



# Seminar

Lichuang Huang

Wie-Biotech

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# Last Month

- AutoDock (vina)
  - Computational
- Weighted genes co-expression
- RNA-protein binding prediction
- Prediction model
- Single-cell analysis
  - Standard processing (Seurat)
  - Cell annotation (Garnett)
  - Cell communication (CellChat)
  - Cell pseudo-time (monocle3)

# Repetition of Technology

# Article

Received: 6 November 2021 | Revised: 20 February 2022 | Accepted: 12 April 2022

DOI: 10.1111/jpi.12803

## ORIGINAL ARTICLE



WILEY

# Single-cell transcriptomic analysis reveals circadian rhythm disruption associated with poor prognosis and drug-resistance in lung adenocarcinoma

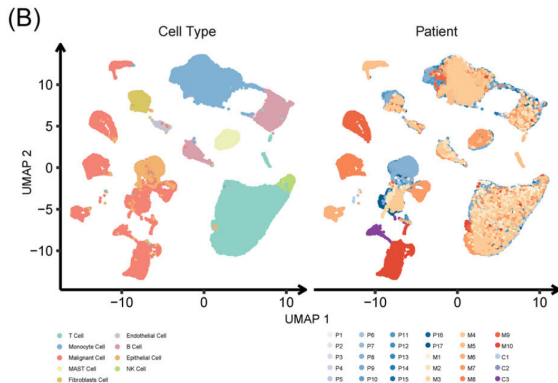
Lei He<sup>1</sup> | Yixian Fan<sup>2</sup> | Yue Zhang<sup>1</sup> | Tongtao Tu<sup>1</sup> | Quan Zhang<sup>3</sup> | Fahu Yuan<sup>4</sup> | Chao Cheng<sup>5</sup>

# Research idea

- CRD and disease (Malignant)
  - Clustering
  - Cell annotation
  - WGCNA
- CRD and therapy
  - ...
  - Pathway enrichment
- CRDscore validation
  - Correlation
- CRD and prognosis
  - TCGA Survival
  - TCGA CRDscore
- Construct prediction model
  - LASSO
  - SVM
- Experimental validation

# Techniques 1

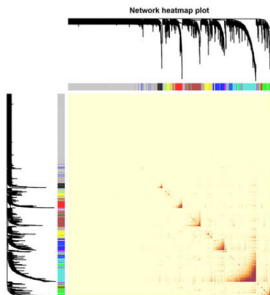
Standard workflow and annotation



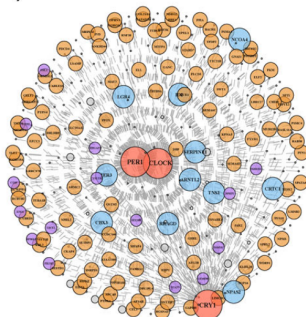
## Techniques 2

Weighted gene co-expression ... (WGCNA)

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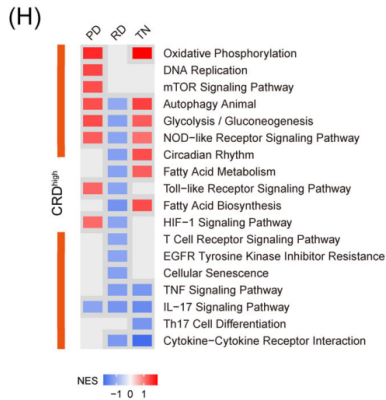
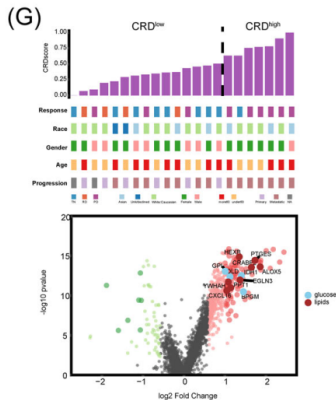


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# Techniques 3

## Differential analysis and Pathway enrichment



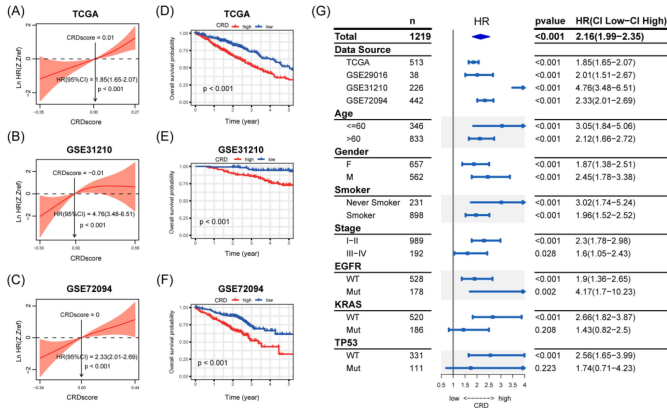


### Cell-cell ligand-receptor (LRs) analysis



# Techniques 5

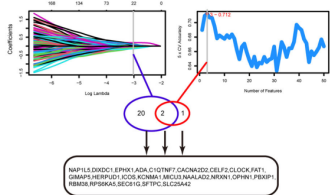
## Survival analysis



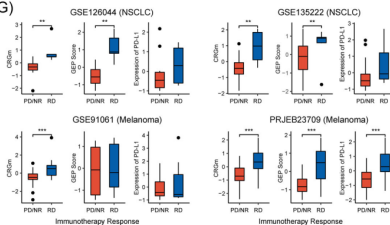
# Techniques 6

## LASSO and SVM

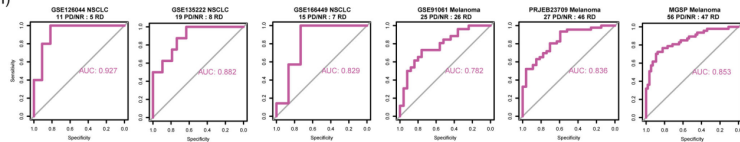
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# Techniques 7

yixianfan / CRDscore

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🔗 yixianfan

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