INTRODUCTION

Breast cancer is the most common and the most deadly cancer type in women. Patients undergo avoidable adjuvant chemotherapy in 70-80% of cases in node-negative early breast cancer. High-throughput gene-expression profiling technologies yield genomic signatures to predict clinical conditions or patient outcome and help refine a therapeutic decision.

We propose an interactome-based algorithm13-17: ITI (Interactome-Transcriptome Integration) to find a generalizable signature for predicting 5 years relapse free survival in breast cancer.

METHODS

We compared performances between signatures found with ITI algorithm and previously established signatures: the Mammaprint 70 genes signature13-17 (70G) and the ER Status 76 genes signature (76G). This test shows that not only ITI has better predictive power, but that ITI is more generalizable. Our signatures have 11.5 to 32.8% genes in common, so they are less unstable.

RESULTS & DISCUSSION

Subnetworks are stored in the ITI web site (bioinformatique.insERM.fr/iti). This resource is the first of its kind to allow linking a human interactome to diseases or clinical situations. It can be mined for isolating potential drug targets, tumor suppressor genes or oncogenes, as well as prognostic signatures for metastasis of breast cancer as well as other diseases. It has the potential of becoming the starting point to establish finer disease models by systems biology techniques.

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