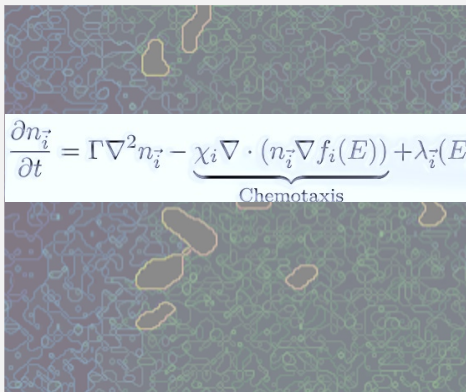
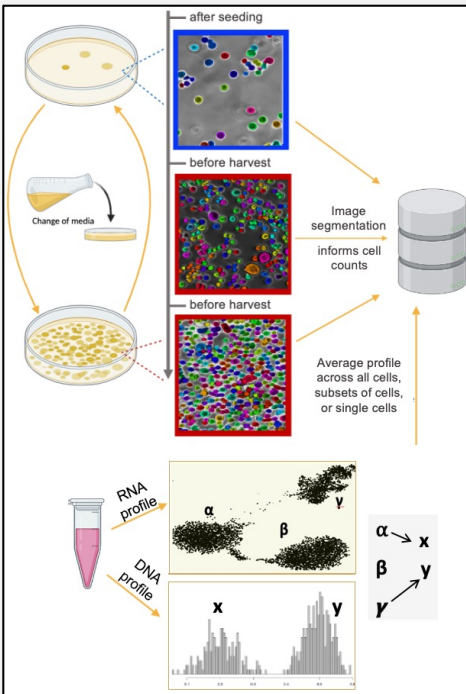
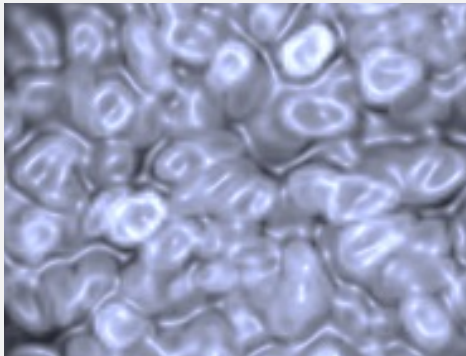


SOFTWARE ARCHITECT



Success in the clinical setting requires an experimental setting in which our therapeutic solutions are challenged with the adaptive nature of cancer. We seek to contribute to a paradigm shift in the way research laboratories define success of pre-clinical studies, not as the maximum reduction in cancer cell population growth, but as the ability to control a population's clonal dynamics over several generations of environmental adaptation. While a plethora of algorithms have been developed to characterize the clonal composition of a cell population, no infrastructure exists to store clone specific measures and to streamline their acquisition while preserving contextual information, such as cell density, time and pedigree. We developed a software called CLONEID to fill this gap. It offers the flexibility to handle a range of resolutions on the cellular composition of profiled samples, integrating measurements obtained from different technologies, or from multi-spatial or longitudinal biopsies, into a comprehensive approximation of coexisting tumor clones. The software provides the infrastructure for efficient collaborations between experimentalists, computational biologists and mathematicians. Experiments to inform mathematical models are carefully planned to ensure they will provide the necessary information for modeling, a process that requires coordination and discussions between experimentalists and computational/mathematical biologists and often takes weeks per experiment. CLONEID provides a workflow to streamline this process. It ensures that the information needed for modeling is permanently stored in a centralized location with minimal extra burden on the experimentalist.

We seek an experienced software engineer to lead development of the beta version of CLONEID. Goal is to distribute the software across up to 10 laboratories and facilitate standardization, access and sharing of the data they generate into a common centralized database. Strong skills in software architecture design, model-based systems engineering, including requirement traceability, behavioral analysis and substantial expertise in Java and relational databases is required. The ideal candidate works according to established software architecture principles (e.g. observer pattern, modular architectures, flexibility tradeoffs), and has a track record of designing and testing flexible architectures. Experience with MagicDraw, MySQL, R and MATLAB are a plus.

Moffitt Cancer Center is the top-ranked NCI-designated comprehensive cancer center in the Southeastern US. The Integrated Mathematical Oncology department at Moffitt integrates mathematicians, computer scientists, and physicists together with evolutionary biologists, geneticist and imaging specialists as well as clinical and experimental oncologists to better understand, predict and treat cancer.

More information under cloneredesign.com.

Please send your CV and cover letter to noemi.andor@moffitt.org