

Performance evaluation of disease progression models

Razvan Valentin Marinescu

Center for Medical Image Computing, University College London

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Measure accuracy of:

- the fitted model parameters that describe the disease process
- predicted stages of subjects

The datasets analysed fall into three broad categories:

- simulated datasets: ground truth is user-defined
- well-phenotyped datasets: diagnoses are confirmed, stages and the disease process are known
 - post-mortem confirmed dementia
 - familial AD (e.g. DIAN)
 - prion disease
- less well-phenotyped datasets: little information on diagnoses, stages or the disease process
 - Rotterdam study
 - ADNI

Simulated datasets:

- same model used for generating and fitting data:
 - direct comparison of fitted parameters with true parameters
- different model:
 - need to transform the true parameters then compare

Well-phenotyped datasets:

- post-mortem confirmed dementia datasets:
 - differential diagnosis
- autosomal dominant dementia datasets:
 - prognostic accuracy of later time points from early data
 - prediction of genetic groups - supervised or unsupervised

Less well-phenotyped datasets:

- Goodness of fit measures: AIC, BIC
- Staging consistency: follow-up stages $>$ baseline stages
- Elapsed time prediction: predict the elapsed time between two visits
- Correlation of stages with clinical or leave-out biomarkers:
 - MMSE
 - CDR-SOB
 - hippocampal volume
- Resampling methods:
 - cross-validation
 - bootstrapping
- Reproducibility for different:
 - models
 - datasets
 - fitting procedures
 - missing data entries

Simulated datasets

- direct comparison between fitted and true parameters

Well-phenotyped datasets

- differential diagnosis
- prognosis of later time points from early data
- prediction of genetic groups

Less well-phenotyped datasets:

- Goodness of fit: AIC, BIC
- Staging consistency
- Elapsed time prediction
- Correlation of stages with clinical or leave-out biomarkers
- Resampling methods
- Reproducibility for different