1. Abstract

Breast cancer is one of the primary threats to women's health worldwide. However, the molecular mechanisms underlying the development of breast cancer remain to be fully elucidated. The present study aimed to investigate specific target gene expression profiles in breast cancer tissues in general and in different breast cancer stages, as well as to explore their functions in tumor development. For integrated analysis, a total of 5 gene expression profiling datasets for 3 different stages of breast cancer (stages I-III) were downloaded from the Gene Expression Omnibus of the National Center for Biotechnology Information. Pre-processing of these datasets was performed using the Robust Multi-array Average algorithm and global renormalization was performed for all studies. Differentially expressed genes between breast cancer patients and controls were estimated using the empirical Bayes algorithm. The Database for Annotation, Visualization and Integrated Discovery web server was used for analyzing the enrichment of the differentially expressed genes in Gene Ontology terms of the category biological process and in Kyoto Encyclopedia of Genes and Genomes pathways. Furthermore, breast cancer target genes were downloaded from the Thomson Reuters Integrity Database. We merged these target genes with the genes in breast cancer datasets. Analysis of anti-breast cancer gene networks was performed using the Genome-scale Integrated Analysis of Gene Networks in Tissues web server. The results demonstrated that the normal functions of the cell cycle, cell migration and cell adhesion were altered in all stages of breast cancer. Furthermore, 12 anti-breast cancer genes were identified to be dysregulated in at least one of the three stages. Among all of these genes, ribonucleotide reductase regulatory subunit M2 (RRM2) exhibited the highest degree of interaction with other interacting genes. Analysis of the network interactions revealed that the transcription factor of RRM2 is crucial for cancer development. Other genes, including mucin 1, progesterone receptor and cyclin-dependent kinase 5 regulatory subunit associated protein 3, also exhibited a high degree of interaction with the associated genes. In conclusion, several key anti-breast cancer genes identified in the present study are mainly associated with the regulation of the cell cycle, cell migration, cell adhesion and other cancer-associated cell functions, particularly RRM2.

2. Abstract

Cancer can be defined as uncontrolled growth of the cells in the human body and can cause in death if the spread is uncontrollable. As the huge amount of breast cancer data available, the integration of data from difference sources becomes one of the challenges in healthcare. The increasing number of data will make the data disorganised, hard to acquire information and share knowledge from a huge database. In recent years, ontology has become more visible within healthcare area. Ontology is a new method designed to improve data integration in a complex database. Ontology integrates and extracts the data from difference sources. There are three ontology methods for data integration, which are single ontology method, multi-ontology method and hybrid ontology method. Hybrid ontology method is a better method as compared to single ontology and multi-ontology. Therefore, this study focused on data integration based on hybrid ontology approach for breast cancer.
(PDF) Development of breast cancer ontology based on hybrid approach. Available from: https://www.researchgate.net/publication/282972440_Development_of_breast_cancer_ontology_based_on_hybrid_approach[accessed Sep 05 2018].

3. Abstract

As the most common cancer among women, breast cancer results from the accumulation of mutations in essential genes. Recent advance in high-throughput gene expression microarray technology has inspired researchers to use the technology to assist breast cancer diagnosis, prognosis, and treatment prediction. However, the high dimensionality of microarray experiments and public access of data from many experiments have caused inconsistencies which initiated the development of controlled terminologies and ontologies for annotating microarray experiments, such as the standard microarray Gene Expression Data (MGED) ontology (MO). In this paper, we developed BCM-CO, an ontology tailored specifically for indexing clinical annotations of breast cancer microarray samples from the NCI Thesaurus. Our research showed that the coverage of NCI Thesaurus is very limited with respect to i) terms used by researchers to describe breast cancer histology (covering 22 out of 48 histology terms); ii) breast cancer cell lines (covering one out of 12 cell lines); and iii) classes corresponding to the breast cancer grading and staging. By incorporating a wider range of those terms into BCM-CO, we were able to indexed breast cancer microarray samples from GEO using BCM-CO and MGED ontology and developed a prototype system with web interface that allows the retrieval of microarray data based on the ontology annotations.

4. **Abstract**

There are increasing efforts directed at providing formal frameworks to consolidate the widening net of terms and relations used in medical practice. While there are many reasons for this, the need for standardisation of protocol and terminology is critical, not only for the provision of uniform levels of health care, but also to facilitate medical science research. In the domain of breast cancer pathology, a summary of current practice by the World Health Organisation states that the variability of the evidence archive (inconsistencies in describing microscopic appearances of phenomena, different diagnostic thresholds for working pathologists) is chief among the barriers to the medical understanding of the symptoms and development of early cancers. Such variability is acknowledged across specialist fields of medicine, motivating standardisation of terminologies for reporting medical practice. The desideratum of making these standards machine-readable has led to their formalisation as ontologies.

Ontologies are computational artefacts designed to provide representations of a domain of interest. Thus, the representation must be a formal description so that it can be encoded, and reused, allowing navigation of the key concepts recorded and retrieval of information indexed against it. This brings the required standardisation by offering a set of labelling options to record observations and events encountered by medical professionals.

Given the twin goals of ontologies -- representation and standardisation -- this paper will consider the key question of their design in the context of the use by experts, of information handling applications built around them. We build on our experience in developing ontologies for decision support software in the area of breast cancer diagnosis and treatment. We will also examine, from this perspective, the suggestion offered in the literature that a set of metaphysically motivated questions should form the basis of ontology building as guarantors of fidelity to reality.

5. Abstract

There are increasing efforts directed at providing formal frameworks to consolidate the widening net of terms and relations used in medical practice. While there are many reasons for this, the need for standardisation of protocol and terminology is critical, not only for the provision of uniform levels of health care, but also to facilitate medical science research. In the domain of breast cancer pathology, a summary of current practice by the World Health Organisation states that the variability of the evidence archive (inconsistencies in describing microscopic appearances of phenomena, different diagnostic thresholds for working pathologists) is chief among the barriers to the medical understanding of the symptoms and development of early cancers. Such variability is acknowledged across specialist fields of medicine, motivating standardisation of terminologies for reporting medical practice. The desideratum of making these standards machine-readable has led to their formalisation as ontologies. Ontologies are computational artefacts designed to provide representations of a domain of interest. Thus, the representation must be a formal description so that it can be encoded, and reused, allowing navigation of the key concepts recorded and retrieval of information indexed against it. This brings the required standardisation by offering a set of labelling options to record observations and events encountered by medical professionals. Given the twin goals of ontologies -- representation and standardisation -- this paper will consider the key question of their design in the context of the use by experts, of information handling applications built around them. We build on our experience in developing ontologies for decision support software in the area of breast cancer diagnosis and treatment. We will also examine, from this perspective, the suggestion offered in the literature that a set of metaphysically motivated questions should form the basis of ontology building as guarantors of fidelity to reality. We find that ontologies intended to support medical practice can only be understood within the context of their intended use. The declarative framework within which they are encoded generates the hope that their meaning transcends the specific application context. We show, however, that these declarative statements are to be understood as end products of chains of procedural engagements between humans, materials and communitarian norms. It is only when this scaffolding that brings this representation into existence becomes routine and consensual (within the community that exchanges information indexed against it) that the concepts stand in for physiological states with independent dynamics. However, as the state of biomedical knowledge is always in a state of flux, and different institutions and practitioners may be out of sync with respect to such modifications, the concepts embedded in the

ontologies are constantly subject to reinterpretation within the context of specific institutional practices. Given the fragmentation of the patient's body when viewed through various specialised lenses, ontologies can provide placeholders for co-ordinating disparate viewpoints to provide suitable medical interventions. The extent to which such interventions reflect any underlying reality, as manifest in measures of their efficacy, is closely wrapped up in the regulatory apparatus of protocol-guided consensus making. The value of ontologies lies in their reflection of, and support for, the sense-making activities that constitute expertise, not in their transparent access to a metaphysical reality.