

Supplementary material

We present the Table S1, S2 and S3 as supplementary material.

Table S1: Potential scale reduction factor (labelled psrf) and their upper 95% confidence limits (labelled upper C.I.) of all the estimated parameter a_{ij} .

Female's families			Female's genus						Male		
a_{ij}	psrf	Upper C.I.	a_{ij}	psrf	Upper C.I.	a_{ij}	psrf	Upper C.I.	Parameters	psrf	Upper C.I.
$a_{1,1}$	1,0011	1,0053	$a_{1,1}$	1	1	$a_{1,4}$	1	1,0001	$a_{1,1}$	1,0007	1,0016
$a_{2,1}$	1,0019	1,0086	$a_{2,1}$	1	1,0002	$a_{2,4}$	1	1	$a_{2,1}$	1,0001	1,0005
$a_{3,1}$	1,0004	1,0023	$a_{3,1}$	1	1,0004	$a_{3,4}$	1	1	$a_{3,1}$	1,0001	1,0002
$a_{4,1}$	1	1	$a_{4,1}$	1,0002	1,0002	$a_{4,4}$	1	1,0001	$a_{4,1}$	1,0004	1,001
$a_{5,1}$	1,0011	1,0054	$a_{5,1}$	1	1	$a_{5,4}$	1	1	$a_{5,1}$	1,0006	1,0009
$a_{6,1}$	1,0001	1,0004	$a_{6,1}$	1,0002	1,0002	$a_{6,4}$	1	1	$a_{6,1}$	1,0001	1,0007
$a_{7,1}$	1,0007	1,0035	$a_{7,1}$	1,0003	1,0011	$a_{7,4}$	1	1,0002	$a_{7,1}$	1	1
$a_{8,1}$	1,0005	1,0025	$a_{8,1}$	1,0003	1,0017	$a_{8,4}$	1,0005	1,0014	$a_{8,1}$	1,0001	1,0005
$a_{9,1}$	1,0019	1,0093	$a_{9,1}$	1	1,0001	$a_{9,4}$	1	1	$a_{9,1}$	1,0004	1,0022
$a_{1,2}$	1,003	1,0148	$a_{10,1}$	1,0005	1,0025	$a_{10,4}$	1,0005	1,0018	$a_{1,2}$	1	1,0002
$a_{2,2}$	1,0031	1,0155	$a_{11,1}$	1,0001	1,0001	$a_{11,4}$	1,0001	1,0001	$a_{2,2}$	1,0003	1,0013
$a_{3,2}$	1	1,001	$a_{12,1}$	1,0005	1,0008	$a_{12,4}$	1,0002	1,0006	$a_{3,2}$	1	1,0001
$a_{4,2}$	1,0004	1,0019	$a_{13,1}$	1,0002	1,001	$a_{13,4}$	1,0003	1,0014	$a_{4,2}$	1,0001	1,0005
$a_{5,2}$	1,0028	1,014	$a_{14,1}$	1,0002	1,0014	$a_{14,4}$	1,0001	1,0008	$a_{5,2}$	1,0002	1,0003
$a_{6,2}$	1,0017	1,0081	$a_{15,1}$	1,0003	1,0012	$a_{15,4}$	1,0002	1,0007	$a_{6,2}$	1,0001	1,0001
$a_{7,2}$	1,002	1,0089	$a_{16,1}$	1,0002	1,001	$a_{16,4}$	1	1	$a_{7,2}$	1	1,0001
$a_{8,2}$	1,0013	1,0065	$a_{17,1}$	1	1	$a_{17,4}$	1	1	$a_{8,2}$	1,0003	1,0006
$a_{9,2}$	1,0034	1,0169	$a_{18,1}$	1,0002	1,0003	$a_{18,4}$	1	1,0001	$a_{9,2}$	1,0001	1,0004
$a_{1,3}$	1,0001	1,0008	$a_{1,2}$	1	1,0001	$a_{1,5}$	1,0004	1,0005	$a_{1,3}$	1,0002	1,001
$a_{2,3}$	1,0009	1,004	$a_{2,2}$	1	1,0002	$a_{2,5}$	1,0001	1,0003	$a_{2,3}$	1,0001	1,0004
$a_{3,3}$	1,0009	1,0043	$a_{3,2}$	1	1,0001	$a_{3,5}$	1,0004	1,0019	$a_{3,3}$	1	1
$a_{4,3}$	1,0004	1,0009	$a_{4,2}$	1	1,0001	$a_{4,5}$	1,0001	1,0007	$a_{4,3}$	1,0002	1,0006
$a_{5,3}$	1,0004	1,0022	$a_{5,2}$	1,0001	1,0004	$a_{5,5}$	1,0002	1,0009	$a_{5,3}$	1	1
$a_{6,3}$	1,0001	1,0006	$a_{6,2}$	1,0001	1,0003	$a_{6,5}$	1,0002	1,0009	$a_{6,3}$	1,0002	1,0004
$a_{7,3}$	1,001	1,0044	$a_{7,2}$	1	1	$a_{7,5}$	1	1	$a_{7,3}$	1	1
$a_{8,3}$	1,0003	1,0016	$a_{8,2}$	1	1,0002	$a_{8,5}$	1,0002	1,0006	$a_{8,3}$	1,0002	1,0002
$a_{9,3}$	1,0011	1,0056	$a_{9,2}$	1	1,0002	$a_{9,5}$	1,0007	1,0031	$a_{9,3}$	1,0002	1,0005
$a_{1,4}$	1,0006	1,0031	$a_{10,2}$	1	1	$a_{10,5}$	1	1	$a_{1,4}$	1	1,0002
$a_{2,4}$	1,0003	1,0011	$a_{11,2}$	1	1	$a_{11,5}$	1,0002	1,0003	$a_{2,4}$	1	1
$a_{3,4}$	1,0004	1,0022	$a_{12,2}$	1	1	$a_{12,5}$	1,0003	1,0005	$a_{3,4}$	1	1
$a_{4,4}$	1,0001	1,0009	$a_{13,2}$	1	1	$a_{13,5}$	1,0002	1,0006	$a_{4,4}$	1,0006	1,0012
$a_{5,4}$	1,0001	1,0007	$a_{14,2}$	1,0001	1,0007	$a_{14,5}$	1	1	$a_{5,4}$	1,0014	1,002
$a_{6,4}$	1,0001	1,0003	$a_{15,2}$	1	1,0002	$a_{15,5}$	1	1,0004	$a_{6,4}$	1	1
$a_{7,4}$	1	1	$a_{16,2}$	1,0002	1,0011	$a_{16,5}$	1	1,0001	$a_{7,4}$	1,0001	1,0001
$a_{8,4}$	1,0002	1,0008	$a_{17,2}$	1,0001	1,0001	$a_{17,5}$	1,0001	1,0004	$a_{8,4}$	1,0001	1,0003
$a_{9,4}$	1,0001	1,0005	$a_{18,2}$	1,0002	1,0011	$a_{18,5}$	1	1	$a_{9,4}$	1,0002	1,0008
$a_{1,5}$	1	1	$a_{1,3}$	1,0001	1,0006	$a_{1,6}$	1,0002	1,0002	$a_{1,5}$	1	1
$a_{2,5}$	1,0002	1,0009	$a_{2,3}$	1	1	$a_{2,6}$	1	1,0002	$a_{2,5}$	1	1
$a_{3,5}$	1,0002	1,0007	$a_{3,3}$	1	1,0001	$a_{3,6}$	1,0001	1,0002	$a_{3,5}$	1	1,0001
$a_{4,5}$	1,0001	1,0007	$a_{4,3}$	1	1,0001	$a_{4,6}$	1,0001	1,0004	$a_{4,5}$	1,0002	1,0007
$a_{5,5}$	1,0004	1,0014	$a_{5,3}$	1,0001	1,0001	$a_{5,6}$	1	1	$a_{5,5}$	1,0002	1,0002
$a_{6,5}$	1	1,001	$a_{6,3}$	1,0004	1,0004	$a_{6,6}$	1	1,0001	$a_{6,5}$	1,0001	1,0001
$a_{7,5}$	1	1,004	$a_{7,3}$	1,0001	1,0007	$a_{7,6}$	1	1,0002	$a_{7,5}$	1,0001	1,0001
$a_{8,5}$	1	1	$a_{8,3}$	1	1	$a_{8,6}$	1,0001	1,0001	$a_{8,5}$	1,0001	1,0001
$a_{9,5}$	1,0001	1,0003	$a_{9,3}$	1	1,0001	$a_{9,6}$	1	1	$a_{9,5}$	1	1,0003
$a_{1,6}$	1,0006	1,0007	$a_{10,3}$	1,0004	1,001	$a_{10,6}$	1	1			
$a_{2,6}$	1,0013	1,0022	$a_{11,3}$	1	1	$a_{11,6}$	1,0002	1,001			
$a_{3,6}$	1	1,001	$a_{12,3}$	1,0003	1,0003	$a_{12,6}$	1	1			
$a_{4,6}$	1	1	$a_{13,3}$	1	1	$a_{13,6}$	1,0001	1,0002			
$a_{5,6}$	1,0008	1,001	$a_{14,3}$	1	1,0001	$a_{14,6}$	1	1			
$a_{6,6}$	1	1,002	$a_{15,3}$	1	1	$a_{15,6}$	1,0001	1,0002			
$a_{7,6}$	1,0002	1,0011	$a_{16,3}$	1,0004	1,0017	$a_{16,6}$	1	1			
$a_{8,6}$	1,0002	1,0007	$a_{17,3}$	1	2 1	$a_{17,6}$	1	1,0002			
$a_{9,6}$	1,0011	1,0033	$a_{18,3}$	1	1,0001	$a_{18,6}$	1	1			

Table S2: Estimated parameters (a_{ij}) and credible interval obtained applying the Proposed Model to the female dataset at genus taxonomic level. The table also contains the percentage of influence that each SPBal $_j$ has on each genus and, in bold, it is represented the percentage of sway that each genus has on the bacterial community

Genus taxonomic level						
a_{ij}	Intercept	SPBal $_1$	SPBal $_2$	SPBal $_3$	SPBal $_4$	SPBal $_5$
o_Bacteroidales; f.; g-	0,7498 (-0,35 , 1,94) 7,26 %	-0,0632 (-0,15 , 0,01) 15,29 %	0,0378 (-0,16 , 0,26) 9,14 %	-0,1482 (-0,36 , 0,06) 35,84 %	0,0464 (-0,15 , 0,25) 11,21 %	0,1180 (-0,17 , 0,39) 28,53 %
Other	1,7632 (0,87 , 2,60) 17,08 %	-0,0382 (-0,10 , 0,02) 4,99 %	-0,1557 (-0,34 , 0,03) 20,37 %	-0,0768 (-0,28 , 0,10) 10,05 %	0,0069 (-0,15 , 0,16) 0,90 %	-0,4869 (-0,84 , -0,15) 63,70 %
o_Clostridiales; f.; g-	-0,0878 (-1,46 , 1,23) 0,85 %	-0,0072 (-0,13 , 0,11) 3,03 %	-0,0567 (-0,36 , 0,23) 23,90 %	0,0430 (-0,21 , 0,32) 18,12 %	0,0735 (-0,23 , 0,40) 30,98 %	-0,0568 (-0,41 , 0,23) 23,97 %
f_Lachnospiraceae; g-	0,0287 (-1,26 , 1,22) 0,28 %	-0,0225 (-0,12 , 0,07) 3,77 %	-0,1609 (-0,41 , 0,06) 26,96 %	-0,2148 (-0,46 , 0,02) 35,98 %	0,0235 (-0,23 , 0,28) 3,94 %	-0,1752 (-0,54 , 0,10) 29,35 %
g_Blautia	-0,0348 (-1,29 , 1,05) 0,34 %	-0,0526 (-0,17 , 0,05) 14,36 %	0,0286 (-0,22 , 0,29) 7,81 %	-0,0465 (-0,28 , 0,17) 12,69 %	0,1385 (-0,12 , 0,42) 37,80 %	-0,1002 (-0,44 , 0,16) 27,34 %
g_Clostridium	-0,0078 (-1,18 , 1,08) 0,08 %	-0,0837 (-0,18 , 0,00) 14,69 %	-0,0653 (-0,29 , 0,14) 11,45 %	-0,2156 (-0,44 , 0,01) 37,85 %	0,0377 (-0,18 , 0,26) 6,62 %	-0,1674 (-0,51 , 0,09) 29,39 %
g_Coproccoccus	-0,0826 (-1,42 , 1,14) 0,80 %	-0,0301 (-0,15 , 0,08) 11,16 %	0,0330 (-0,22 , 0,30) 12,24 %	0,0169 (-0,21 , 0,25) 6,28 %	0,0920 (-0,19 , 0,39) 34,12 %	-0,0976 (-0,43 , 0,15) 36,20 %
g_Dorea	-0,9311 (-2,72 , 0,42) 9,02 %	-0,0274 (-0,16 , 0,09) 14,71 %	-0,0351 (-0,35 , 0,27) 18,85 %	0,0107 (-0,31 , 0,29) 5,72 %	0,0519 (-0,27 , 0,38) 27,91 %	-0,0610 (-0,43 , 0,24) 32,80 %
g_Eubacterium	-0,6798 (-2,46 , 0,59) 6,59 %	-0,0422 (-0,17 , 0,07) 33,00 %	0,0028 (-0,30 , 0,30) 2,18 %	-0,0250 (-0,33 , 0,24) 19,51 %	0,0546 (-0,25 , 0,37) 42,71 %	0,0033 (-0,35 , 0,31) 2,59 %
g_Roseburia	0,3644 (-0,68 , 1,52) 3,53 %	-0,0362 (-0,13 , 0,05) 7,46 %	0,1517 (-0,07 , 0,41) 31,24 %	-0,0199 (-0,22 , 0,19) 4,11 %	0,0980 (-0,13 , 0,35) 20,17 %	-0,1798 (-0,46 , 0,05) 37,02 %
g_Ruminococcus	-0,5185 (-2,10 , 0,65) 5,02 %	-0,0510 (-0,18 , 0,07) 13,93 %	0,0760 (-0,22 , 0,40) 20,79 %	0,0019 (-0,29 , 0,26) 0,52 %	0,2103 (-0,11 , 0,56) 57,49 %	-0,0266 (-0,38 , 0,26) 7,26 %
f_Ruminococcaceae; g-	0,2119 (-0,94 , 1,47) 2,05 %	-0,0342 (-0,14 , 0,06) 14,74 %	-0,0091 (-0,26 , 0,24) 3,93 %	0,0123 (-0,20 , 0,24) 5,29 %	0,0387 (-0,21 , 0,30) 16,69 %	-0,1376 (-0,47 , 0,11) 59,35 %
g_Clostridium	-0,3507 (-1,96 , 1,05) 3,40 %	-0,0232 (-0,15 , 0,09) 7,45 %	0,0616 (-0,22 , 0,37) 19,81 %	0,1107 (-0,16 , 0,40) 35,61 %	0,0431 (-0,26 , 0,35) 13,86 %	-0,0724 (-0,45 , 0,22) 23,27 %
g_Phascolarctobacterium	0,2522 (-0,83 , 1,36) 2,44 %	-0,0852 (-0,17 , 0,00) 14,76 %	0,0527 (-0,15 , 0,27) 9,13 %	-0,0917 (-0,31 , 0,12) 15,89 %	0,0478 (-0,16 , 0,27) 8,29 %	-0,2997 (-0,63 , -0,01) 51,93 %
g_Desulfovibrio	-0,1352 (-1,48 , 1,04) 1,31 %	-0,0303 (-0,15 , 0,07) 10,44 %	0,0804 (-0,18 , 0,37) 27,70 %	0,0047 (-0,24 , 0,25) 1,62 %	0,1415 (-0,13 , 0,44) 48,76 %	-0,0333 (-0,38 , 0,25) 11,48 %
g_Clostridium	-0,5888 (-2,34 , 0,69) 5,70 %	-0,0034 (-0,13 , 0,12) 0,87 %	-0,2154 (-0,56 , 0,10) 55,62 %	-0,0306 (-0,34 , 0,24) 7,90 %	0,0554 (-0,28 , 0,41) 14,31 %	-0,0825 (-0,48 , 0,23) 21,29 %
g_Akkermansia	0,4689 (-0,43 , 1,49) 4,54 %	-0,7168 (-0,86 , -0,58) 32,70 %	0,3378 (0,19 , 0,49) 15,41 %	-0,1117 (-0,30 , 0,07) 5,10 %	0,8178 (0,67 , 0,97) 37,31 %	0,2079 (-0,03 , 0,43) 9,49 %
g_Bacteroides	3,0652 (2,30 , 3,81) 29,70 %	-0,0890 (-0,15 , -0,03) 20,70 %	0,0608 (-0,08 , 0,22) 14,14 %	-0,0689 (-0,23 , 0,06) 16,02 %	-0,0028 (-0,13 , 0,13) 0,64 %	-0,2084 (-0,44 , 0,01) 48,49 %

Table S3: Estimated parameters (a_{ij}) and credible interval obtained applying the Proposed Model to the Male dataset. The table also contains the percentage of influence that each SPBal $_j$ has on each family and, in bold, it is represented the percentage of influence that each family has on the bacterial community

Family taxonomic level					
a_{ij}	Intercept	SPBal $_1$	SPBal $_2$	SPBal $_3$	SPBal $_4$
f_Alcaligenaceae	0,1563 (-2,21 , 2,28) 2,15 %	0,1563 (-0,36 , 0,98) 12,87 %	-0,3031 (-1,07 , 0,30) 24,95 %	-0,5221 (-1,37 , 0,22) 42,98 %	0,2332 (-0,94 , 1,57) 19,20 %
f_Bacteroidaceae	0,8131 (-1,32 , 3,20) 11,20 %	0,8131 (-0,78 , 0,45) 32,49 %	-0,2503 (-0,97 , 0,29) 10,00 %	-0,8869 (-1,72 , 0,00) 35,44 %	0,5522 (-0,40 , 1,76) 22,07 %
f_Lachnospiraceae	1,0084 (-1,11 , 3,44) 13,89 %	1,0084 (-0,42 , 0,90) 44,65 %	-0,0450 (-0,78 , 0,62) 1,99 %	-0,2582 (-1,05 , 0,56) 11,43 %	-0,9467 (-2,51 , 0,33) 41,92 %
f_Porphyrimonadaceae	0,3775 (-2,09 , 2,75) 5,20 %	0,3775 (-0,76 , 0,63) 36,48 %	-0,1091 (-0,90 , 0,58) 10,55 %	-0,4222 (-1,29 , 0,37) 40,80 %	0,1260 (-1,25 , 1,57) 12,18 %
Other	0,4171 (-2,03 , 2,87) 5,74 %	0,4171 (-0,62 , 0,88) 40,41 %	0,0209 (-0,74 , 0,78) 2,03 %	-0,3362 (-1,20 , 0,46) 32,57 %	-0,2579 (-1,93 , 1,15) 24,99 %
f_Rikenellaceae	0,1962 (-2,50 , 2,71) 2,70 %	0,1962 (-0,79 , 0,86) 26,58 %	-0,0332 (-0,87 , 0,78) 4,49 %	-0,2370 (-1,18 , 0,62) 32,13 %	0,2715 (-1,41 , 2,09) 36,80 %
f_Ruminococcaceae	0,8821 (-1,21 , 3,15) 12,15 %	0,8821 (-0,58 , 0,68) 51,91 %	-0,1941 (-0,95 , 0,42) 11,42 %	-0,3469 (-1,11 , 0,41) 20,42 %	-0,2760 (-1,65 , 0,97) 16,25 %
f_Veillonellaceae	0,2825 (-2,04 , 2,43) 3,89 %	0,2825 (-0,21 , 1,20) 31,10 %	-0,2180 (-0,98 , 0,42) 24,00 %	-0,2962 (-1,09 , 0,41) 32,61 %	0,1116 (-1,28 , 1,53) 12,28 %
f_Prevotellaceae	3,1272 (1,50 , 4,70) 43,07 %	3,1272 (-0,13 , 0,93) 67,13 %	-0,4606 (-1,13 , 0,03) 9,89 %	-0,4815 (-1,10 , 0,07) 10,34 %	0,5891 (-0,21 , 1,59) 12,65 %