Realization of Common Platform Technology, Facilities, and Equipment that creates Innovative Knowledge and Products

Quantitative approach for genome evolution dynamics based on multiscale mathematical model

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Summary :

A current gold-standard approach in disease research is essentially rely on statistical analysis of "snapshot data" during dynamic disease progression. In order to quantitatively understand disease progression as "genome evolution" and extract "nonlinear system" behind real datasets, we will develop novel dynamical approach combing population dynamics theory and population genetics theory with time-series data. In particular, we will analyze time-series of deep-sequence datasets obtained from virus infected patients (e.g. HTLV-1 and HCV) and contribute the establishment of new diagnosis criteria and prediction of disease progression. To achieve our project, we first need to derive mathematical formulation of multiscale model and perform its numerical calculation based on individualbased model. Then, we generate "artificial sequences" using the simulator and estimate parameters to reproduce real datasets deep-sequences. Integrating current high-throughput bv technics including next-generation sequencer and mathematical sciences, we make a paradigm shift in future disease researches. 図1.POCを達成するための研究開発の全体像



