Computing and Visualizing the Generalized Singular Value Decomposition in Python

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Abstract

The human genome project has been completed, but there are barriers between researchers who study the genetic sequences and clinicians who treat cancers. First of all, there is low reproducibility in genetic studies, caused by different sequencing techniques and batch effects. Secondly, it is difficult for clinicians who do not have a computational background to interpret existing computational methods. To minimize these disconnections, a computational model should be developed to find the significant genes in a genome that separate batch and experimental effects from biological effects. The proposed solution is to use the generalized singular value decomposition (GSVD) to reveal genetic patterns on the transformation of genes, and to separate the tumor-exclusive genotype from experimental inconsistencies.

Here we developed a computation and visualization toolkit to improve computing and visualizing the GSVD in Python.