

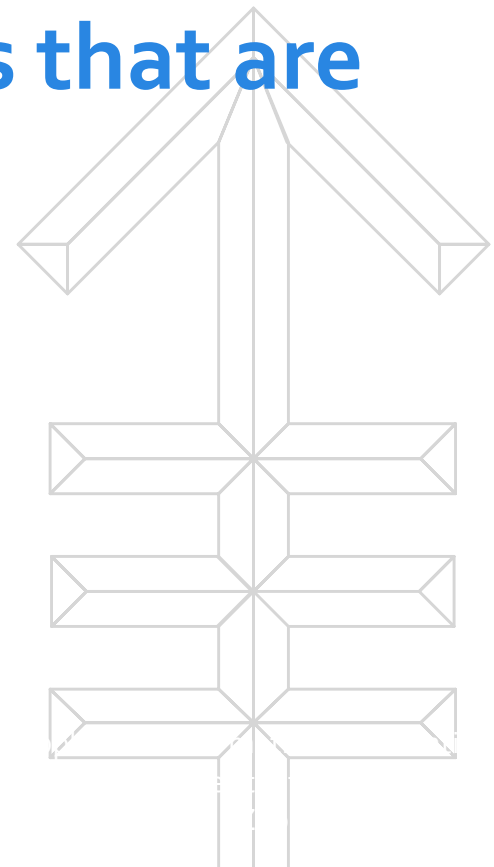


Memorial Sloan Kettering
Cancer Center™

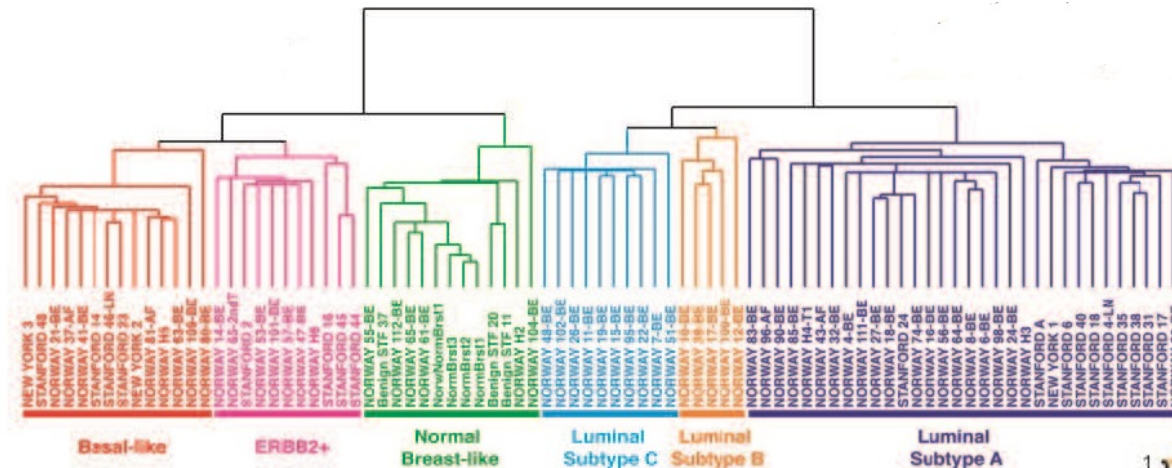
COLUMBIA UNIVERSITY | MAILMAN SCHOOL
of PUBLIC HEALTH
BIOSTATISTICS

Application of a method for identifying disease subtypes that are etiologically heterogeneous

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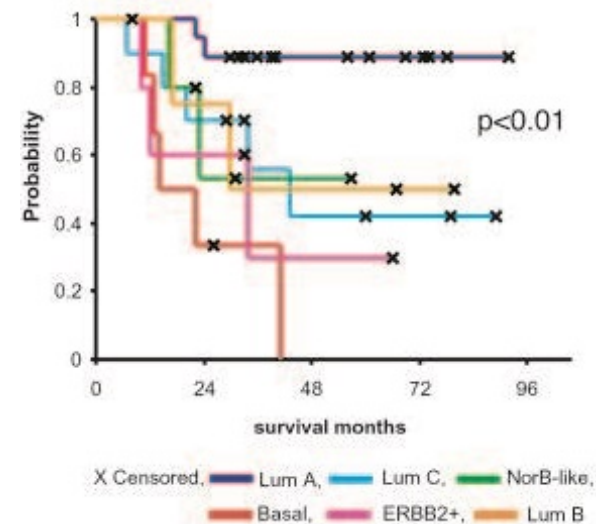


Breast cancer is biologically diverse and subtypes of disease risk and prognosis are recognized



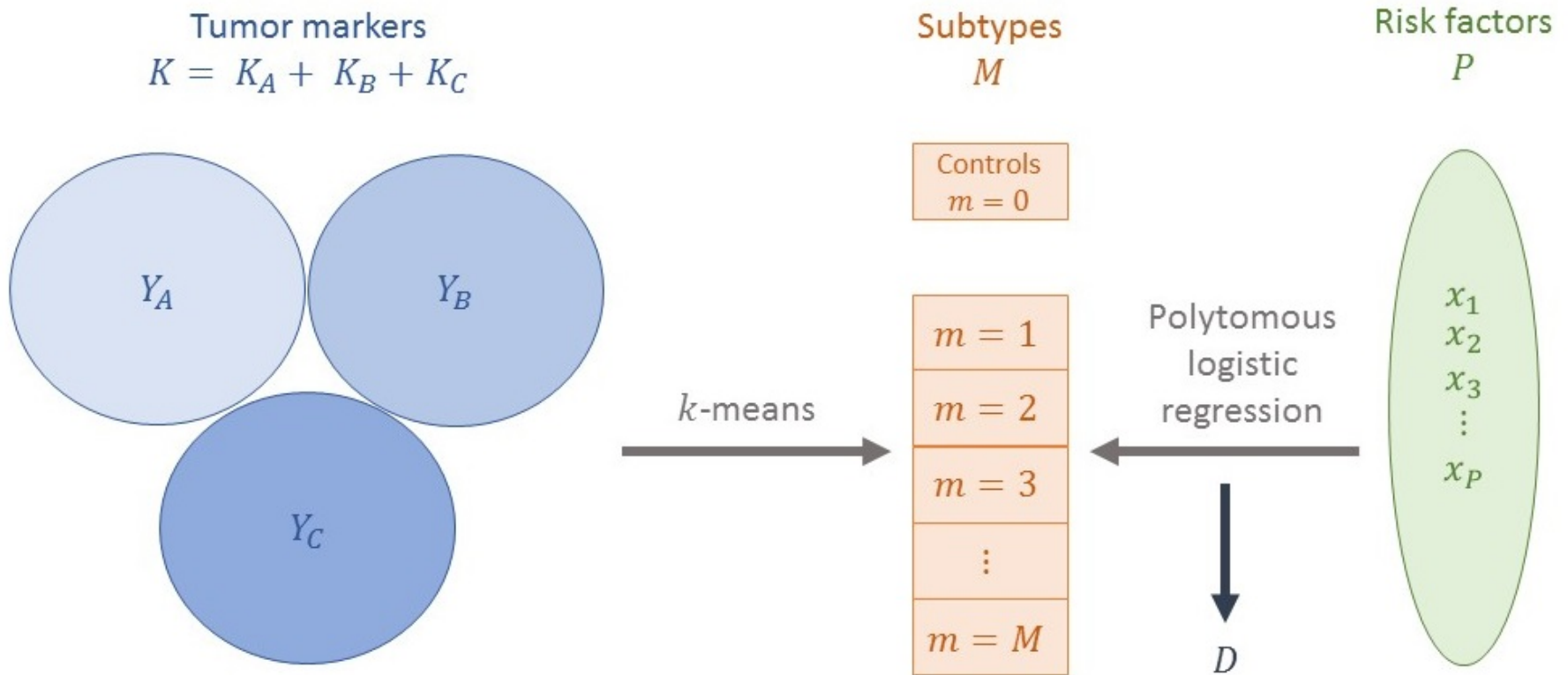
Primary molecular subtypes of breast cancer can be approximated with 4 classes based on 3 IHC markers:

- Estrogen receptor (ER)
- Progesterone receptor (PR)
- Human epidermal growth receptor (Her2)

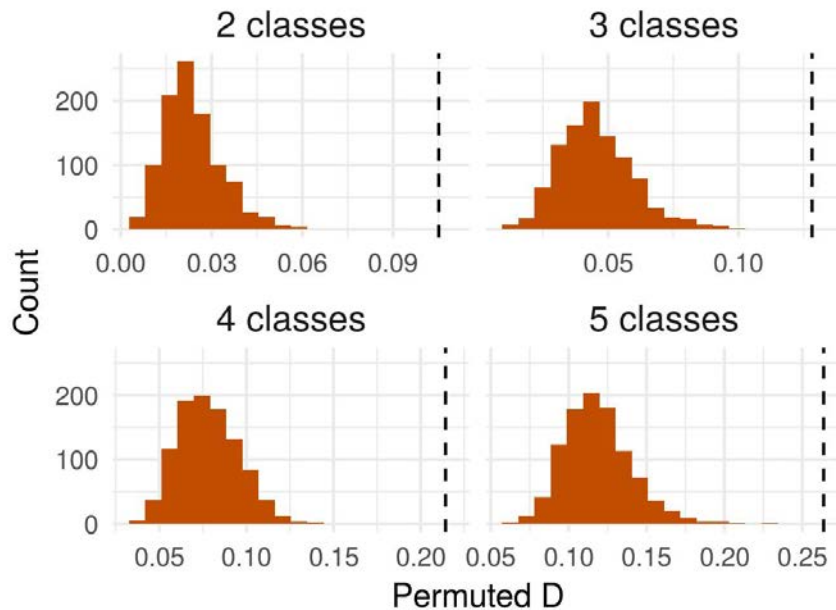


Sorlie et al (2001). Gene Expression Patterns of Breast Carcinomas Distinguish Tumor Subclasses with Clinical Implications. PNAS (19): 10869-74.

Seek to cluster tumor marker data and optimize a scalar measure of etiologic heterogeneity, D



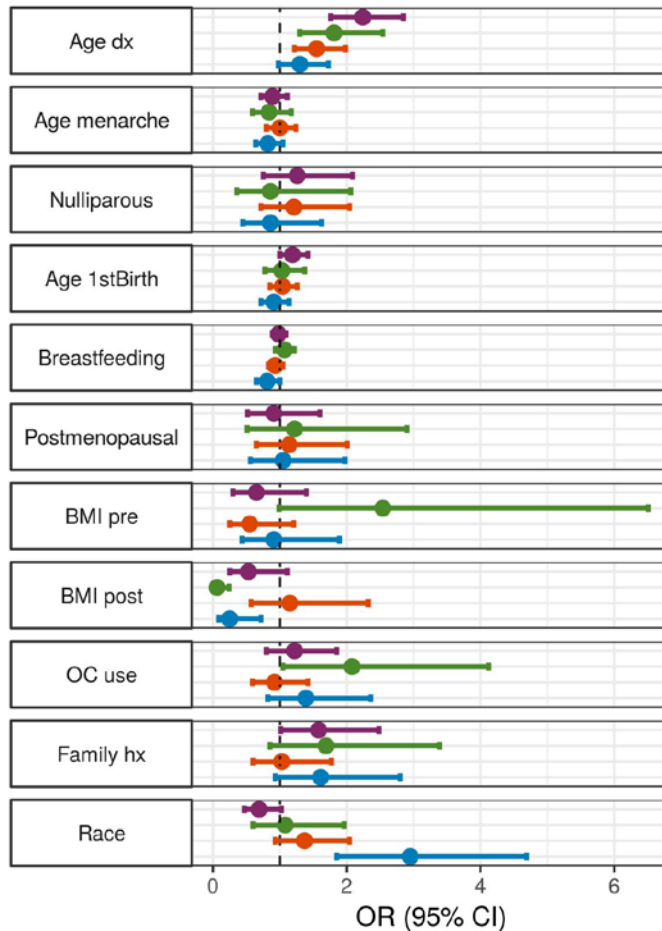
Discovery analysis selects 112 genes and identifies 4 classes



Class size	D difference	P-value
3 VS 2	0.023	0.454
4 VS 2	0.109	0.002
5 VS 2	0.159	0.012
4 VS 3	0.086	0.007
5 VS 3	0.135	0.015
5 VS 4	0.049	0.358

- 532 breast cancer cases included in clustering
- Top-ranked genes of 406 total selected for inclusion based on individual gene D

Age at diagnosis, menopausal status, and race are driving the heterogeneity across subtypes



Class size

D

Discovery

0.214

Validation

0.245

Traditional IHC 4-class

0.148

- Validation produces reasonably similar gene rankings
- Optimal 4-class D exceeds that in traditional IHC 4-class
- ER is a key gene in distinguishing subtypes

