Journal Name

COMMUNICATION

Supplementary Information

Dynamically resolved self-assembly of S-layer proteins on solid surface

The growth rate of the S-layer islands is related to the flux of monomers from the solid-liquid interface to the edge of the S-layer island. When the separation between neighbouring S-layer islands becomes smaller, this flux is reduced, and reaches 0 (zero) when neighbouring islands touch. This is also referred to as diffusion field overlap and is well known for 2D growth where the flux is from the surface.

In order to make a correction for the reduced flux, the tetramer attachment rate of the S-layer island,

$$\sqrt{N_T} * R$$

must be multiplied with a function that is 1 at large separation distance and which will reach to 0 at a separation distance of 0, approaching to 0 linearly in island separation. Furthermore, the transition from 1 to 0 will occur over a characteristic distance determined by the diffusion length.

Ideally, a hyperbolic tangent function of the island separation divided by the diffusion length would be used. However, this requires an additional input in the form of a time dependent island separation and unless the experimental setup contains such large number of S-layer islands that the distribution will reach the ensemble average, the time dependent separation distance will be dependent on the experiment.

Instead, we use the fact that the island separation is inversely related to the island size, with maximum separation at zero island size, and zero separation at maximum island size. The correction term

$$\frac{N_{T,m} - N_T}{N_{T,m}}$$

equals 1 at 0 island size and linearly approaches zero at maximum island size.

Similarly, the island separation is inversely related to the number of S-layer islands, with maximum separation at zero islands, and zero separation when the maximum number of islands is reached. Thus, the correction term then becomes

$$\frac{N_{SL,m} - N_{SL}}{N_{SL,m}}$$