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| --- | --- |
| Review: | |
| year | Title |
| 2013 | Computational Deconvolution :Extracting Cell Type-Specific Information from Heterogeneous Samples |
| 2015 | A Critical Survey of Deconvolution Methods for Separating cell-types in Complex Tissues |
| 2018 | Quantifying tumor-infiltrating immune cells from transcriptomics data |
| 2018 | Computational deconvolution of transcriptomics data from mixed cell populations |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Method | Data | Country/university | Citation (2018.10) | journal |
| CIBERSORT | 2015 | Stanford | 470 | Nature methods |
| TIMER | 2016 | Harvard | 97 | Genome Biology |
| EPIC | 2017 | Switzerland | 11 | Elife |
| cellMix | 2013 | South Africa (Gaujoux) | 107 | Bioinformatics |
| ESTIMATE | 2013 | MD Anderson CC | 328 | Nature comm. |
| ICeD-T | 2018 | North Carolina Univ. | 0 | BiorXiv |
| EDec | 2016 | Baylor college of med | 13 | Cell report |
| MySort | 2018 | Taiwan | 0 | bmcbioinformatics |
| ImmuneCC | 2017 | Beijing | 10 | Scientific reports |
| From Review: Quantifying tumor-infiltrating immune cells from transcriptomics data. | | | | |
| TIminer | 2017 | Austria | 10 | Bioinformatics |
| xCell | 2017 | UCSF | 37 | Genome Biology |
| MCP-counter | 2016 | France | 67 | Genome Biology |
| DeconRNASeq | 2013 | Novartis Institutes for BioMedical Research, USA | 65 | Bioinformatics |
| PERT | 2012 | Canada | 54 | PLoS computational biology |
| quanTIseq | 2017 | Austria | 2 | BiorXiv |
| deconf | 2010 | Germany | 68 | bmcbioinformatics |
| ssKL | 2004 | MIT and Harvard | 1217 | PNAS |
| DSA | 2013 | Baylor college of med. | 56 | bmcbioinformatics |
| MMAD | 2014 | OSU | 33 | Bioinformatics |
| From review : Computational Deconvolution :Extracting Cell Type-Specific Information from Heterogeneous Samples | | | | |
| SPEC | 2011 | Yale University | 41 | bmcbioinformatics |
| CTEN | 2012 | Tokyo | 62 | bmcgenomics |
| ssGSEA | 2010 | MIT and Harvard | 4021 | Cancer cell |
| collapseRows | 2011 | UCLA | 177 | Bmcbioinformatics |
| Abbas | 2009 | UCSF | 222 | PloS one |
| methyISpectrum | 2012 | Oregon state Univ. | 1088 | bmcbioinformatics |
| qpure | 2012 | Australia | 52 | PloS one |
| ABSOLUTE | 2012 | MIT and Harvard | 738 | Nature Biotechnology |
| csSAM | 2010 | stanford | 300 | Nature method[brief comm] |
| PSEA | 2011 | Switzerland | 103 | Nature method[brief comm] |
| DeMix | 2013 | MD Anderson | 42 | bioinformatics |
| ISOpure | 2013 | Canada | 47 | Genome medicine |
| DSection | 2010 | Finland | 55 | bioinformatics |
| ssNMF | 2012 | South Africa (Gaujoux) | 68 | Infection, Genetics and Evolution |



