Inferring the presence of metabolites

January 30, 2023

We seek to infer the presence or absence of M metabolites in S species. We denote by x_{sm} whether metabolite m = 1, ..., M is present $(x_{sm} = 1)$ or absent $(x_{sm} = 0)$ in species s = 1, ..., S. To infer the full vector $\mathbf{x} = (x_{11}, ..., x_{1M}, ..., x_{SM})$, we assume that related species share a similar set of metabolites and that metabolites related in their synthesis share a similar distribution across species. Let $\mathbb{P}(x_{sm} = 1|y_{sm}) = y_{sm}$ be the probability with which metabolite m is present in species s. We then assume that

logit
$$y_{sm} = \mu_m + \epsilon_{sm}$$

where μ is a metabolite-specific intercept and ϵ_{sm} is normally distributed with mean 0 and co-variance $\operatorname{cov}(\epsilon_{sm}, \epsilon_{s'm'}) = \alpha \sigma_{ss'} + \beta \sigma_{mm'}$ between each combination of species and metabolite. Here, $\sigma_{ss'}$ and $\sigma_{mm'}$ are known measures of covariance between species s and s' and between metabolites m and m', respectively, and α and β are positive scalars.

We consider two sets of data informative about x: i) Presence-absence data obtained with mass-spectrometry and ii) presence-only reports of specific metabolites in specific specie. Let $\mathbf{d}_{sj} = (d_{sj1}, \dots, d_{sjM})$ be the presence-absence vector of each metabolite m obtained with mass-spectrometry run $j = 1, \dots, J_s$ performed on species s. Assuming a false-positive and false-negative error rates ϵ_{01} and ϵ_{10} , respectively, we have

$$\mathbb{P}(\boldsymbol{d}_{sj}|\boldsymbol{x},\epsilon_{01},\epsilon_{10}) = \prod_{m} \left[x_{sm} \left(\epsilon_{10}^{1-d_{sjm}} (1-\epsilon_{10})^{d_{sjm}} \right) + (1-x_{sm}) \left(\epsilon_{01}^{d_{sjm}} (1-\epsilon_{01})^{1-d_{sjm}} \right) \right].$$

To model the presence only data, it must be put in relation to the expected research effort. Let p_{sm} denote the known number of presence-only reports for metabolite m in species s and n_{sm} the unknown number of research projects that aimed at discovering metabolite m in species s. Assuming a false-positive and false-negative error rates π_{01} and π_{10} , respectively, we have

$$\mathbb{P}(p_{sm}|n_{sm},\pi_{01},\pi_{10}) =$$