**Recalled Batch Scenario:** The recalled PIF batch profile collected from Jongenburger et al. (2011). To replicate the recalled batch profile, we simulate one lognormally distributed cluster covering 42% of production with 1.779±0.675 log(CFU/g) Cronobacter concentration (mean±sd), and used -5 log(CFU/g) as the background level.

**Reference Batch Scenario:** The reference batch profile collected from Jongenburger et al. (2011). The batch is one with one contamination cluster with 2.44 ± 0.8 log(CFU/g) concentration (mean ± sd) and 1% prevalence.

**Prevalence:** Proportion of lot that is contaminated. For example, 100% prevalence means the whole lot is contaminated. 1% prevalence means a small portion of the lot is contaminated.

The **mean** and **standard deviation** are used to assign a contamination level to the contamination cluster. The contamination levels are drawn from a lognormal distribution.

If you have previously measured the contamination level or have historical data of microbial load in your lot, please input it here.

The number of **equally sized (g) samples** that will be throughout the production of the lot. A greater number of samples means that the sampling plan is more stringent.

The production **time (x-axis)** will be split into ***n (user input)***equally sized stratum. For example, if my production time is **20 hrs.** and I select “Number of Strata” as **5.** Then each stratum will be 20/5 = **4 hrs.**

The number of **equally sized (g) samples** that will be taken for each stratum. Example. If I have 4 strata, and I select “**Number of sample points per strata”** as **5**, then I will be taking a total of 4 X 5 = **20 total samples per production lot**