**Relative abundance findings (anaerobic digester sludge):**

* Highest abundance methanogens:
  1. Acetoclastic
     + Methanosaeta
     + Methanosarcina
  2. Hydrogenotrophic
     + Methanospirillium
     + Methanoculleus
     + Methanoregula
  3. Methylotrophic
     + Methanococcoides
* Highest abundance bacteria:
  1. Fermenters
     + Clostridium
  2. Acetogenic
     + Treponema
     + Eubacterium
  3. Hydrolysers
     + Halothermothrix
* Most abundant systems:
  1. Central carbon metabolism
  2. One-carbon metabolism
  3. CO2 fixation
  4. Fermentation
  5. Organic acids

**Nutrient abundance findings (incoming sewage):**

**Overall findings:**

Bacteria are found in a much higher abundance overall than archaea, showing archaea with a relative abundance of approximately 6% compared to bacterial abundance of 93% (Guo et al., 2015), with similar results shown in previous studies. Incoming sewage has a drastically different community make up than activated sludge. Communities between different digesters can have rather large differences.

Initial inoculation communities have a large effect on future community structure, however further alterations can be made to community structure but primarily through incoming nutrients rather than incoming communities (Shchegolkova et al., 2016). Approximately 97% of faecal taxa and abundance is represented in sewage communities (Shchegolkova et al., 2016). Avoiding high Gordonia abundance will reduce foaming and bulking significantly, according to Shchegolkova et al. 12% - 15% of all sewage material is from human faecal matter. This ties in to the previous point of an 97% faecal taxa mirror in sewage communities.