

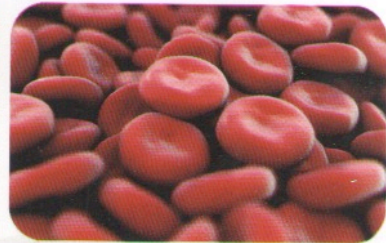
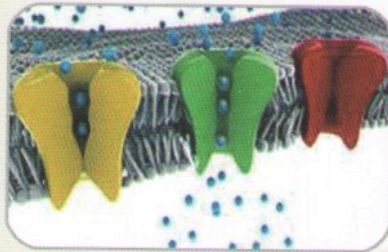


2016第十四届国际新药发明科技年会

BIT's 14th Annual Congress of International Drug Discovery Science & Technology-2016

时间: 2016年11月16-19日 Time: November 16-19, 2016

地点: 中国南京国际青年会议酒店 Venue: Nanjing International Youth Conference Hotel, China



2016首届国际现代中医药大会

BIT's 1st Annual World Congress of Modern Chinese Medicine-2016



2016第三届国际高科技针灸与中西医结合大会

BIT's 3rd Annual World Congress of High-Tech Acupuncture and Integrative Medicine-2016



2016第九届国际癌症免疫治疗研讨会

BIT's 9th International Symposium of Cancer Immunotherapy-2016



2016第十届国际再生医学与干细胞大会

BIT's 10th World Congress of Regenerative Medicine & Stem Cells-2016



2016第六届世界微生物大会

BIT's 6th Annual World Congress of Microbes-2016



Conference Abstract Book 会刊



Title: A New Multiple Testing Method for Discovering Cancer Biomarkers

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Abstract

Case-control tests take important roles in various studies of multi-omics and translational medicine. A new method is here presented for tackling a large number of individual tests, targeting at two major challenges.

1. Multiple hypothesis testing Genome-wide biomarker screening demands joint multiple tests, e.g., each gene g in a set G of genes is tested, resulting in a list of p -values $\{p_g\}$. We want to maximize the number of discovered genes while controlling the false discovery rate (FDR), which is widely studied but still a present challenge (see Nature Methods, 577-581, July 2016). Widely used procedures, such as Benjamini Hochberg (BH) (1995) and Storey (2004), suffer inaccuracy and suboptimal power. As summarized in Figure, our method estimates FDR by integrating $\{p_g\}$ from a perspective that differs from the previous ones, by one of two easy implementations:

- (a) map p_i into pp_i , use BH/Storey on $\{pp_i\}$ to get FDR by Eq.(2).
- (b) directly get FDR by Eq.(1).

2. Testing with a small size of samples Even testing merely one aim (e.g., one gene) on a pair $X^+||X^-$ of case-control populations with a small sample size, the resulted p -value p_0 is unreliable and can be improved by this new method on a list of p -values p_1, \dots, p_n with each obtained by a test on a case-control pair permuted from $X^+||X^-$. Then, p_0 is modified into its posteriori counterpart pp_0 by Eq.(2) with p_0 in place of p_i .

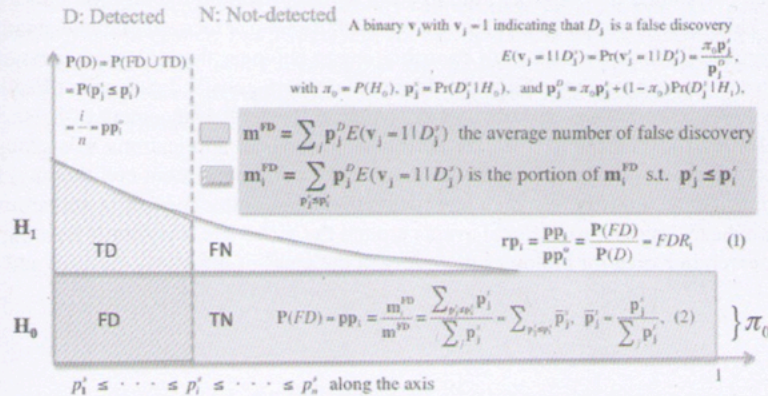


Figure A new method for estimating FDR. The superscript s indicates that the measure is obtained in the space of statistics s , e.g., p_i^s or pp_i^s is the probability that s_i falls in its rejection area while pp_i or p_i^s is the p -value obtained in the p -space of $\{p_i\}$. Further details about $r p_i$ and pp_i are also referred to Xu, L. Appl Inform (2015) 2:4.

Biography

Lei Xu, Zhiyuan Chair Professor of CSE Department. and Director of Brain Inspired Computing and Bio-Health Informatics Center, SJTU; Also, a Guest Professor of Institute of Biophysics, CAS; Ph.D., Tsinghua Univ(1986), Postdoc (1987) and Associate Professor (1988), Peking Univ as well as Postdoc and Visiting Scientist in Finland, Canada and USA (Harvard and MIT) during 1989-93. Joined CUHK as Senior Lecturer in 1993, Professor in 1996, and Chair Professor during 2002-16. Published more than 350 papers and given over 50 keynote/invited/ tutorials at intl. conferences in his research areas. Received several national and international academic awards, including 1993 National Nature Science Award, 1995 Leadership Award from intl. neural network society and 2006 APNNA Outstanding Achievement Award. Elected to Fellow of IEEE (2001); Fellow of intl. Association for Pattern Recognition (2002) and of European Academy of Sciences (EAS) (2002), as well as serve as a member of EAS scientific committee (2014-17).

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