OPEN ACCESS Freely available online

ISSN: 2168-9431
Single Cell Biology

Opinion Article

Essential Role of Proteins in Gene Expression of a Cell

Elin Buil Rogy*

Department of Cell Biology, University of Pittsburgh, Pennsylvania, United States

DESCRIPTION

The process by which the genome's sequence is translated into proteins is known as gene expression. A finely controlled process called gene expression enables a cell to react to its changing surroundings. It serves as both a volume control that raises or lowers the level of proteins produced as well as an on/off switch to regulate when proteins are created. Compared to transcripts proteins play a more direct role in the maintenance of cellular activities. Single-cell RNA sequencing offers an objective categorization of diverse biological states at the transcriptional level but it is not always correlated with the expression of cell-surface proteins. Assessing transcriptional similarities and differences within a population of cells has been a major use of scRNA-Seq. To profile the expression of genes at the transcriptional and translational levels the quantification of protein expression is combined with an absolute measurement of the same gene's mRNA levels in the same cell.

Measuring mRNA is a common method for determining gene expression for genome-wide investigations in a single cell. Recent improvements in amplification techniques have substantially enhanced detection and quantification of mRNA. This objective has been greatly advanced by single cell transcriptome analysis methods based on cDNA microarray and mRNA sequencing. While scRNAseq offers thorough snapshots of gene expression, gene transcription is stochastic, characterized by bursts of different sizes and speeds mRNA molecule half-lives differ dramatically between genes. Single-Cell Protein and RNA Co-Profiling which permits detection of specific intracellular proteins and high multiplex global mRNA in single cells. These can be divided into two categories of expression programmes that are easy to spot in scRNA-Seq data.

Expression programs

1. GEPs(Gene Expression Programs) that identify a particular cell type like hepatocytes or melanocytes (identity programs). A systematic search for GEPs (Gene Expression Programs) may turn up unexpected or unusual activity patterns that reflect crucial biological aspects of the native biological tissue. It might make it possible to characterize the frequency of each GEP (Gene Expression Program) across different cell types in the tissue. Finally, by preventing the erroneous inclusion of activity programme genes in identity programmes accounting for activity programmes may improve the inference of identity programmes.
2. Cell GEPs (Gene Expression Programs) express specific gene expression program in every cell that performs a specific activity such as cell division or immune cell activation (activity programs) regardless of cell type.

Matrix factorization would model the gene expression data matrix as the product of two lower rank matrices one encoding the relative contribution of each gene to each programme and the second giving the proportions in which the programmes are combined for each cell. The cells express one or more activity GEPs (Gene Expression Programs) in addition to their expected cell type GEPs (Gene Expression Programs) and could correctly model the doublets as a combination of the identity GEPs (Gene Expression Programs) for the combined cell types.

CONCLUSION

The variation of RNA and protein expression are complex and co-dependent processes. To study the factors that determine the differences between mRNA and the variation in protein expression we considered translation from mRNA to protein. To profile the expression of genes at the transcriptional and translational levels the quantification of protein expression is combined with an absolute measurement of the same gene's mRNA levels in the same cell. Using matrix factorization to simultaneously derive identities and activity programs from scRNA-Seq Data activity programs could improve the inference of identity programs by avoiding the spurious incorporation of activity program genes into the latter.

Correspondence to: Elin Buil Rogy, Department of Cell Biology, University of Pittsburgh, Pennsylvania, United States; E-mail: buil.erogy@gmail.com

Received: 06-Jun -2022, Manuscript No. SCPM-22-17365; **Editor assigned:** 08-Jun-2022, Pre QC No. SCPM-22-17365 (PQ); **Reviewed:** 23-Jun-2022, QC No. SCPM-22-17365; **Revised:** 30-Jun-2022, Manuscript No. SCPM-22-17365 (R); **Published:** 07-Jul-2022, DOI: 10.35248/2168-9431.22.11.030

Citation: Rogy EB (2022) Essential Role of Proteins in Gene Expression of a Cell. Single Cell Biol. 11:030.