

# Limitations and opportunities for identifying outcome prognostic factors in the context of small samples



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## BACKGROUND AND OBJECTIVE

Identification of prognostic factors is essential for advances in clinical research but rare diseases or genomics mutations studies face the limits of small numbers of patients, for which current methods coming from biostatistics and machine learning may be challenged. Indeed, small populations having high variability, that constraints analyses in terms of robustness and estimates with a possible production of uncertain results.

**GOAL:** This work aims to address the need for a synthesis around limitations and opportunities for up-to-date statistical and machine learning methods in the context of small samples.

## METHODS

A literature review based on relevant keywords in the context of small sample size was performed on Google Scholar and PubMed, such as “small data”, “small sample”, “small population” merged with “issues”, “bias”, “limits” and “problems” related or not to the identification of prognostic factors. The criteria used for selecting methodological papers included the date of publication and number of citations. Then, the first selection allowed to select others papers based on associated references or on new key-words identified in previously identified articles. These principle was repeated several times to refine the search.

## RESULTS

As of today, the following limits in low sample size for prognostic identification were identified in relevant literature which corresponds to 15 articles retained out of 22 identified. These limits are described below in the tables :

### 1) Overfitting leading to false-positive results and instability.

### 2) High-dimensionality of the sample

« Overfitting » is a production of an analysis that corresponds too closely of a dataset and may fail to generalize in an other dataset. An overfitted model is characterized by a high number of parameters relative to what the data needs.

The high-dimensionality is when your number of features is too large according to the number of patients, that questions usual statistical models and machine learning algorithms.

| Opportunity : To reduce overfitting and increase confidence in results   |  | Opportunity : To deal with high-dimensionality of a small sample   |  |
|--|--|--|--|
| Type of methods  | Examples of methods  | Type of methods  | Examples of methods  |
| Stricter variables selection protocols, which means no mixing of data to determine and assess prognostic factors               | <input type="checkbox"/> Train/test split<br><input type="checkbox"/> Complete Cross-validation<br><input type="checkbox"/> Nested Cross-validation (most advisable)   | Dataset transformation methods which allows to avoid the primary amount of data  | <input type="checkbox"/> Data augmentation methods<br><input type="checkbox"/> Virtual samples   |
| Methods adding external knowledge to increase confidence in results  | <input type="checkbox"/> Cross-referencing of data sources<br><input type="checkbox"/> Meta-analyses by combining estimates from regression (based on the literature) with coefficients of estimated regression on the studied dataset<br><input type="checkbox"/> Addition of prior information through Bayesian methods<br><input type="checkbox"/> Clinical knowledge from experts/clinicians | Feature transformation methods combining supervised and unsupervised methods to reduce data dimensions   | <input type="checkbox"/> Supervised methods : Linear Discriminant Analysis, Partial Least Square Discriminant Analysis<br><input type="checkbox"/> Unsupervised methods : Factor Analysis, Clustering of variables, Non-negative matrix factorization  |
| Ensemble methods based on the aggregation of different results to obtain a more stable and accurate result by a voting system. | <input type="checkbox"/> At the feature-scale with principles of Bagging and Boosting, algorithms such as Random-Forest, SVM-RFE, XGBoost...<br><input type="checkbox"/> At the method scale with the principle of stacking to obtain the best model   | Methods based on sparsity to reduce number of variables in the most reliable way   | <input type="checkbox"/> Lasso, Ridge regressions<br><input type="checkbox"/> Adaptative Lasso<br><input type="checkbox"/> Group Lasso<br><input type="checkbox"/> Sparse Group Lasso<br><input type="checkbox"/> Group PLS<br><input type="checkbox"/> Sparse Group PLS   |
| Regularized regressions which explicitly penalize overly complex models and test the model ability to generalize               | <input type="checkbox"/> Lasso<br><input type="checkbox"/> Ridge<br><input type="checkbox"/> Elastic Net   | Rule of thumb to have a sufficient number of events in data  | <input type="checkbox"/> One in ten rule : the rule states that one predictive variable can be studied for every ten events  |
| Noise injection methods where adding a noise has a regularization effect to the training set                                   | <input type="checkbox"/> Jitter  | Feature selection families to reduce dimensions:   | <input type="checkbox"/> Filter : statistical criteria (e.g. p-value), distance and information measures (e.g. Gain Ratio)<br><input type="checkbox"/> Wrapper : sequential search (e.g. stepwise methods, best first strategies method), exponential search (exhaustive methods...) and random search (e.g. genetic algorithms) |
| Sampling methods to gain stability for identified prognostic factors   | <input type="checkbox"/> Sampling with replacement such as Bootstrap   | <input type="checkbox"/> Filter : univariate or multivariate analysis based on criteria<br><input type="checkbox"/> Wrapper : research of optimal subset by combining iterative search and an algorithm to assess performance<br><input type="checkbox"/> Embedded : variable selection process contained in methods | <input type="checkbox"/> Embedded : regularized methods (e.g. Lasso, Ridge) and machine learning algorithms (Decision Tree, Random forest...)  |
| Dataset transformation methods which allows to avoid the primary amount of data  | <input type="checkbox"/> Data augmentation methods<br><input type="checkbox"/> Virtual samples   |  |  |

### 3) Lack of accuracy with large confidence intervals

Accuracy in statistics usually refers to the extent to which the results of a test are similar after several tests. In the case of small samples, there are large variations due to the lack of data and data heterogeneity.

| Opportunity : To deal with accuracy                                     |   |
|---|---|
| Type of methods   | Examples of methods   |
| Methods to increase precision of results based on external knowledge    | <input type="checkbox"/> Meta-analyses by combining estimates from regression (based on the literature) with coefficients of estimated regression on the studied dataset<br><input type="checkbox"/> Addition of prior information through Bayesian methods |
| Estimation methods to refine confidence intervals                       | <input type="checkbox"/> Bootstrap confidence interval estimates  |
| Epidemiological rule of thumb to ensure there are enough events in data | <input type="checkbox"/> “One in ten rule”  |

## CONCLUSION

Many methods adapted to the search for prognostic factors attempt to deal with problems related to small sample sizes. Faced with this great diversity, further research is needed to better guide the statistician.

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