NATIONAL CANCER INSTITUTE
Technology Transfer Center

# CODEFACS and LIRICS: Computation Tools for Identifying Cell-Type Specific Gene Expression Levels in Tumors and Other Types of Samples


## Summary

The National Cancer Institute (NCI) seeks co-development partners or licensees for CODEFACS, a transcriptomics deconvolution tool for analyzing cell-type specific gene expression in complex tissues, and LIRICS, a supporting framework for analyzing immune interactions in the tumor microenvironment.


## NIH Reference Number

E-044-2020

## Product Type

- Research Tools


## Keywords

- CODEFACS, LIRICS, Deconvolution, Gene Expression, Immunotherapy, Tumor Microenvironment, TME, Ligand-Receptor Interaction, Cell-cell Interaction, Ruppin


## Collaboration Opportunity

This invention is available for licensing and co-development.

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## Description of Technology

The tumor microenvironment (TME) is a complex mixture of cell types whose interactions affect tumor growth and clinical outcome. Recent studies using fluorescence-activated cell sorting (FACS) and single-cell RNA sequencing (RNAseq) to elucidate tissue composition and cell-cell interactions in the TME led to improved biomarkers of patient response and new treatment opportunities. However, the use of FACS is limited to simultaneously measuring the expression of a few protein markers, whereas the use of single-cell RNAseq has been limited due to cost and scarcity of fresh tumor biopsies. In contrast, bulk tumor gene expression from preserved biopsies accompanied by clinical outcome metadata is abundant. Several algorithms have shown promise in accurately reconstructing cell-type-specific gene expression profiles from bulk gene expression.

Researchers at National Cancer Institute (NCI) have developed CODEFACS (COnfident DEconvolution For All Cell Subsets), a transcriptomics computation tool that can confidently estimate cell type abundance and deconvolve cell-type-specific gene expression profiles of individual cancer patients from bulk gene expression measurements. A complementary, second software tool LIRICS (LIgand-Receptor Interaction between Cell Subsets) prioritizes clinically relevant ligand-receptor interactions between cell types from the deconvolved data. These tools uncovered TME ligand-receptor interactions associated with improved patient survival and high sensitivity to immune checkpoint blockade therapy. These excellent tools for understanding the TME can inform diagnosis and treatment strategies. They are available for co-development or licensing opportunities.

**Potential Commercial Applications**

- Development of improved immune checkpoint blockade therapies against cancer
- Development of improved therapies against cancer involving the TME
- Improved determination and analysis of cell-type abundance and cell-type-specific gene expression from bulk gene expression
- Identifying cell-cell and ligand-receptor interactions within complex tissues, including the TME
- Identifying cell type specific biomarkers, drug targets and drug repurposing opportunities to improve diagnosis and clinical outcome
- Applicable non-cancerous disease, including preeclampsia, pregnancy-related complications, autoimmune disorders, ageing and neurodegenerative disorders.

**Competitive Advantages**

- Higher gene coverage for all cell types than existing related technologies
- Improved predictive accuracy of patient response to therapy
- Built-in confidence ranking system to compare prediction accuracies

**Inventor(s)**

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**Development Stage**

- Discovery (Lead Identification)

**Patent Status**

- **PCT:** PCT Application Number PCT/US2020/062238, Filed 25 Nov 2020

**Therapeutic Area**

- Immune System and Inflammation

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