From Knowledge Management to Translational Research by Combining Clinical and Experimental Data with Public Available Knowledge for Breast Cancer Research

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Abstract and Objective

Breast cancer therapy is confronted with the problem, that after surgical treatment and adjuvant therapy metastases occur in nearly 20% of patients independently of the lymph node status. The prognostic and predictive factors available allow prediction of recurrence with only moderate accuracy. This results in the fact, that the major proportion of patients gets adjuvant therapy of different kind although only a minority needs it. To predict metastasis risk we want to identify a risk pattern consisting of different biomarkers of postmenopausal breast cancer patients. Additionally data from public databases and knowledge from MEDLINE is combined with the experimental data in the BioXM platform.

Keywords:

Breast cancer, Metastases risk, Knowledge management, Data integration

Introduction

Approximately 20% of all adjuvantly treated breast cancer patients develop metastases [1], but due to the lack of specific knowledge all those patients have to get extensive therapy.

The aim of this study is to identify a risk pattern consisting of epigenetic, genetic [2], metabolomic, and transcriptomic markers (inclusive miRNAs) determined in white blood cells WBCs, serum samples and paraffin embedded tissues of postmenopausal breast cancer patients with metastases in comparison to patients without metastases after a period of 5 years. This should allow us to identify different risk classes of getting metastases. In addition markers will be evaluated as indicators for the efficacy of standard adjuvant therapies. We want to identify predisposing features for metastases formation as well as easily approachable tumor markers responsible for haematogenic spread of cancer.

Methods

We use the application BioXM [3] for comprehensive knowledge management and data integration of all available clincal and experimental data combined with public available and integrated data from public databases like MEDLINE, KEGG, EntrezGen, UniGene, UniProt, OMIM, PubChem, miRBase and others.

Results

We provide a comprehensive knowledge management platform for breast cancer metastases risk prediction research for our clinical partners. All mentioned methods can be reused in following studies. We implemented a variety of import scripts and tailored R-scripts in BioXM, which allow to analyze the clinical and the experimental data with different statistical and data mining methods.

Conclusion

Integration of different data types is necessary for effective analyses of our breast cancer studies. BioXM can be used for data integration and leveraging links to public available data. Different types of analyzes can be, once implemented, reused with other data.

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References

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