Final project proposal

### The Data:

We have data from 6 replicons from 4 different species of bacteria: \ecoli, \bass, \strep, and \smel.

All of the bacteria have their genome contained in one chromosome except \smel which is a multirepliconic bacteria. A multirepliconic bacteria means that the genome is made up of multiple replicons or chromosome like structures. For this reason, each replicon of \smel (chromosome, pSymA, pSymB) will be analyzed separately. So we effectively have 6 bacterial datasets.

\begin{table}[H]

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\begin{tabular}{ll}

\toprule

Bacteria & Replicon Name \\

\midrule

\ecol & Chromosome \\

\bass & Chromosome \\

\strep & Chromosome \\

\smel & Chromosome \\

\smel & pSymA \\

\smel & pSymB \\

\bottomrule

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