The CIBERSORT algorithm is a computational tool used to analyze gene expression data from mixed cell populations and infer the relative abundance of different cell types within the population. The algorithm was developed by a team of researchers led by Dr. Ash Alizadeh at Stanford University in 2013.

The CIBERSORT algorithm uses a machine learning approach to deconvolute gene expression profiles of mixed cell populations. It works by comparing gene expression signatures of known cell types to a mixed cell population, and inferring the relative abundance of each cell type within the population. The algorithm uses a support vector regression method to estimate the proportions of each cell type in the sample, and it has been shown to be highly accurate and robust across a range of cell types and tissues.

CIBERSORT has been widely used in cancer research, where it has been used to analyze gene expression data from tumor samples to identify different immune cell populations present in the tumor microenvironment. This information can be used to gain insight into the immune response to the tumor and potentially guide the development of new immunotherapies.

Overall, the CIBERSORT algorithm provides a powerful tool for analyzing gene expression data from mixed cell populations and has the potential to advance our understanding of a wide range of biological processes, including cancer and other diseases.

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