

# scDEcrypter: Detecting latent viral states in scRNA-seq

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## Introduction

Detecting infected cells in viral scRNA-seq data is challenging because viral transcripts are often sparse or undetected, leaving most infection labels unknown and limiting downstream differential expression analyses. scDEcrypter is a statistical framework we developed to address this problem by modeling infection status, and optionally other partitioning variables such as cell type. The method uses a penalized multiway mixture model, anchored by a small set of confidently labeled cells, to recover latent infection states with high accuracy even when viral reads are extremely limited. To avoid double-dipping, scDEcrypter employs a data-splitting strategy, using one subset of cells for parameter estimation and another independent subset for differential expression testing. A fast approximate likelihood ratio test is then used to identify infection-associated genes within each cell type. scDEcrypter can improve power, robustness, and biological interpretability. If you use scDEcrypter in published research, please cite:

## Run scDEcrypter

### Install the package

```
library(devtools)
devtools::install_github("https://github.com/LZHONG25/scDEcrypter")
library(scDEcrypter)
```