[372] Functional maps: a novel way of visualizing patterns of recurrence of breast cancer.

Gray LC, Vaidya JS, Houghton J, Baum M University of Texas Health Science Center, Houston, TX; University College, London, United Kingdom

Background: We applied the mathematical technique of multidimensional scaling (MDS) to graphically depict patterns in over 1000 breast cancer recurrences within a randomized trial of the treatment of early breast cancer (ATAC).
Methods: Recurrences in the breast, chest, axilla, supraclavicular node, bone, lung, liver, and other soft tissues were modeled much as if an expanding wave of disease spread over a fluid surface. The result is termed a "functional map". The surface of this map is a computer-generated rearrangement of the body such that distances on the surface represent the probabilities of recurrent disease. The various sites of possible recurrence are points on this surface. Different types of primary tumors are represented as different starting points for disease that expands as concentric ellipses on the surface of the functional map. A succinct visual depiction of underlying patterns in recurrences is thus obtained through a mathematically derived landscape where disease spreads to the next nearest area. This functional map is, in a sense, the tumors' "view" of the body.
Results: This model has a high level of statistical significance ($p \ll 0.01$), explaining between two-thirds and three-quarters of the variance in over 1000 recurrences. There are visually striking differences in patterns of recurrences depending on estrogen receptor status and histological grade of the primary tumor. The tumors in these patients (especially ER+ve tumors) seem to "view" the bone as "closer" than any other site of the body. The maps show an additive interaction between estrogen receptor status and grade, more variability in ER-ve tumors, and absence of unique patterns due to positive nodes, age, months to recurrence, and previous chemotherapy. The trends identified by MDS could be confirmed with standard analyses.
Discussion: MDS provides diagrams that succinctly summarize the data and reveal patterns that are difficult to appreciate otherwise. Subsets of cases with recurrences in different places are easily identified using these maps. The predicted course of disease is succinctly visualized. With the increasing availability of genomic and micro-array data, MDS could be used to provide a unified "picture" including both the genotype and phenotype of disease.

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