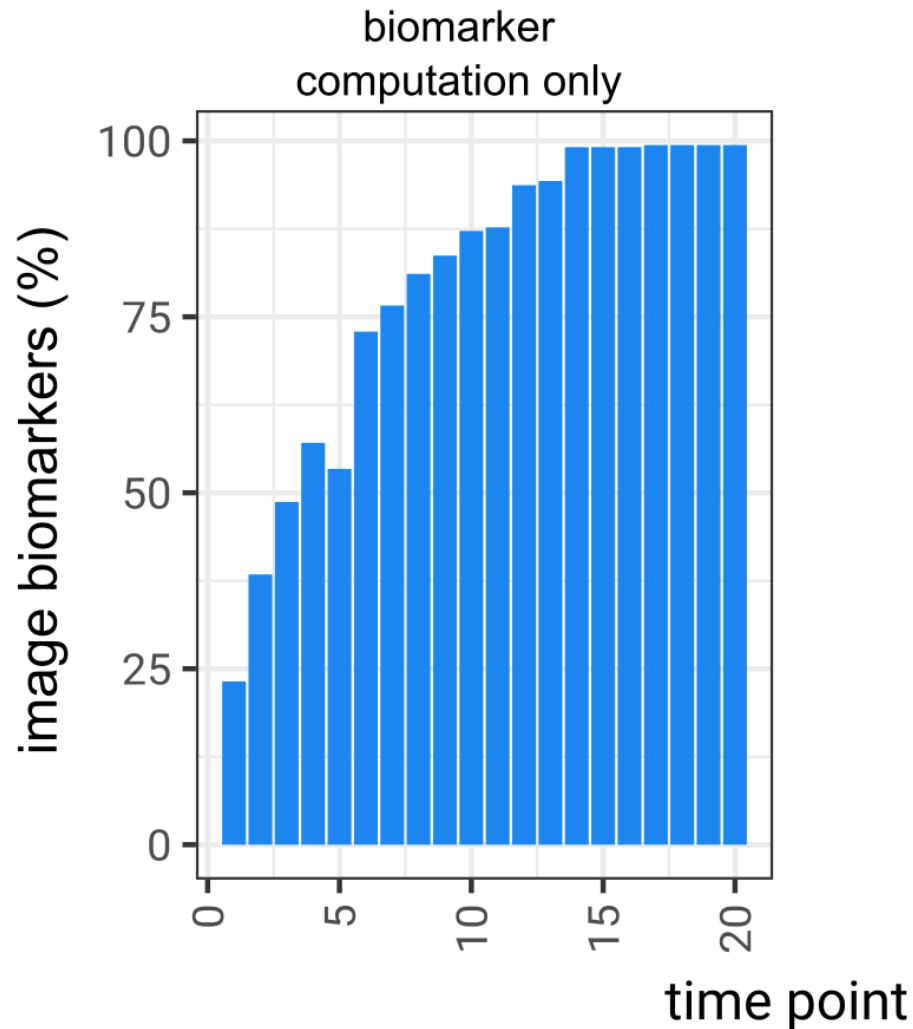
feature  
computation



# Image biomarker standardisation initiative



# Image biomarker standardisation initiative



*Annals of Internal Medicine* RESEARCH AND REPORTING METHODS

Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis (TRIPOD): The TRIPOD Statement

Gary S. Collins, PhD; Johannes B. Reitsma, MD, PhD; Douglas G. Altman, DSc; and Karel G.M. Moons, PhD

*Annals of Internal Medicine* RESEARCH AND REPORTING METHODS

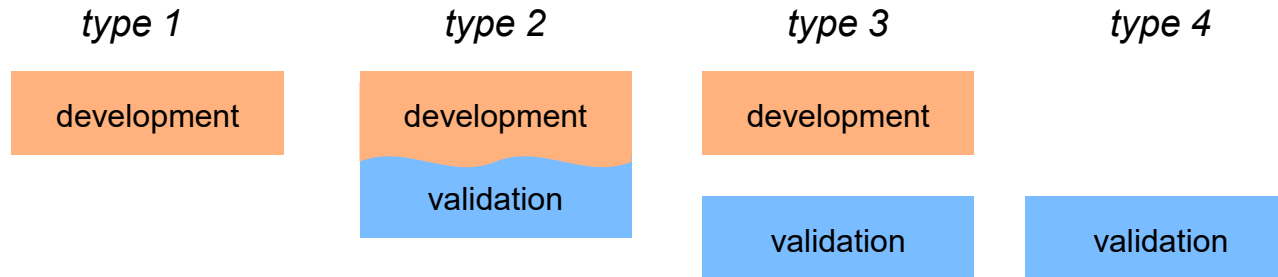
Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis (TRIPOD): Explanation and Elaboration

Karel G.M. Moons, PhD; Douglas G. Altman, DSc; Johannes B. Reitsma, MD, PhD; John P.A. Ioannidis, MD, DSc; Petra Macaskill, PhD; Ewout W. Steyerberg, PhD; Andrew J. Vickers, PhD; David F. Ransohoff, MD; and Gary S. Collins, PhD

- The TRIPOD papers describe:
  - how to create **unbiased** diagnostic and prognostic models
  - how to **report** them
- Use TRIPOD to improve the quality of your research



# The importance of validation



- Example 1: type 1 with univariate feature selection
- Example 2: type 1 with LASSO feature selection (*less features in model*)
- Example 3: type 2 with LASSO and cross-validation
- Example 4: type 2 with feature selection on all data, and cross-validation
- Example 5: type 3 with external validation of 1-4

example	validation set	reported validation	external validation
1	development	0.71 (0.65-0.77)	0.53 (0.43-0.62)
2	development	0.68 (0.62-0.74)	0.55 (0.44-0.65)
3	validation folds	0.51 (0.38-0.64)	0.55 (0.43-0.65)
4	validation folds	0.63 (0.50-0.77)	0.55 (0.46-0.64)

- Many radiomic studies are not reproducible
- Radiomics is susceptible to variability
- The influence of variability can be reduced, but requires:
  - technological development (e.g. auto-segmentation)
  - harmonisation
  - methodological rigour
  - effort and collaboration

# Questions



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STAATSMINISTERIUM  
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