Request For Applications:  
Cancer Systems Biology Training Program

Sponsored by The Cancer Cell Map Initiative, UCSF and UC San Diego Health Sciences

Overview

The Cancer Cell Map Initiative (CCMI; www.ccmi.org) is pleased to accept applications for our Cancer Systems Biology Training Program (www.ccmi.org/training-program). Applications are solicited from graduate students, postdoctoral fellows and senior scientists (titles such as project scientist or research scientist) at UCSF or UC San Diego wishing to develop and apply systems biology approaches to address a compelling biomedical question in cancer. Proposals are welcome from trainees in CCMI-funded labs or from trainees proposing a collaborative project with at least one CCMI faculty member (www.cmi.org/investigators).

The CCMI will provide funds to support 50% of the trainee’s salary. Trainees will be required to participate in the CCMI’s annual External Advisory Committee Meeting, every other month All Hands Meetings and potentially other CCMI events. They will also have to submit a brief annual report. Funds will be provided for one year with trainees able to re-apply for future years.

Goals

Although much attention has been devoted to sequencing tumor genomes, understanding cancer involves more than cataloging frequently mutated genes. It is critical to understand the many interactions between these genes and the corresponding proteins, and how these complex networks give rise to tumor initiation, progression and metastasis. The CCMI is applying systematic approaches to comprehensively map the molecular networks that underlie cancer and will use these maps as a key resource for precision medicine.

This program is intended to support the exploration of innovative, high-risk concepts that are already part of CCMI research programs or that complement ongoing studies (more details are available at www.ccmi.org/research, ccmi.org/research-core and bit.ly/CCMIpubs). Possible topics of notable interest based on recent CCMI publications are as follow:

- Extending DrugCell (Kuenzi et al., Cancer Cell 2020; drugcell.ucsd.edu) to include new features about cancer cells (e.g., copy number alterations, mRNA expression levels and epigenetic modifications) or drugs and drug combinations;
- Development of novel approaches to map genetic interactions in cancer (Tutuncuoglu and Krogan, Genome Med 2019, Shen and Ideker, J Mol Biol 2018, Du et al., Nat Methods 2017 and Shen et al., Nat Methods 2017) to comprehensively identify and validate key hierarchical structures and systems (Zheng et al., bioRxiv 2020); and

Submission Information

Use the NIH’s structure (Significance, Innovation and Approach) or a similar format to describe a single Specific Aim in two pages or less. Proposals should clearly state the significance of the biomedical problem in cancer and why it will benefit from a systems biology approach. The proposal should include a succinct description of the research plan along with proposed experiments, methods and
analysis. Please describe the available reagents and assays needed to support the research or describe what will need to be developed. Applications will be scored based on standard NIH criteria with an emphasis on the potential for groundbreaking science and synergy with CCMI research efforts.

In addition to the two-page research proposal, please also provide an NIH biosketch and letter(s) of support from faculty mentor(s). For proposals from trainees in CCMI-funded labs, a single letter is sufficient. For trainees outside the CCMI proposing a collaborative project, letters should be provided from both their main faculty mentor and the collaborating CCMI faculty member.

All documents should be submitted as one PDF to hello@ccmi.org by 11:59 PM PT January 31, 2021. Please also direct any questions to hello@ccmi.org.

About The Cancer Cell Map Initiative (CCMI)

The CCMI is generating comprehensive maps of the key protein-protein and genetic interactions underlying cancer, and is developing computational methods using these maps to identify new drug targets and groups of patients with shared outcomes (Fig. 1). Protein-protein interaction maps – the complete set of proteins that bind to another protein – tell us about the physical structure of cancer cells. Genetic interaction maps – knowing how deleting one gene impacts how cells respond to the loss of another gene – tell us about how groups of genes function as pathways and networks. New drug targets and patient subtypes will then be identified using a variety of machine learning algorithms. Unsupervised methods such as clustering and network propagation will be used to identify patient subtypes and drug targets, respectively, and supervised methods like neural networks will be trained to predict outcomes based genetic information.

The CCMI’s initial research efforts are focused on head and neck squamous cell carcinoma (HNSCC) and breast cancer. HNSCC is the sixth most common malignancy worldwide with only a 40% survival rate; breast cancer is the most common type of cancer in the US leading to over 40,000 deaths. For both, we will generate unbiased, comprehensive physical interaction maps of the forty most commonly mutated proteins in that cancer type. Genetic interaction maps will be generated for the same forty genes plus an additional thirty druggable targets. These interaction maps will also be used along with other comprehensive datasets to infer data-driven hierarchical maps of the protein complexes, pathways and other subsystems present in cancer cells. These ontologies will then be used as features by sophisticated machine learning algorithms to predict patient outcomes like drug response.

Figure 1 | Overview of the CCMI’s research efforts.