



# Jornadas sobre Biología Computacional y Ciencia de datos

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

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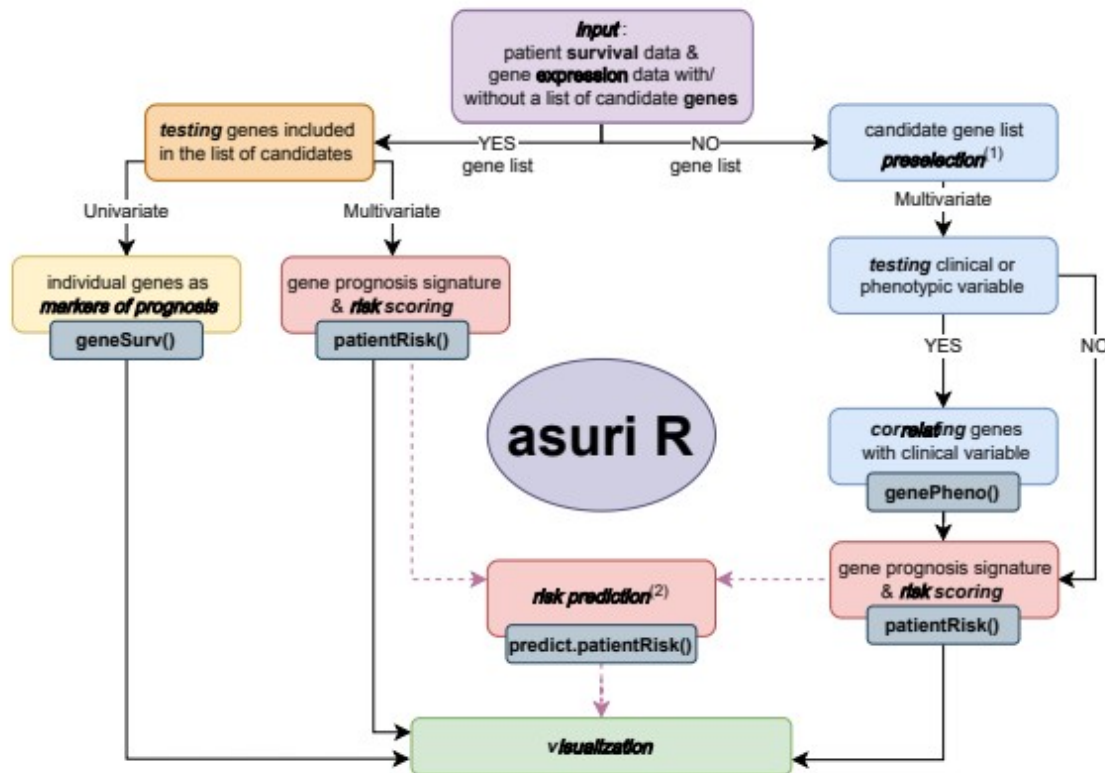


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# Motivation

- 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 can not 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 oncoPrint (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

Bueno-Fortes S, Berral-Gonzalez A, Sánchez-Santos JM, Martín-Merino M, De Las Rivas J. Identification of a gene expression signature associated with breast cancer survival and risk that improves clinical genomic platforms. *Bioinform Adv.* 2023 Mar 22;3(1).

### Questions ???

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