

	Objective Function	Deconvolution Type	Solver	Marker Selection	Value	Ref
CIBERSORT	$\arg \min_{\beta, v, \epsilon} C \sum_m  a_m - s_m \cdot \beta _{\epsilon} + \frac{1}{2}   \beta  ^2 + v\epsilon$	Reference	svm	Differentially-expressed (DE'ed), prioritized by fold change, not expressed in non-hematopoietic cells	$\beta^+$	13
CIBERSORTx	$\arg \min_{\beta, v, \epsilon} C \sum_m  a_m^* - s_m \cdot \beta _{\epsilon} + \frac{1}{2}   \beta  ^2 + v\epsilon$	Reference	svm	DE'ed, prioritized by fold change, not expressed in non-hematopoietic cells	$\beta^+$	29
EPIC	$\arg \min_{\substack{\beta \\ \text{s.t. } \beta_m \geq 0 \forall m \\ \sum_m \beta_m \leq 1}} \sum_m w_m^{\text{EPIC}} (a_m - s_m \cdot \beta)^2$	Referene	constrOptim	DE'ed, not expressed in non-hematopoietic tissues, similarly expressed in healthy and malignant tissues	$\beta$	14
MCP-Counter		Enrichment		DE'ed across hierarchy of purified expression profiles, specific to cell type	$\frac{1}{ M_c } \sum_{m \in M_c} a_m$	15
quanTIseq	$\arg \min_{\substack{\beta \\ \text{s.t. } \beta_m \geq 0 \forall m \\ \sum_m \beta_m \leq 1}} \sum_m (a_m - s_m \cdot \beta)^2$	Reference	lsei	Correlated with random fractions in simulated admixtures, specific to cell type, expressed in tumors, not expressed in non-hematopoietic tissues,	$\beta$	17
xCell		Enrichment		not very highly expressed DE'ed, specific to cell type, not expressed in carcinomas	ssGSEA mapped to linear scale	18
Aginome-XMU	DNN trained to predict random fractions in simulated admixtures	Other		None	Fractions predicted by DNN	30
Biogem	$\arg \min_{\beta} \sum_m [w_H(a_m - s_m \cdot \beta)]^2 (a_m - s_m \cdot \beta)^2$	Reference	rlm		$\beta$	33
DA_505	$\arg \min_{b_c} (  \tilde{p}_c - \tilde{A}_{M_c} \cdot b_c  ^2) + \lambda_2   b_c  ^2 + \lambda_1   b_c  _1$	Other		Identified by RF regression against random fractions in simulated admixtures	$A_{M_c} \cdot b_c$	
mitten_TDC19		Enrichment		Correlated with random fractions in simulated admixtures	$\sum_{m \in M_c} a_m$	

$M_c$ : set of markers for cell type $c$ $A_{M_c}, \tilde{A}_{M_c}$ : input or simulated admixture matrices, respectively, subset to markers for cell type $c$ $a, a^*$ : input or batch-corrected admixture expression vector, respectively $a_m$ : expression for marker $m$ in admixture $a$	$S$ : marker $\times$ cell type signature matrix $s_m$ : expression vector for marker $m$ across cell types (i.e., column of $S$ ) $\beta^+ \equiv (\beta_0^+, \beta_1^+, \dots)$ with $\beta_i^+ \equiv \max(\beta_i, 0)$  $ e _{\epsilon} \equiv 0$ if $ e  < \epsilon$ ; $ e  - \epsilon$ otherwise	$w_H(e) \equiv 1$ if $ e  < k$ ; $k/ e $ otherwise $w_m^{\text{EPIC}}$ : weight giving marker $m$ importance relative to its variability $\tilde{p}_c$ : vector of proportions of cell type $c$ in simulated admixtures
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