DNA coded randomized algorithms

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Abstract: The traditional understanding of cells of the same type has been that they react similarly when exposed to the same signals. As experimental methodologies have become more quantitative, this view has been challenged by data establishing the ubiquity of heterogeneity in the potential of apparently identical cells. The source and ramifications of this diversity is presently a topic of active study in subjects from cancer to immunology.

In this talk we describe two tools that we have designed to aid in this investigation, providing some of the mathematical detail that led to one of them. Both are randomised algorithms that can be coded in mammalian DNA and are being implemented in labs in the Netherlands and Australia. One enables the inference of the the average number of divisions a population of cells has undergone and is based on theorems regarding the average generation of an age-dependent branching process. The other enables familial identification of cells by, essentially, placing a deck of cards and drug-inducible instructions for shuffling into DNA.

No prior biological knowledge is required to understand this talk and an attempt to provide motivation will be provided throughout.