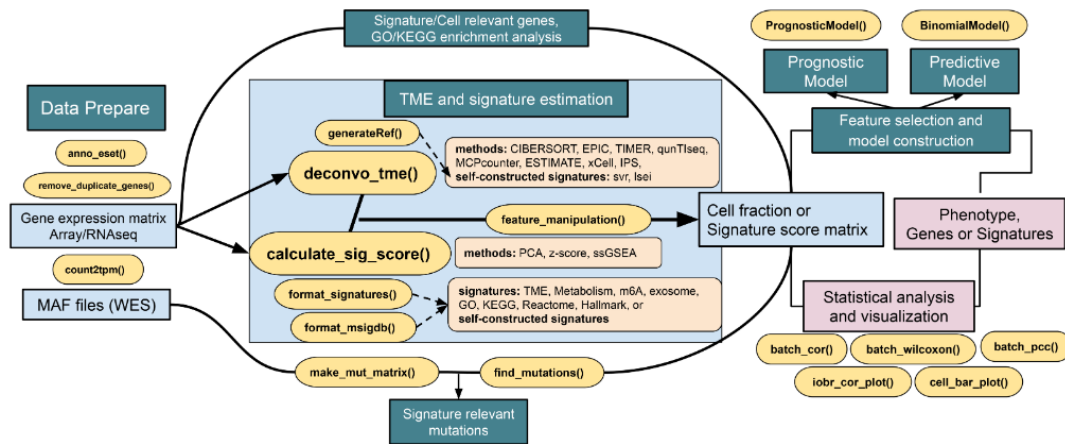


IOBR (Immuno-Oncology Biological Research)

当今肿瘤免疫学研究中，免疫细胞浸润分析是一个重要的领域。IOBR 包用于对肿瘤微环境和免疫肿瘤学特征进行全面分析。



IOBR (Immuno-Oncology Biological Research)

IOBR 包里有啥

1. IOBR 收集了 255 个已发表的特征基因集，涉及肿瘤微环境、肿瘤代谢、m6A、外泌体、微卫星不稳定性 and 三级淋巴结构。
2. IOBR 整合了 8 种已发表的计算肿瘤微环境（TME）背景的方法学： CIBERSORT, TIMER, xCell, MCPcounter, ESITMATE, EPIC, IPS, quanTIseq;
3. IOBR 采用了三种计算方法来计算特征分数，包括 PCA、z-score 和 ssGSEA;
4. IOBR 整合了变量转换、可视化、批量生存分析、特征选择和统计分析等多种方法。
5. IOBR 还整合了亚组特征的批量可视化的方法。

method	license	citation
CIBERSORT	free for non-commercial use only	Newman, A. M., Liu, C. L., Green, M. R., Gentles, A. J., Feng, W., Xu, Y., ... Alizadeh, A. A. (2015). Robust enumeration of cell subsets from tissue expression profiles. <i>Nature Methods</i> , 12(5), 453–457. https://doi.org/10.1038/nmeth.3337 
ESTIMATE	free (GPL2.0)	Vegesna R, Kim H, Torres-Garcia W, ..., Verhaak R. (2013). Inferring tumour purity and stromal and immune cell admixture from expression data. <i>Nature Communications</i> 4, 2612. http://doi.org/10.1038/ncomms3612 
quanTiseq	free (BSD)	Finotello, F., Mayer, C., Plattner, C., Laschober, G., Rieder, D., Hackl, H., ..., Sopper, S. (2019). Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. <i>Genome medicine</i> , 11(1), 34. https://doi.org/10.1186/s13073-019-0638-6 
TIMER	free (GPL 2.0)	Li, B., Severson, E., Pignon, J.-C., Zhao, H., Li, T., Novak, J., ... Liu, X. S. (2016). Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 17(1), 174. https://doi.org/10.1186/s13059-016-1028-7 
IPS	free (BSD)	P. Charoentong et al., Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade. <i>Cell Reports</i> 18, 248-262 (2017). https://doi.org/10.1016/j.celrep.2016.12.019 
MCPCounter	free (GPL 3.0)	Becht, E., Giraldo, N. A., Lacroix, L., Buttard, B., Elarouci, N., Petitprez, F., ... de Reyniès, A. (2016). Estimating the population abundance of tissue-infiltrating immune and stromal cell populations using gene expression. <i>Genome Biology</i> , 17(1), 218. https://doi.org/10.1186/s13059-016-1070-5 
xCell	free (GPL 3.0)	Aran, D., Hu, Z., & Butte, A. J. (2017). xCell: digitally portraying the tissue cellular heterogeneity landscape. <i>Genome Biology</i> , 18(1), 220. https://doi.org/10.1186/s13059-017-1349-1 
EPIC	free for non-commercial use only (Academic License)	Racle, J., de Jonge, K., Baumgaertner, P., Speiser, D. E., & Gfeller, D. (2017). Simultaneous enumeration of cancer and immune cell types from bulk tumor gene expression data. <i>ELife</i> , 6, e26476. https://doi.org/10.7554/eLife.26476 