Feature selection by replicate reproducibility and non-redundancy

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Feature selection

Unsupervised  **Supervised**

Filter methods

- evaluated on intrinsic properties of the data
- fast and simple
- e. g. selection of highly variable genes

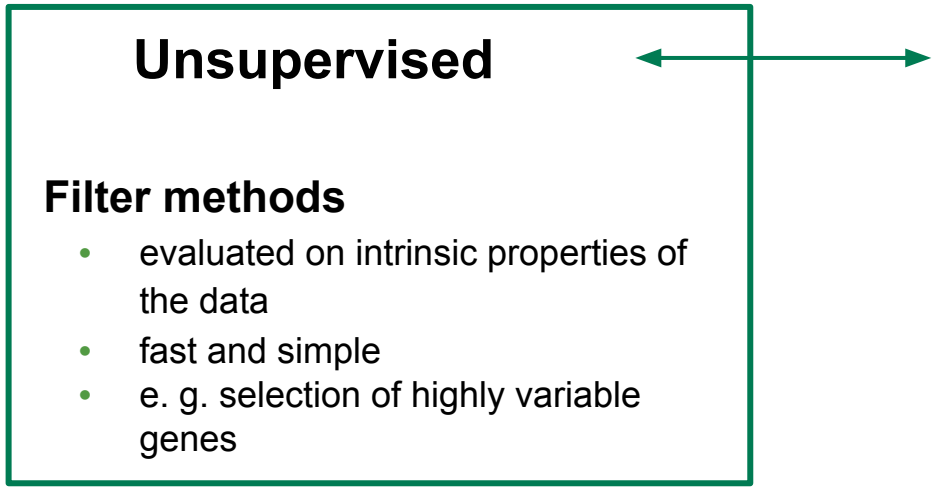
Wrapper methods

- feature subsets evaluated on performance of a model
- search algorithms combined with classifier
- computationally expensive

Embedded methods

- feature selection embedded in a model
- e. g. decision trees, lasso regression

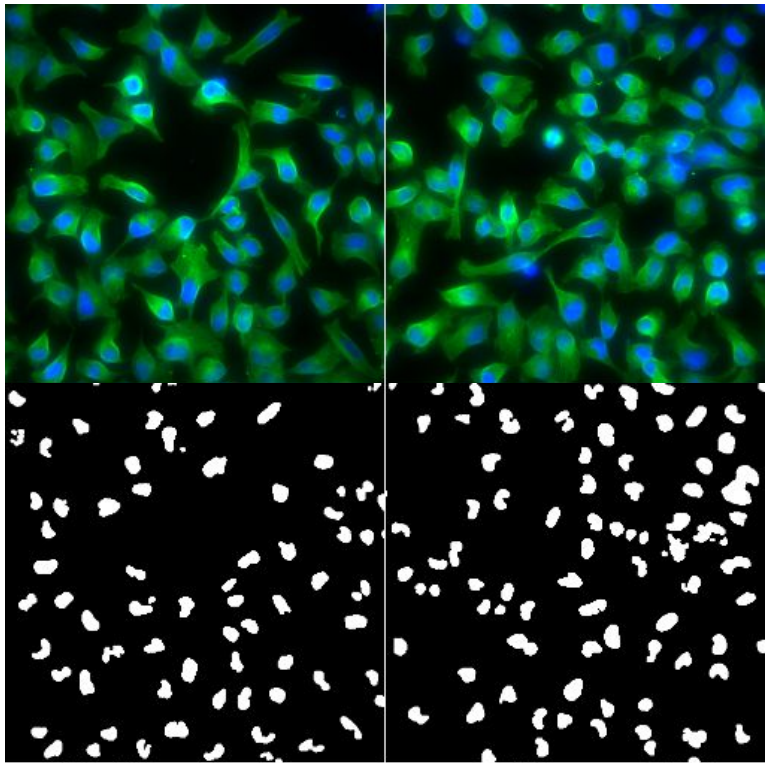
Feature selection



Embedded methods

- feature selection embedded in a model
- e. g. decision trees, lasso regression

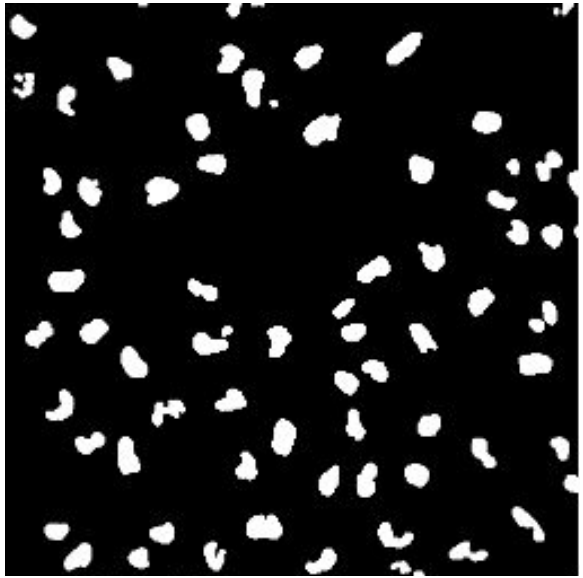
Feature selection applied to image analysis



Pau et al. 2010, EBImage—an R package for image processing with applications to cellular phenotypes

- Intrinsically high dimensional
- Analysis with neural networks
- Feature extraction (e.g. EBImage)
  - Highly correlated features
  - Noisy features

Feature selection applied to image analysis



Examples of extracted features:

- Cell count

Shape:

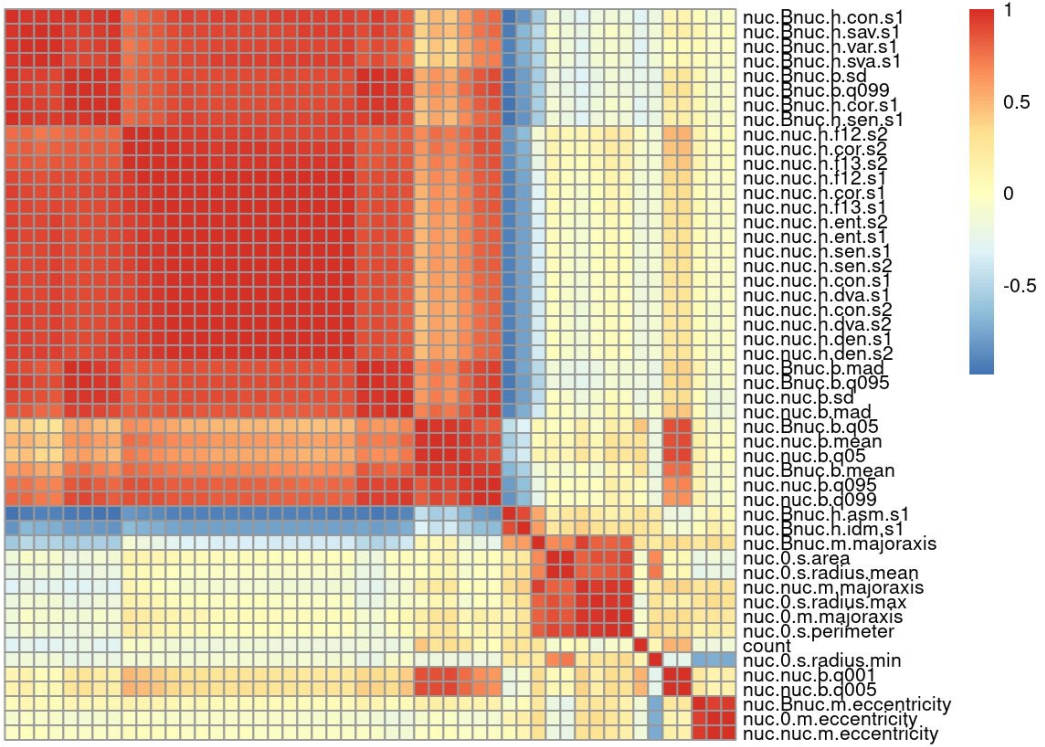
- Major axis length
- Eccentricity
- Area

Spatial independent:

- Quantile intensity
- Mean intensity

Pau et al. 2010, EBImage—an R package for image processing with applications to cellular phenotypes

Feature extraction produces highly correlated features



Data from: Laufer, C. et al. 2013. Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping.

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Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping

Christina Laufer, Bernd Fischer, Maximilian Billmann, Wolfgang Huber & Michael Boutros

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A map of directional genetic interactions in a metazoan cell

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Research Article · Mar 6, 2015

FeatSeekR: R package for unsupervised feature selection

Goal:

- Non-redundant feature subset with high replicate reproducibility

Method:

- Pre-select feature set
- Model each feature as a function of the selected features
- Project out dimension of the selected features
- Selection based on reproducibility of the signal across replicates
- Stop if there is only noise left

FeatSeekR: R package for unsupervised feature selection

Input:

- Data: $(X_{n\times p})^r$
- Selected features: $(S_{n\times q})^r$

Rank features according to reproducibility between replicates:

- Fit linear model:

$$x^r_{t,i} = S^r_t \beta^r_{t,i} + \epsilon^r_{t,i} \quad with \quad i = 1 \dots p$$

- Select feature i with highest reproducibility between replicates:

$$\max_i(g(\epsilon^1_i, \dots, \epsilon^r_i))$$

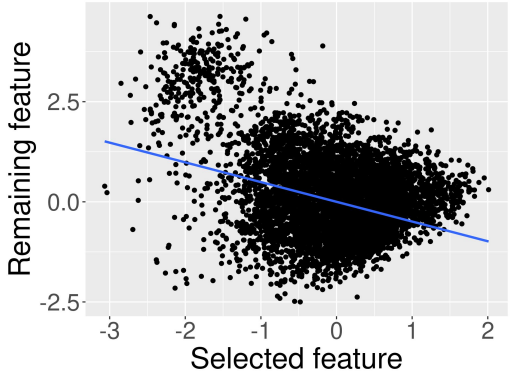
- Project out dimension spanned by previously selected features by setting:

$$x^r_{t+1,i} = \epsilon^r_{t,i}$$

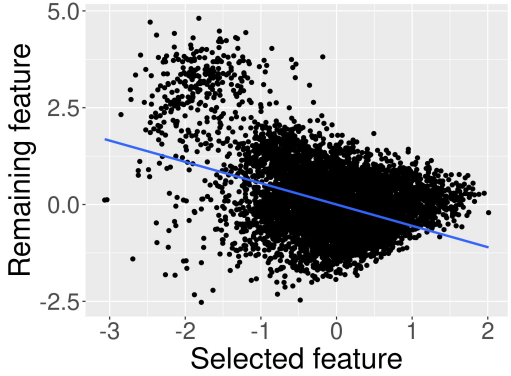
Iteration 1

1.) Fit linear model

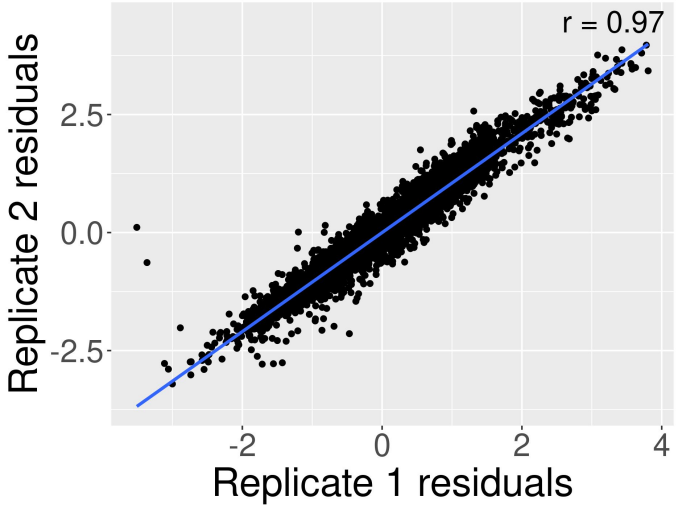
R1



R2



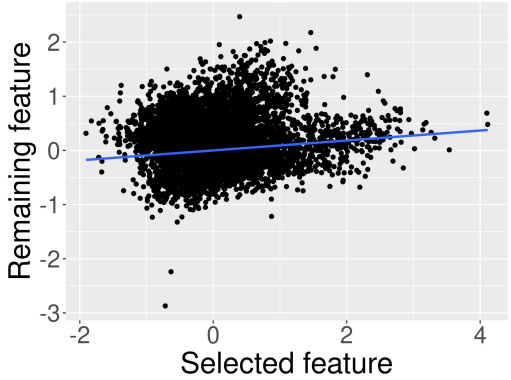
2.) Evaluate replicate reproducibility



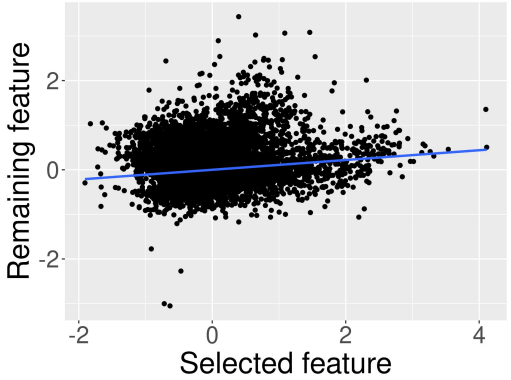
Iteration 5

1.) Fit linear model

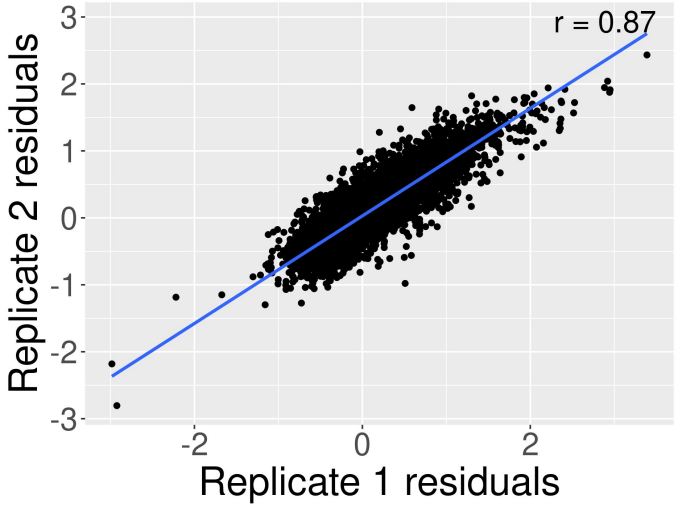
R1



R2



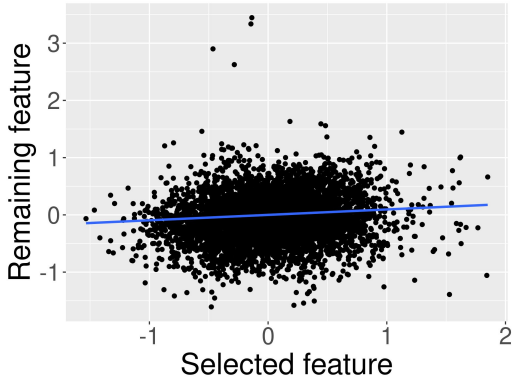
2.) Evaluate replicate reproducibility



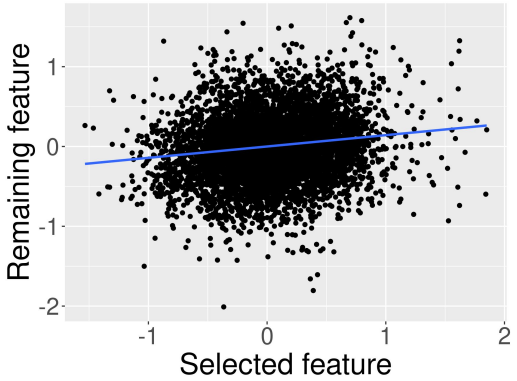
Iteration 10

1.) Fit linear model

R1



R2



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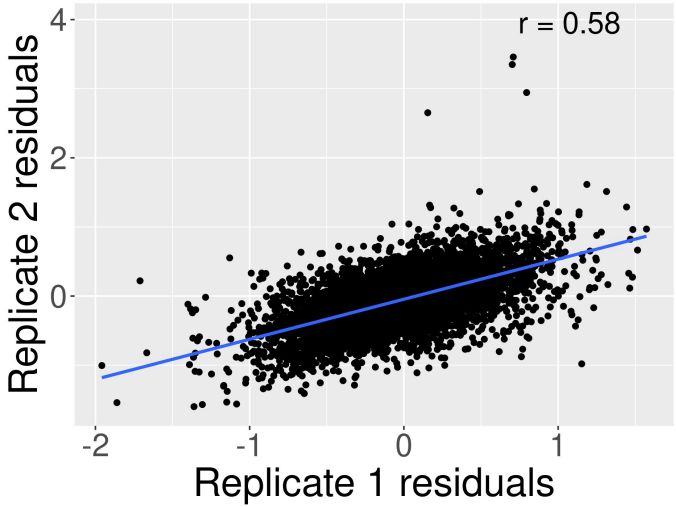
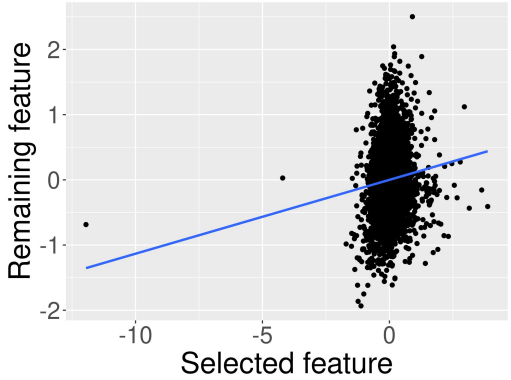


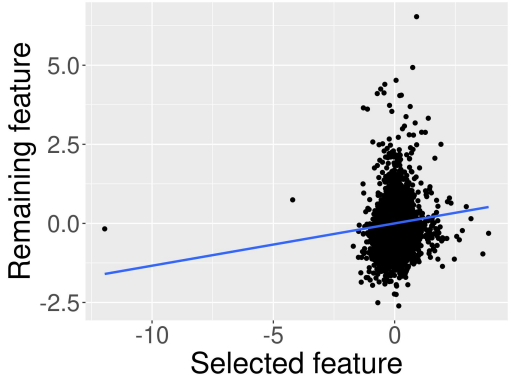
Iteration 18

1.) Fit linear model

R1



R2



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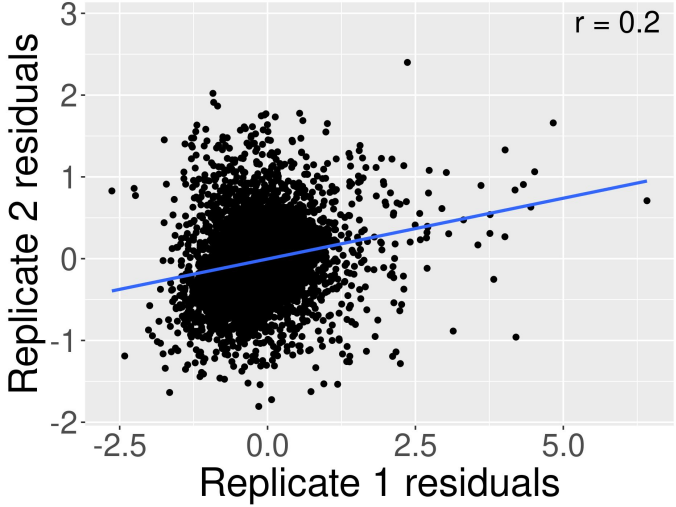
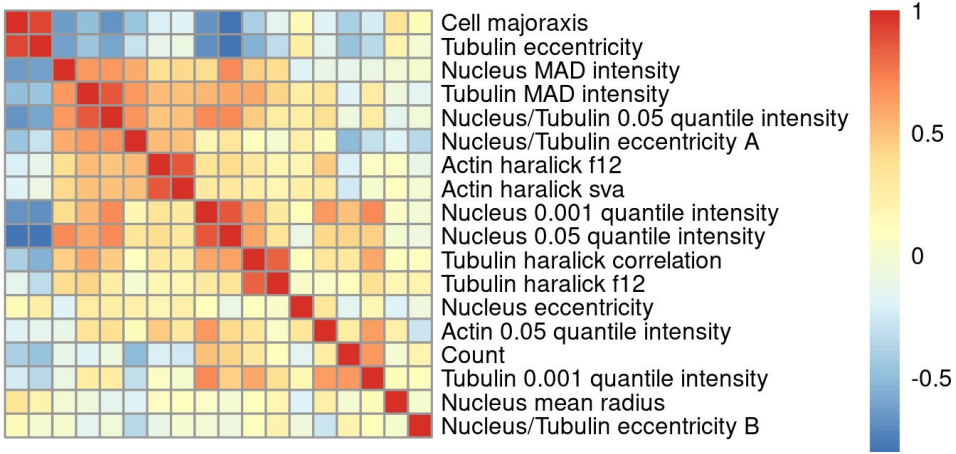


FeatSeekR identifies non-redundant and reproducible feature set



- 5820 samples
- 2 replicates
- 216 features

Data from: Laufer, C. et al. 2013. Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping.

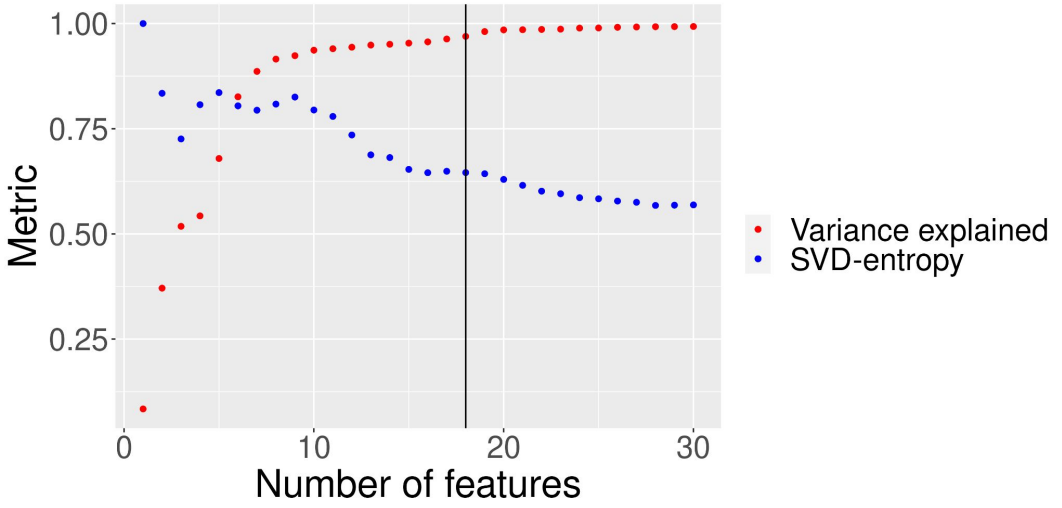
FeatSeekR identifies non-redundant and reproducible feature set

Variance explained:

$$\frac{\sum_{i=1}^{p} R^2_{adj,i}}{p}$$

Non-redundancy by SVD entropy:

$$E = -\frac{1}{log(q)} \sum_{i=1}^{q} V_i \, log(V_i)$$



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