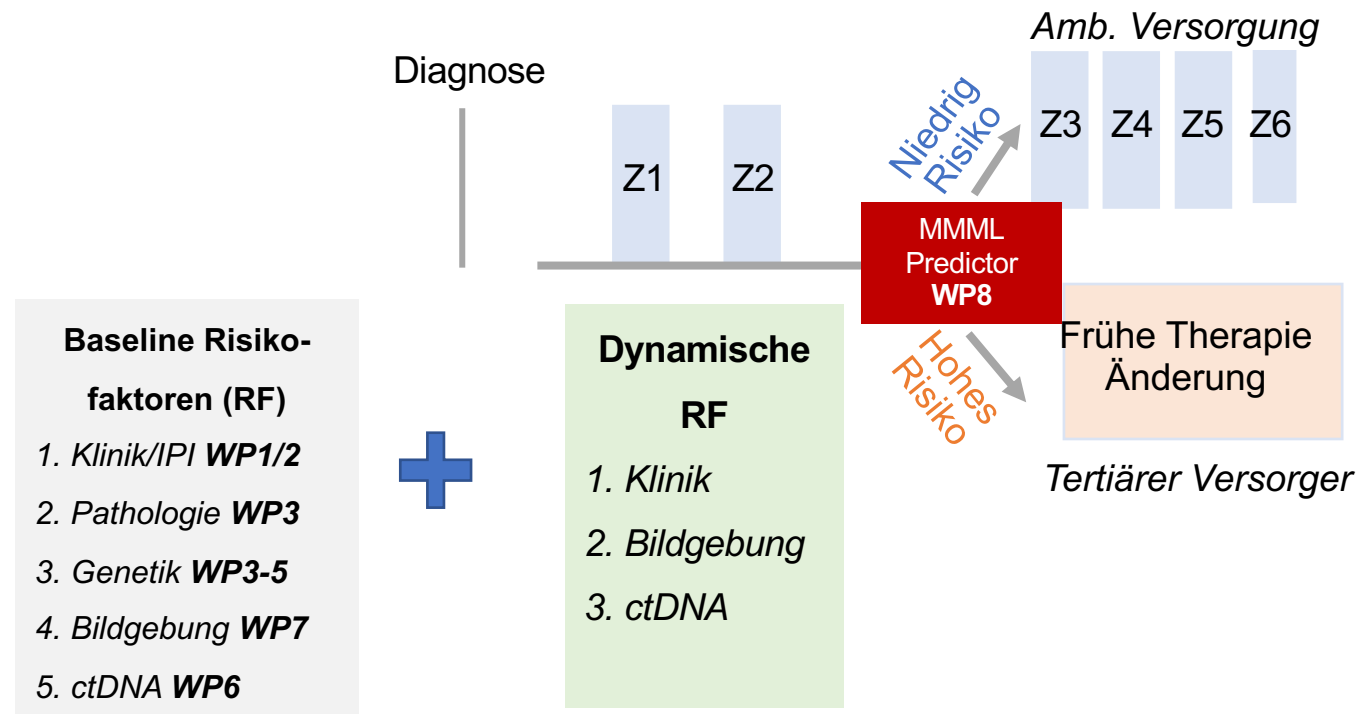


Machine learning based identification of high risk patients (WP8)

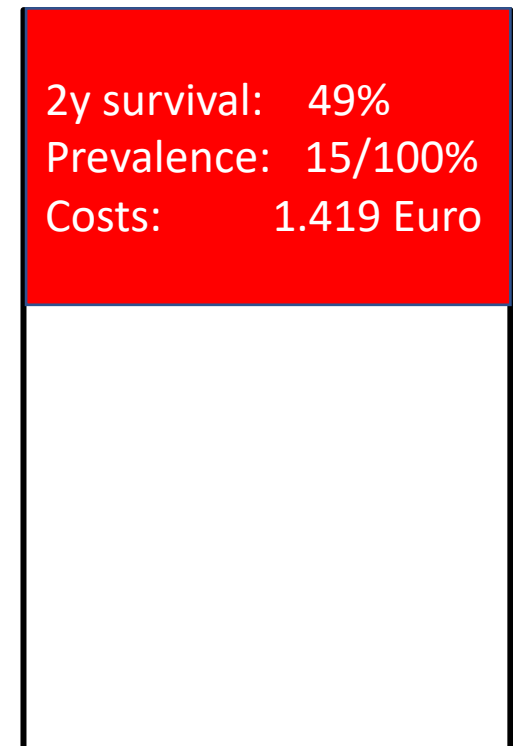
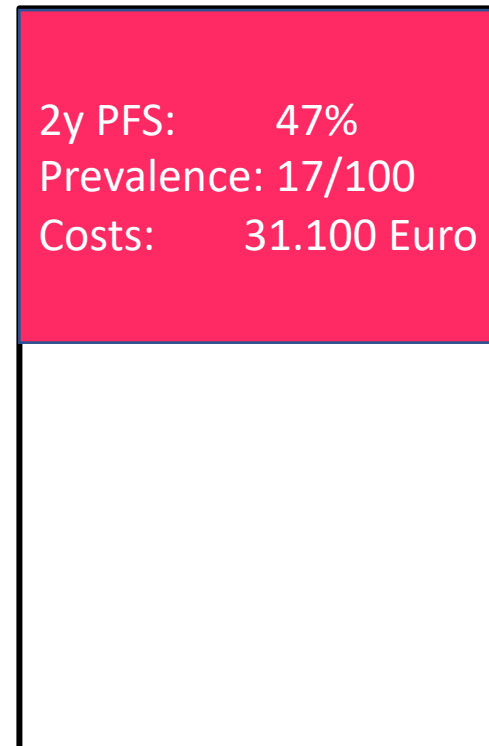
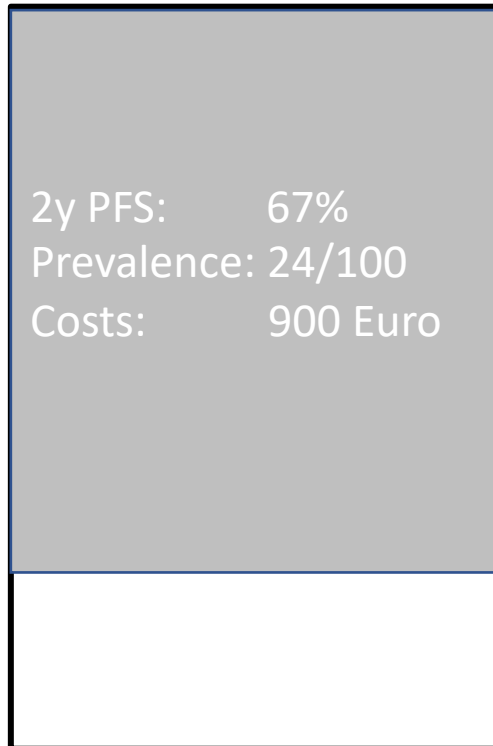
*Für die Antragsteller des MMML Verbundes / GLA
Rainer Spang*

German Lymphoma Alliance e.V.
Arbeitsgruppen: Aggressive Lymphome, Pathologie, Biologie, Biometrie, Bildgebung

The MMML Predictor



Very High Risk



Machine Learning based Risk Predictor

Age

Initial PET

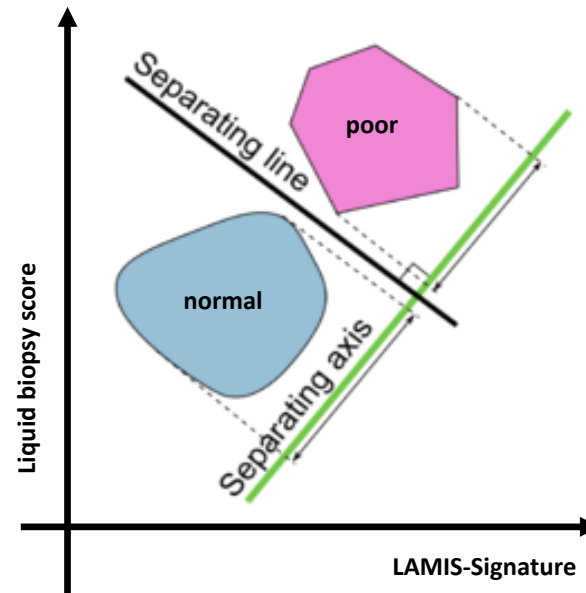
Standard Pathology

Expression Signatures

Genomics Host/Somatic

Liquid biopsies

Second PET/CT



Data Integration

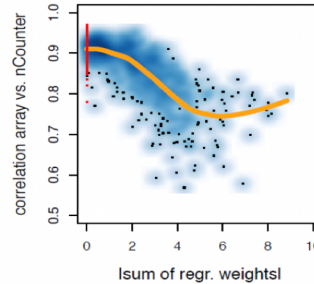
2y survival < 50%

< 1500 Euro

Prediction Accuracy

Validation

$$y_i = \beta_0 + \sum_j \beta_j (x_{ij} + \gamma_i)$$
$$y_i = \beta_0 + \sum_j \beta_j x_{ij} + \underbrace{\gamma_i \sum_j \beta_j}_{=0}$$



Our work horse is Zero-Sum Regression a more robust derivative of the LASSO

Altenbuchinger et al. Bioinformatics 2019a
Altenbuchinger et al. Bioinformatics 2019b
Staiger et al. Leukemia 2019 (LAMIS)

Work Package

Data Integration

2y survival < 50%

< 1500 Euro

Prediction Accuracy

Validation/Leipzig

Plan A

Late Integration

Binary Zero-Sum Regression

Weighted L1-Penalization

Nested Monotone Regression

Independent Cohort

Plan B/Improvements

Intermediate Integration (train on residuals)

Constrained Coordinate Descent (Cox Zero-Sum)

Constrained Coordinate Descent (Zero-Sum)

Fall: 04-YB13-71641b

Hoch Risiko: **91,3%**

Genexpression: **75,9%**

Liquid Biopsy: **99,9%**

Pathologie: **98,1%**



Fall: X14-9950-AZG9c

Hoch Risiko: **1,2%**

Genexpression: **0,9%**

Liquid Biopsy: **3,0%**

Pathologie: **5,8%**



Fall: 66-9UJ50-HPARe

Hoch Risiko: **69,9%**

Genexpression: **18,1%**

Liquid Biopsy: **99,6%**

Pathologie: **2,0%**

