Reproducible research

Jeff Leek

@jtleek

www.jtleek.com

Why reproducible research?

Genomic signatures to guide the use of chemotherapeutics

Anil Potti^{1,2}, Holly K Dressman^{1,3}, Andrea Bild^{1,3}, Richard F Riedel^{1,2}, Gina Chan⁴, Robyn Sayer⁴, Janiel Cragun⁴, Hope Cottrill⁴, Michael J Kelley², Rebecca Petersen⁵, David Harpole⁵, Jeffrey Marks⁵, Andrew Berchuck^{1,6}, Geoffrey S Ginsburg^{1,2}, Phillip Febbo^{1,2,3}, Johnathan Lancaster⁴ & Joseph R Nevins^{1,2,3}

Using *in vitro* drug sensitivity data coupled with Affymetrix microarray data, we developed gene expression signatures that predict sensitivity to individual chemotherapeutic drugs. Each signature was validated with response data from an independent set of cell line studies. We further show that many of these signatures can accurately predict clinical response in individuals treated with these drugs. Notably, signatures developed to predict response to individual agents, when combined, could also predict response to multidrug regimens. Finally, we integrated the chemotherapy response signatures with signatures of oncogenic pathway deregulation to identify new therapeutic strategies that make use of all available drugs. The development of gene expression profiles that can predict response to

ARTICLE LINKS

Supplementary info

ARTICLE TOOLS

- Send to a friend
- Export citation
- Export references
- Rights and permissions
- A Order commercial reprints

SEARCH PUBMED FOR

- Anil Potti
- Holly K Dressman
- Andrea Bild
- Richard F Riedel
- Gina Chan
- Robyn Sayer

DERIVING CHEMOSENSITIVITY FROM CELL LINES: FORENSIC BIOINFORMATICS AND REPRODUCIBLE RESEARCH IN HIGH-THROUGHPUT BIOLOGY

By Keith A. Baggerly* and Kevin R. Coombes*

U.T. M.D. Anderson Cancer Center

High-throughput biological assays such as microarrays let us ask very detailed questions about how diseases operate, and promise to let us personalize therapy. Data processing, however, is often not described well enough to allow for exact reproduction of the results, leading to exercises in "forensic bioinformatics" where aspects of raw data and reported results are used to infer what methods must have been employed. Unfortunately, poor documentation can shift from an inconvenience to an active danger when it obscures not just methods but errors. In this report, we examine several related papers purporting to use microarray-based signatures of drug sensitivity derived from cell lines to predict patient response. Patients in clinical trials are currently being allocated to treatment arms on the basis of these results. However, we show in five case studies that the results incorporate several simple errors that may be putting patients at risk. One theme that emerges is that the most common errors are simple (e.g., row or column offsets); conversely, it is our experience that the most simple errors are common. We then discuss steps we are taking to avoid such errors in our own investigations.

Annals of Applied Statistics

Genomic signatures to guide the use of chemotherapeutics

Anil Potti^{1,2}, Holly K Dressman^{1,3}, Andrea Bild^{1,3}, Richard F Riedel^{1,2}, Gina Chan⁴, Robyn Sayer⁴, Janiel Cragun⁴, Hope Cottrill⁴, Michael J Kelley², Rebecca Petersen⁵, David Harpole⁵, Jeffrey Marke⁵, Geoffrey S Ginsburg^{1,2}, Phillip Febbo^{1,2}, Wohnan Lancaster⁴ & Joseph R Nevins^{1,2,3}

Using in vitro de a seculativa de la microarre data, la microarre data from an independent set of cell line studies. We further show that many of these signatures can accurately predict clinical response in individuals treated with the drugs. Notably, signatures developed to predict response to individual agents, when combined, could also predict response to multidrug regimens. Finally, we integrated the chemotherapy response signatures with signatures of oncogenic pathway deregulation to identify new therapeutic strategies that make use of all available drugs. The development of gene expression profiles that can predict response to

ARTICLE LINKS

Supplementary in



Byport citation

Export references

Rights and permissions

Order commercial reprints

SEARCH PUBMED FOR

- Anil Potti
- Holly K Dressman
- Andrea Bild
- Richard F Riedel
- Gina Chan
- Robyn Sayer

From the article:

Cancer trial errors revealed

2006 Anil Potti, a cancer geneticist at Duke University in Durham, North Carolina, and others file patent applications on the idea of using gene-expression data to predict sensitivity to cancer drugs. Potti is first author on a paper in Nature Medicine.

2007 Potti is last author on a paper in the Journal of Clinical Oncology (JCO)². Duke begins three clinical trials to test Potti's predictors in patients with breast or lung cancer.

SEPTEMBER 2009 Keith Baggerly and Kevin Coombes, statisticians at the University of Texas M. D. Anderson Cancer Centre in Houston,

publish a paper in Annals of Applied Statistics³ stating that they could not replicate Potti's claims. Duke suspends the trials and asks a review panel to investigate.

NOVEMBER 2009 Potti places data underlying the *JCO* paper online. Baggerly writes to Sally Kornbluth, Duke vice-dean for research, and Michael Cuffe, Duke vice-president for medical affairs, to point out differences from raw data.

DECEMBER 2009 An unredacted copy of the report by Duke's review panel, later obtained by *Nature*, shows that the panel replicated Potti's claims using his data, but were unaware that those data contained discrepancies.

JULY 2010 The Cancer Letter reveals that Potti made false claims about his CV. Trials are suspended and an investigation begins. Harold

JANUARY 2010 Duke restarts clinical trials.

Varmus, director of the National Cancer Institute in Bethesda, Maryland, asks the Institute of Medicine to review Duke's trials.

NOVEMBER 2010 JCO paper is retracted. Duke closes the trials permanently. Potti resigns.

DECEMBER 2010 Institute of Medicine study begins, but will now focus more generally on criteria for genomics predictor.

JANUARY 2011 Nature Medicine paper is retracted.

Reference: http://www.nature.com/news/2011/110111/full/469139a/box/1.html





News » Health & Science » Research

Second Potti suit filed against Duke

By Julian Spector on September 23, 2011



Two lawsuits have now been filed in Durham Superior Court against Duke University, Duke University Health System and other members of the Duke Medicine community.

Former patients of discredited Duke cancer researcher Anil Potti have filed complaints in early September. The first suit was filed by eight joint plaintiffs Sept. 7. A second suit, was filed the same day by a single plaintiff—breast cancer patient Joyce Shoffner of Wake County.

Lawyer Robert Zaytoun of Raleigh, N.C. filed the 82-page lawsuit on behalf of Shoffner. The suit states that in seeking treatment for breast cancer, Shoffner participated in clinical trials based on the research of Anil Potti.

"There is a lot of common information alleged in the [two] complaints," Zaytoun said. "The reason for





