Inferring the presence of metabolites

February 14, 2023

1 Idea and concept

We seek to infer the presence or absence of M metabolites in S species. We denote by x_{sm} whether metabolite $m = 1, \ldots, M$ is present ($x_{sm} = 1$) or absent ($x_{sm} = 0$) in species $s = 1, \ldots, S$. To infer the full vector $\boldsymbol{x} = (x_{11}, \ldots, x_{1M}, \ldots, x_{SM})$, 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

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

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 $\boldsymbol{x}$: i) Presence-absence data obtained with mass-spectrometry and ii) presence-only reports of specific metabolites in specific specie. Let $\boldsymbol{d}_{sj} = (d_{sj1}, \ldots, d_{sjM})$ be the presence-absence vector of each metabolite m obtained with mass-spectrometry run $j = 1, \ldots, J_s$ 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

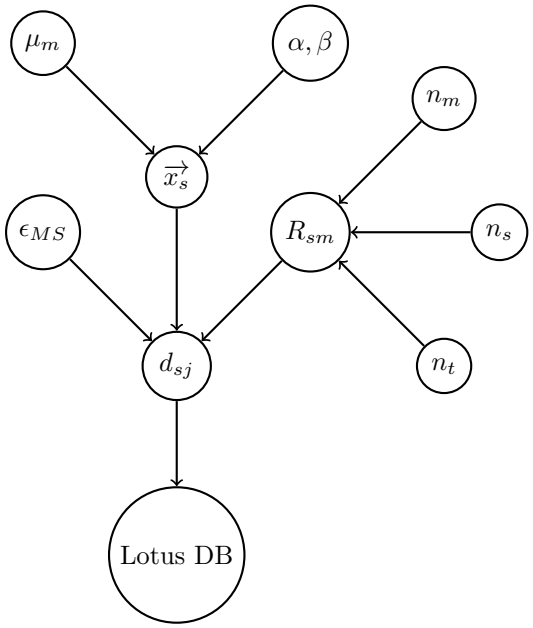
$$\mathbb{P}(p_{sm}|n_{sm}, \pi_{01}, \pi_{10}) =$$

We would have the covariance matrix such as :

$$\operatorname{cov}(\epsilon_{smt}, \epsilon_{s'm't'}) = \alpha\sigma^P_{ss'} + \beta\sigma^M_{mm'} + \gamma\sigma^E_{ss'} + \ldots \tag{1}$$

With P the phenotype between two species, E an environment factor between two species and M the TODO

2 DAG scratch



3 Ideas scratch

$$\begin{array}{c} \\ x_{sm}=0 \\ x_{sm}=1 \end{array} \begin{array}{c} \begin{array}{cc} L_{sm}=NA & L_{sm}=1 \end{array} \\ \begin{pmatrix} 1 & 0 \\ 1-R_{sm} & R_{sm} \end{pmatrix} \end{array}$$

With x_{sm} a molecule present or not present in a specific species. L_{sm} the presence or absence of a molecule in a species that is present or not in the Lotus database. Finally, R_{sm} the research effort made for that specific molecule. R_{sm} being a function of the number of papers made on a specific molecule or species : $f(n_s, n_m)$.