

Failing to bridge the gap between test tubes, animals, and human biology

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Reasoning used in many highly cited cancer publications to support the relevance of animal and test tube experiments to human cancer is questionable, according to a study by researchers from Université Libre de Bruxelles published in the open-access journal *PLoS Computational Biology* on October 20th 2011.

Most experimental biomedical research is performed on animals or on cells living in test tubes due to the limits ethics guidelines place on experimental investigation on humans. Bridging the gap between these experiments and human biology is a major hurdle. A connection is often made using the prognostic value of [molecular markers](#)—sets of genes whose activation is related to particular biological processes. Researchers first determine a cancer marker and then assess the ability of the marker to predict survival. The fact that the marker is prognostic is considered to be evidence that the particular biological process is an important driver of cancer.

The authors question this reasoning by highlighting that most whimsical molecular markers, for example genes associated with mice social behavior, are prognostic in human breast cancer. Moreover, they studied 47 markers published in leading scientific journals, representing various biological processes supposedly relevant to breast cancer. They confirmed their prognostic value, but found that 60% of them are not better than random markers devoid of any biological rationale. Thus, the prognostic ability of molecular markers in human breast cancer seems to convey little meaningful information relevant to the [biological processes](#)

of breast cancer progression.

The study recognizes that some molecular markers are truly prognostic and act as a useful guide to breast cancer treatment, even though they may fail to support the causal role of specific biological mechanisms in human [breast cancer](#) progression.

More information: Venet D, Dumont JE, Detours V (2011) Most Random Gene Expression Signatures Are Significantly Associated with Breast Cancer Outcome. PLoS Comput Biol 7(10): e1002240.
[doi:10.1371/journal.pcbi.1002240](https://doi.org/10.1371/journal.pcbi.1002240)

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