

The ESTIMATE algorithm is a computational tool used to estimate the relative abundance of stromal and immune cells in tumor tissues based on gene expression data. The acronym ESTIMATE stands for Estimation of STromal and Immune cells in MAlignant Tumor tissues using Expression data.

The ESTIMATE algorithm was developed by a team of researchers led by Dr. Andrew Teschendorff at University College London in 2013. The algorithm uses gene expression signatures of stromal and immune cells to infer the relative abundance of these cell types within a tumor sample.

The ESTIMATE algorithm works by first identifying a set of genes that are specifically expressed by stromal and immune cells. It then calculates a stromal score and an immune score for each tumor sample based on the expression levels of these genes. The stromal score reflects the relative abundance of stromal cells, such as fibroblasts, in the tumor tissue, while the immune score reflects the relative abundance of immune cells, such as T cells and B cells.

The ESTIMATE algorithm has been shown to be highly accurate in estimating the relative abundance of stromal and immune cells in a range of tumor types, including breast cancer, lung cancer, and ovarian cancer. It has also been used to investigate the relationship between the tumor microenvironment and patient survival, as well as to identify potential therapeutic targets for cancer treatment.

Overall, the ESTIMATE algorithm provides a valuable tool for analyzing gene expression data from tumor tissues and has the potential to improve our understanding of the complex interactions between tumor cells and the surrounding microenvironment.

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