Identification of Robust Gene Expression Signatures to Improve Survival Analysis and Risk Prediction in Cancer Patients

Santiago Bueno-Fortes, Alberto Berral, Javier De Las Rivas (Cancer Research Center of Salamanca)
José Manuel Sánchez-Santos (University of Salamanca)
Manuel Martín-Merino (University Pontificia of Salamanca)

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Motivation

• Several gene expression signatures have been proposed for survival and risk prediction. Some of them have been included in commercial platforms.

• They work as black-boxes:
  
  • The influence of gene markers in the risk is unclear.
  
  • The risk score cannot be related to the standard clinico-pathological tumor markers.

• The agreement among the gene signatures and even the risk predictions is small and they are quite unstable.
Set of tools developed in R

- Test the association of a list of genes with risk and survival.

- Identify robust survival gene signatures that correlate well with clinical markers.

- Risk prediction and stratification based on these gene signatures.

- Visualization
Case study: Robust Gene Expression Signatures and Risk Prediction in Breast Cancer

• We have obtained a robust survival gene signature that correlates well with IHC clinical markers in breast cancer (ER, PR and HER2)

• The list of survival markers (34 genes) improves the risk prediction and patient stratification of genomic platforms such as oncotype (16 genes) and prosigna (50 genes)

• Some genes identified have recently been studied in the literature as survival markers in breast cancer and linked to IHC clinical variables
References and Questions


Questions ???

• Manuel Martín-Merino <mmartinmac@upsa.es> (University Pontificia of Salamanca)

• Javier De Las rivas <jrivas@usal.es> (Cancer Research Center of Salamanca)