AI and Human Health – Cancer Therapy

Participants

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Assets

- **Matthew Ringel – Professor, Clinician Endocrinology, CTSA, CCC**
  - Expertise in thyroid cancer, has cell lines and clinical datasets
  - Single cell sequencing, RNA, microRNA
  - Evaluates response to treatments
- **Xiaolin Cheng – Assoc. Prof.**
  - Expertise in virtual screening
  - Molecular target design
- **Lijun Cheng – Asst. Prof.**
  - Expertise in graphical and network models
    - Target identification, CRISPR screening for pancreatic, breast and prostate cancers and sarcomas
- **Sam Davanloo– Asst. Prof.**
  - Efficient optimization of algorithms
  - Ability to scale up models with large amounts (hundreds of thousands) of variables
  - Decision support for optimal solutions
- **Kevin Sweet — Licensed Genetic Counselor**
  - Tumor, germ line genetic/genomic data; large datasets
  - Access to patients
  - Connection to Foundation 1 Program

Link and Leverage Our Big Ideas (Looking for top three)

1. How do we identify critical response pathways for surviving (cancer) treatments? Define adaptive response mechanisms to therapeutic challenges (hypoxia, radiation, drug stressors)

2. How do germline mutations (disease predispositions) interact with somatic line events in a cell/tumor? Link complexity of germline to complexity of tumor itself (germline – somatic genomics)

3. Tumor heterogeneity: what drives it?

4. What causes or prevents the reawakening of symptoms after lapse (thyroid cancer as an example) – "inflection"

5. Why does disease in one person in a family look different from that in other family members? Germline is constant, somatic is different (link with #2 above) how does ethnicity/racial background play a role (genomics)?

6. How do you decide when, which, and how much to knock out genes and proteins? Develop a mathematical model that can help you choose how to get to a desired endpoint (e.g., survival; link with #1 & #2 above)

Big Ideas to investigate:

1. How do we define the level of (gene?) inhibition necessary to achieve biological endpoints?

2. What are the critical pathways that define the adaptive response to therapeutic challenge?

Technology opportunity: create a computational model that allows more rapid ability to analyze complex data sets

Big needs/next steps:

Get to know each other and each other's languages better

Get to know the data: what is available? What is the shape of the data? Which data should we focus on and can it talk to other data types (different levels)?

- Lijun, Xiaolin: identify potential optimization needs (including algorithms not perfectly suited); optimize bottlenecks that limit us from getting to these endpoints (RNA levels?)
- Lijun, Xiaolin, Sam: meet and powwow to define the best dataset to test – determine the expertise needed (e.g., pancreatic cancer?)
- Everyone reconvene to assess translational possibilities and directions