A common microbial stochastic mechanism is phase variation, in which gene expression is controlled by a reversible genetic mutation, re-arrangement, or modification. It may play an important potential role in bacterial specialization and differentiation, and the generation of structured bacterial populations. A characteristic of this process is the formation of sector-like patterns in bacterial colonies. A stochastic phase variation mechanism has been previously encoded in a mathematical model for predicting mutation rates in the presence of fitness differences, describing the colonies at the overall population level and ignoring sectoring. Our goal was to model the spatial attributes of phase variation, to detect and describe the patterns obtained, and provide a method for running simulations for different types of mutation rates and fitness differences.

Two independent parameter scan procedures were executed. The first procedure scanned the parameter space to find the best value of the maximum height (h) of the colony. The second procedure searched for the best value of the probability of the offspring to stay with the parent (w) or be displaced to a neighbouring position.

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References:

Fig. 1. CSPN model for phase variation in bacterial colonies using a circular geometry.

Fig. 4. Different values for the parameter h (a, b) and w (c, d) considering a circular geometry.

Fig. 3. Final state images for stochastic models using rectangular (left) and circular (right) geometries illustrating the development of sector-like patterns. Density ratios of the two phenotypes is encoded by colour where yellow indicates patches with high density of one phenotype and dark purple of the other.

Fig. 5. Detecting and analysing sectors in models using rectangular (left) and circular (right) geometries.

Fig. 6. Distribution of the distance from the centre using rectangular (left) and circular (right) geometries.