

Modelling Team Update

23/07

Progress

- Since last meeting we have:
 - Implemented run & tumble motion
 - With/without chemotaxis
 - Implemented interactions between objects (bacteria and particles)

Run & Tumble Motion

- Parameters:
 - Run time
 - Can vary depending on direction of motion with respect to aspartate gradient
 - Speed is fixed
 - Tumble time
 - Tumble angle

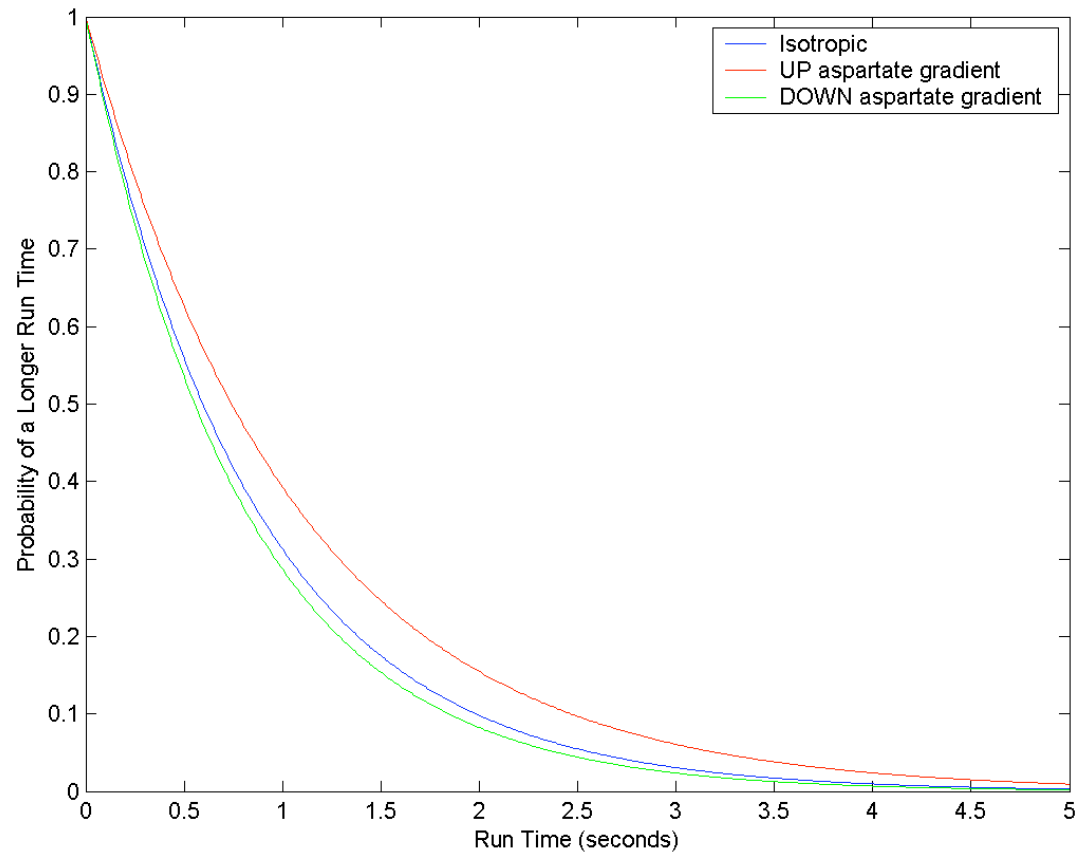
Run & Tumble Motion

- Run Time
 - Current model: run length determined at the start of a run; approximated as an exponentially distributed random variable
 - Isotropic case: mean of distribution is fixed, independent of direction
 - With chemotactic gradient: length is sampled from one of two exponential distributions with different means, depending on direction

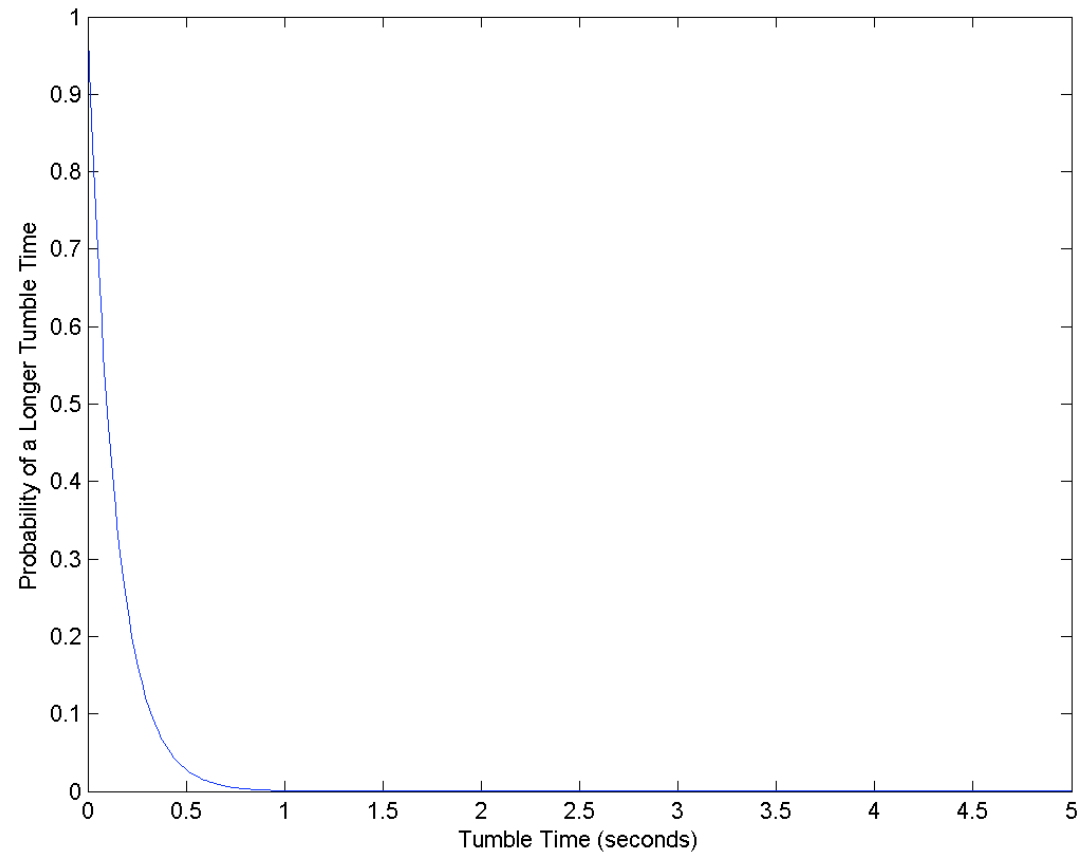
Run & Tumble Motion

- Tumble time
 - Also exponentially distributed random variable
- Tumble angle
 - Random variable sampled from a gamma distribution
 - Bi-directional
- Tumble time is independent of tumble angle (!)

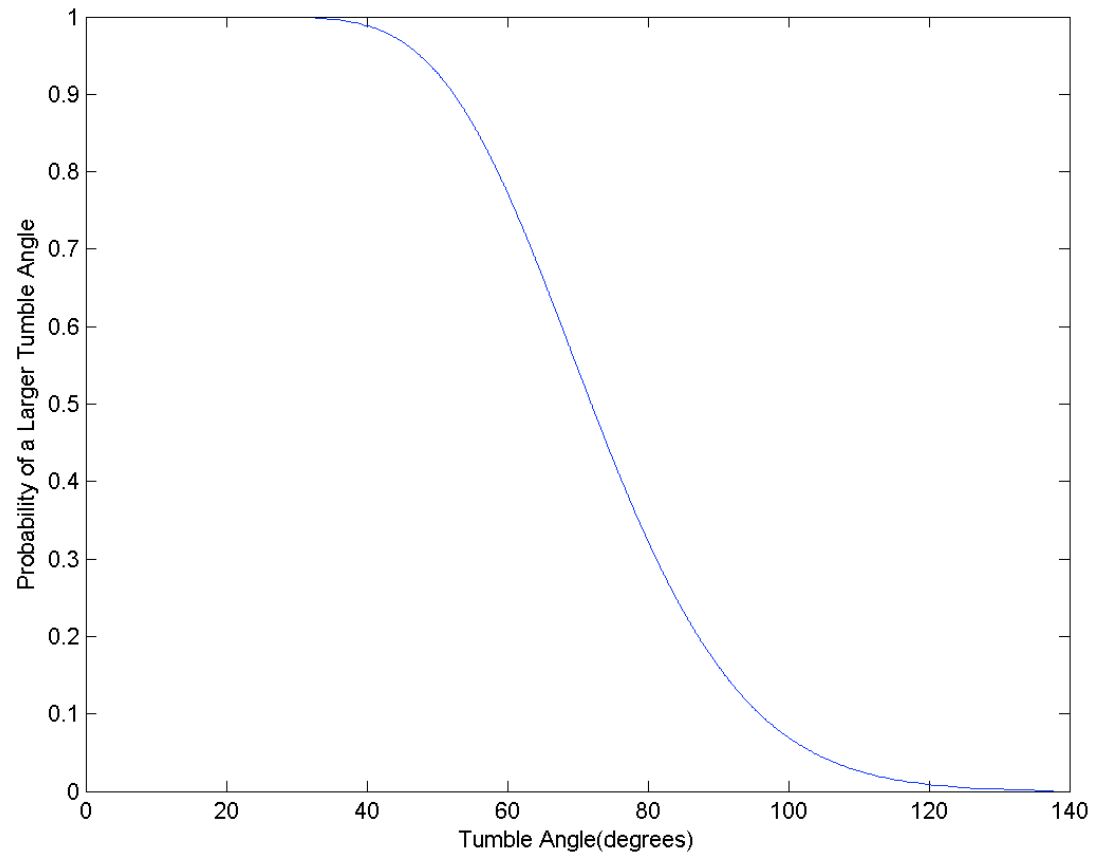
Run Times



Tumble Times



Tumble Angle



Interactions

- Interactions modelled through forces between objects
 - Attractive at short range, repulsive when objects overlap
- Motion is determined by resolving forces
 - No acceleration (inertia is irrelevant at very low Reynolds number)
 - Velocity is a function of: force, object radius, viscosity
 - Found using Stokes' Law for spheres moving at low Reynolds Numbers

Next Stages

- Tracing motion of particles
- Impose boundary conditions
- Implement signalling between bacteria