Venet et al., "Most random gene expression signatures are significantly associated with breast cancer outcome", PLOS Computational Biology 7(10):e1002240, 2011

Session Intro

The session will discuss the paper by Venet et al. on the observation that most random signatures appear to be as predictive as any reported breast cancer prognostic signatures. This is an interesting paper because it calls into question whether any of the reported signatures is more meaningful/useful than random ones. A corollary of this observation is that: If you write a paper that reports a breast cancer prognostic signature (or present a method to do so), and evaluates based purely on prediction performance, the journal/reviewer should reject the paper without review.

I hope this catches your attention ☺, and read (and more importantly, think about) the Venet et al. paper carefully.

Session Plan

I am dividing the session into three parts as given below.

Although I have provided some possible topics/pointers for each aspect, I leave each presenting team to decide on what they want to talk about (i.e., it is perfectly ok to leave out some topics/points and/or include other topics/points.) Also, the presenting team need not just make presentations; they are encouraged to figure out how to engender more class interactions and lead discussions.

Part I, Background information:

This part deals with background knowledge of cancer biology and statistics that is needed to understand the paper. I have highlighted some keywords below for you to look up background literature, Wikipedia, etc.

- Breast cancer

- Hall marks of cancer

- Cox's proportional hazard

- Breast cancer prognostic signatures

Presentation team #8: HE YINGZHI, LI XIANG, ZHAO ZITONG

The team members can decide who present what. Each presentation should be brief (say 5 minutes.) You can focus on any aspect of the topic, with the objective of making it easier for the class to understand the Venet et al. paper. **Total time limit: 15 minutes (presentation) + 5 minutes (audience questions.) Total slide count: 10 slides max.**

Part II, The paper by Venet et al.

This part presents the Venet et al. paper itself. We want to know some key technical details and the key messages, such as:

- Details of how Venet et al. determine whether a signature (reported or random) is significant

- Details of how Venet et al. determine the contribution of proliferation genes in significant signatures

- What the main findings of Venet et al. are.

Presentation team #5: KHOOI XIN ZHE, QIN HANGYU

I leave you to decide how you want to organize the presentation. **Total time limit: 15 minutes (presentation) + 5 minutes (audience questions.) Total slide count: 10 slides max.**

Part III, Possible points for discussion

This part discusses the Venet et al. paper, hopefully in depth. We want to know whether there is any methodological issue, any doubt on the conclusions/key messages, any suggestion for improving the paper. Some pointers for discussion include:

- Any methodological issue? E.g. is there a hypothesis in this paper, and has it been well tested?

- Any issue on the key messages?

- What more can you do to show the impact of proliferation-associated genes on breast cancer survival signatures?

- Are all proliferation-associated genes born equal in terms of impact on breast cancer survival signatures?

- What more could be done in terms of evaluation of breast cancer survival signatures?

Presentation team #1: AISHWARYA JAYAGOPAL, CAO XIAO, LIU ZHUANGHUA

I leave you to decide how you want to organize the presentation. **Total time limit: 15 minutes (presentation) + 5 minutes (audience questions.) Total slide count: 10 slides max.**