

Counting the Patterns of DNA Rearrangement

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Genome rearrangements can induce evolutionary variety, but can also lead to deleterious effects – such as cancer. Certain unicellular organisms undergo a massive genome-wide rearrangement during sexual reproduction, during which the genome becomes fragmented into over 250,000 pieces that can become permuted and inverted before reassembling. The outcomes of these recombination processes can be recorded as oriented rearrangement maps, that belong to an equivalence class of rearrangement patterns. In order to study the complexity of the scrambled patterns, we merge the non-scrambled sections of the resulting genome and form a reduced pattern. In this talk I will enumerate the number of reduced rearrangement maps and patterns, and discuss the complexity of the scrambled patterns found in the ciliate *Oxytricha trifallax*.

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