Table 1 The current code availability of each software (similar to Table 1 of [52]). As ISOpure and DeMix are similar, they are listed first; all other software is listed according to the year of publication. ISOpure is available in both MATLAB and R, and some methods have source code incorporated into the CellMix package, available at `https://r-forge.r-project.org/scm/viewvc.php/pkg/CellMix/?root=cellmix&sortdir=down`.

Method	Year published	Language(s)	Source
ISOpure (Quon)	2013	R	`http://cran.r-project.org/web/packages/ISOpureR/index.html`
		MATLAB	`http://people.csail.mit.edu/geraldquon/software.shtml#isopure`
DeMix (Ahn)	2013	R	`http://odin.mdacc.tmc.edu/~wwang7/DeMix.html`
Abbas	2009	R	CellMix: `https://r-forge.r-project.org/scm/viewvc.php/pkg/CellMix/?root=cellmix&sortdir=down`
deconf (Repsilber)	2010	R	CellMix & `http://www.biomedcentral.com/1471-2105/11/27`
Clarke	2010	R	`www.biomed.miami.edu/site/clients/UMMM/user/65/doc/mixture_estimation.zip`
csSAM (Shen-Orr)	2010	R	CellMix & `http://cran.r-project.org/web/packages/csSAM/index.html`
DSection (Erkkilä)	2010	R, MATLAB	CellMix & `http://informatics.systemsbiology.net/DSection`
Gong	2011	R	CellMix: `https://r-forge.r-project.org/scm/viewvc.php/pkg/CellMix/?root=cellmix&sortdir=down`
PSEA (Kuhn)	2011	R	`http://www.bioconductor.org/packages/release/bioc/html/PSEA.html`
ssNMF (Gaujoux)	2012	R	CellMix: `https://r-forge.r-project.org/scm/viewvc.php/pkg/CellMix/?root=cellmix&sortdir=down`
PERT (Qiao)	2012	Octave	`http://people.csail.mit.edu/geraldquon/software.shtml#pert`
DeconRNASeq (Gong)	2013	R	`http://master.bioconductor.org/packages/release/bioc/html/DeconRNASeq.html`
DSA (Zhong)	2013	R	CellMix & `https://github.com/zhandong/DSA`
TEMT (Li)	2013	Python	`https://github.com/uci-cbcl/TEMT`
ESTIMATE (Yoshihara)	2013	R	`http://sourceforge.net/projects/estimateproject/`
UNDO (Wang N.)	2014	R	`http://master.bioconductor.org/packages/release/bioc/html/UNDO.html`