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A Bayesian approach to optimized sample sizes for analyzing the genetic heterogeneity of bacteria isolated from fecal samples

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- the problem
 - of genetic heterogeneity in multiple bacterial isolates of a sample



- need to answer:
 - How many isolates have to be genotyped in order to be 95% confident that all genotypes are found?

The Approach



The Data

the data:

- genotyping gastrointestinal *E.coli* isolated from 5 sheep using ERIC fingerprints
- N=88 observations from fecal samples

- N=10 max. # isolates typed per sample
- i= 6 max # of genotypes found per sample
- Need the **probabilities** for finding j isolates while typing N isolates per sample!
- i = 6 "true" max # of genotypes per sample
- building priors based on
 expert opinion
- assemble.....
- soft information, f.e. from expert opinion or pilot data as prior knowledge,
- 'hard'information from the sheep data
- probability function
- to cacluate the posterior likelihood distribution for finding all genotypes in a given sample while analyzing a fraction *N*
- using a Gibbs sampler in f.e. WinBUGS (Spiegelhalter et al. 2000)



The Results

1.0

Figure 1: How many isolates does it take in order to find all genotypes with 95% probability?

feces:16rumen:11small intestines:5large intestines:10



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