

Chemotactic responses (accumulation index) are described by the values given in this dataset for each replicate experiment. The accumulation index is calculated based on bacterial cell positions in every image over the chemotaxis time series (3,600s) and is defined as:

$$\beta(t) = \frac{N_L(t) - N_R(t)}{N_L(T) + N_R(T)}$$

Where $\beta(t)$ represents the accumulation index which describes directionality of cell motility. A positive value indicates a net movement to the left side of the channel and is calculated by subtracting the number of cells on the right side of the channel (N_R) at each time point (t) from the number of cells on the left side of the channel (N_L) at the same time point. Only cells within 200 μ m from the left and right edges of the channel are counted. The difference is then divided by the sum of all particles on the left ($N_L(T)$) and right ($N_R(T)$) side of the channel (within 200 μ m from either edge) at the final time point to normalize the data. $\beta(t)$ is calculated for all images in the time series. The individual replicate data as well as the average and the standard error between replicates are given for each condition and are displayed in separate columns.

The accumulation index describes directional chemotaxis of the *V. alginolyticus* population in response to intact *Synechococcus* WH8102 cells. The analysis found that *V. alginolyticus* exhibited a stronger chemotactic bias towards *Synechococcus* WH8102 when they were infected with the cyanophage S-SSM5 which provides support to the overall hypothesis of the project that viral infection of picophytoplankton may result in attraction of heterotrophic microbes thereby altering carbon flux.