## <sup>1</sup> **Supplementary Methods**

## <sup>2</sup> **Classifiers**

<sup>3</sup> We implemented the following classifiers in the machine learning framework and compared their performance: (1)

<sup>4</sup> random forest; (2) logistic regression; (3) L1-regularized (LASSO) logistic regression; (4) L2-regularized (Ridge)

<sup>5</sup> logistic regression; (5) Elastic net regularized logistic regression. Random forest was implemented using the

<sup>6</sup> randomForest R package with 1000 trees. The hyperparameter 'mtry' (number of variables randomly sampled as <sup>7</sup> candidates at each split) was tuned using the caret R package with repeated cross-validation. Logistic regression

8 was implemented using the glm function in R. The regularized logistic regression models were implemented using

<sup>9</sup> the glmnet R package. The hyperparameter 'lambda' in the LASSO and Ridge models was tuned using the

<sup>10</sup> cv.glment function. The hyperparameters 'alpha' and 'lambda' were tuned using the caret R package with repeated

<sup>11</sup> cross-validation.

## <sup>12</sup> **Bayesian Approach**

Let  $G = 1$  if a genus is present (relative abundance  $> 0.001$ ) and 0 if absent,  $B = 1$  if a women has preterm birth (PTB) and 0 if term birth. We can have the conditional probability of PTB giving a genus is absent for dataset *i* to be

$$
p_i(B = 1 | G = 0) = p_i^0 = \frac{u_i}{1 + u_i}
$$

 $_{13}$  where  $u_i$  is the odds of PTB giving a genus is absent for dataset  $i$ .

Define *r* as the odds ratio between a genus is present and absent and it is the same for different datasets. Thus, the conditional probability of PTB giving a genus is present for dataset *i* can be written as

$$
p_i(B = 1|G = 1) = p_i^1 = \frac{u_i r}{1 + u_i r}
$$

<sup>14</sup> We assume both  $u_i$  and  $r$  have prior distributions,  $p(u_i)$  and  $p(r)$ , respectively. We are interested in calculating

 $_1$ s the posterior distribution of  $r$ . Given dataset  $i$ , let  $N_i$  is the total number of subjects in study  $i$ ,  $n_i$  is the number of

 $\cdot$  subjects that with certain genus present.  $M_i$  is the number of PTB subjects in study  $i$ ,  $m_i$  is the number of PTB

<sup>17</sup> subjects that with certain genus present. Thus, we can have the likelihood function

$$
p(N_i, n_i, M_i, m_i | u_i, r)
$$
  
=  $(p_i^0)^{M_i - m_i} (1 - p_i^0)^{(N_i - n_i) - (M_i - m_i)} (p_i^1)^{m_i} (1 - p_i^1)^{n_i - m_i}$   
=  $\frac{u_i^{M_i - m_i}}{(1 + u_i)^{N_i - n_i}} * \frac{(u_i r)^{m_i}}{(1 + u_i r)^{n_i}}$   
=  $\frac{u_i^{M_i} r^{m_i}}{(1 + u_i)^{N_i - n_i} (1 + u_i r)^{n_i}}$  (1)

## 18 Thus, the posterior distribution of  $u_i$  and  $r$  can be written as

$$
p(u_i, r | N_i, n_i, M_i, m_i) = \frac{p(N_i, n_i, M_i, m_i | u_i, r) p(u_i, r)}{p(N_i, n_i, M_i, m_i)} = \frac{p(N_i, n_i, M_i, m_i | u_i, r) p(u_i) p(r)}{\int_{u_i} \int_{r} p(N_i, n_i, M_i, m_i | u_i, r) p(u_i) p(r)}
$$
\n(2)

<sup>19</sup> Furthermore, we can integrate out  $u_i$  and obtain the posterior distribution for odds ratio  $r$ ,

$$
p(r|N_i, n_i, M_i, m_i) = \int_{u_i} p(u_i, r|N_i, n_i, M_i, m_i)
$$
  
= 
$$
\frac{p(r) \int_{u_i} p(N_i, n_i, M_i, m_i|u_i, r) p(u_i)}{\int_{u_i} \int_r p(N_i, n_i, M_i, m_i|u_i, r) p(u_i) p(r)}
$$
 (3)

<sup>20</sup> We assume the  $log(u_i)$  follows a uniform prior distribution for each dataset. For  $r$ , we let the first dataset has the  $21$  uniform prior distribution, then calculate the posterior distribution of  $r$ . Next we let the posterior distribution of the

<sub>22</sub> odds ratio from the first dataset be the prior distribution for the second dataset, and update the posterior distribution

<sup>23</sup> of *r*. Repeated the process until the last dataset and obtain the final posterior distribution of *r*.