Johns Hopkins breast cancer program longitudinal repository

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Public Abstract:
Breast cancer results from the combination of genetic and environmental factors. Increasingly, we recognize it as a collection of subtypes with different clinical and biological behavior. Markers like the estrogen and the HER2 receptor helps identify the subtypes like triple negative, ER-positive, and HER2-positive that will then allow doctors and patients to make decisions about best treatment options, including targeted therapy like the anti-estrogen tamoxifen and the HER2 antibody trastuzumab, respectively. New knowledge allows us to use molecular measures like gene expression to further separate subtypes of breast cancer. In the past, many of these assays required fresh frozen tissue. However, technological developments allow researchers to use routine pathology specimens stored in formalin to measure new molecular markers. Blood tests measuring for the presence of circulating proteins, free DNA, and whole cancer cells are also being developed and could help impact treatment decisions. While much can be learned from the anecdotal clinical experience of individual doctors, from retrospective chart review, and from the evaluation of tissue and blood specimens not needed for patient care, this informal system does not allow high quality research studies. Therefore, a prospective, well-annotated repository with high quality tissue and blood samples and linked to clinical data is needed. Such studies done with approval by research boards could improve our understanding about cancer development, help plan improved diagnostic tests, and help with studies testing new treatment options. Preliminary findings from research institutions like Hopkins can then serve as the basis to develop studies to be conducted through large research groups supported by the NIH, Komen, and other research organizations.