Biomarker 筛选与验证

Boyun Tang

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基于表达谱芯片的 Biomarker 筛选

评价准则

- 较好的预后预测 (Good prognostic value / prediction accuracy)
- 稳定的生物学解读 (Functional similarity / Semantic similarity)



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难点与挑战

- 属于高维拟合问题 $p\gg N$
- Response 值多为截尾数据

许多已发表的肿瘤相关 Gene Signature 并不严谨

OPEN & ACCESS Freely available online

PLOS COMPUTATIONAL BIOLOGY

Most Random Gene Expression Signatures Are Significantly Associated with Breast Cancer Outcome

David Venet¹, Jacques E. Dumont², Vincent Detours^{2,3}*

1 IRIDIA-CODE, Université Libre de Bruxelles (U.L.B.), Brussels, Belgium, 2 IRIBHM, Université Libre de Bruxelles (U.L.B.), Campus Erasme, Brussels, Belgium, 3 WELBIO, Université Libre de Bruxelles (U.L.B.), Campus Erasme, Brussels, Belgium

• 随机化的重复验证很重要



文献

The NEW ENGLAND JOURNAL of MEDICINE

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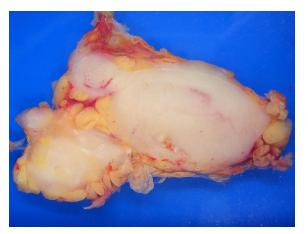
VOL. 351 NO. 21

Prediction of Survival in Follicular Lymphoma Based on Molecular Features of Tumor-Infiltrating Immune Cells

Sandeep S. Dave, M.D., George Wright, Ph.D., Bruce Tan, M.D., Andreas Rosenwald, M.D., Randy D. Gascoyne, M.D., Wing C. Chan, M.D., Richard I. Fisher, M.D., Rita M. Braziel, M.D., Lisa M. Rimsza, M.D., Thomas M. Grogan, M.D., Thomas P. Miller, M.D., Michael LeBlanc, Ph.D., Timothy C. Greiner, M.D., Dennis D. Weisenburger, M.D., James C. Lynch, Ph.D., Julie Vose, M.D., James O. Armitage, M.D., Erlend B. Smeland, M.D., Ph.D., Stein Kvaloy, M.D., Ph.D., Harald Holte, M.D., Ph.D., Jan Delabie, M.D., Ph.D., Joseph M. Connors, M.D., Peter M. Lansdorp, M.D., Ph.D., Qin Ouyang, Ph.D., T. Andrew Lister, M.D., Andrew J. Davies, M.D., Andrew J. Norton, M.D., H. Konrad Muller-Hermelink, M.D., German Ott, M.D., Elias Campo, M.D., Emilio Montserrat, M.D., Wyndham H. Wilson, M.D., Ph.D., Elaine S. Jaffe, M.D., Richard Simon, Ph.D., Liming Yang, Ph.D., John Powell, M.S., Hong Zhao, M.S., Neta Goldschmidt, M.D., Michael Chiorazzi, B.A., and Louis M. Staudt, M.D., Ph.D.

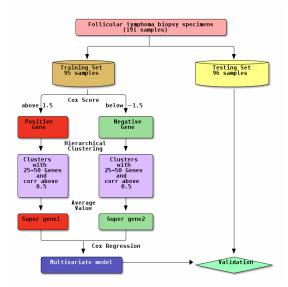


Follicular Lymphoma



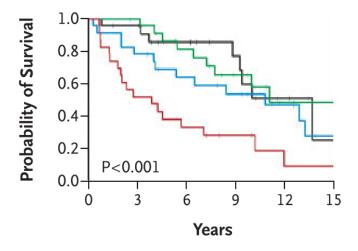
Median survival is around 10 years, but the range is wide, from less than one year, to more than 20 years. Some patients may never need treatment. The overall survival rate at 5 years is 72-77%.

文章思路

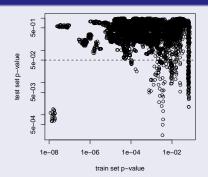




结果

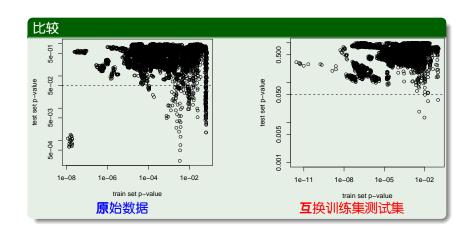


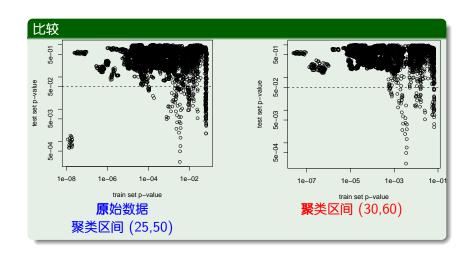
疑点



- Total points (Clustering pairs): 11628
- Points on testing set with p < 0.05: 239







结论

- 看似完美的数据,未必可靠,很可能仅仅是由于过拟合
- 稳健的分析结果,必须经得起Permutation test的反复验证。

参考链接

- http://www.nejm.org/doi/full/10.1056/NEJMoa041869
- http://www-stat.stanford.edu/~tibs/FL/report/