

5.2b SES and Microbiome - twin discordance

LESS STRINGENT

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Paired discordance of OTUs using EdgeR

Education

```
## Coefficient: DiscordanceLDep
##          Kingdom      Phylum           Class
## denovo604 k_Bacteria p_Firmicutes c_Clostridia
## denovo495 k_Bacteria p_Firmicutes c_Clostridia
## denovo88  k_Bacteria p_Firmicutes c_Clostridia
## denovo165  k_Bacteria p_Firmicutes c_Clostridia
## denovo8   k_Bacteria p_Bacteroidetes c_Bacteroidia
## denovo76  k_Bacteria p_Firmicutes c_Clostridia
## denovo111 k_Bacteria p_Firmicutes c_Clostridia
## denovo173 k_Bacteria p_Tenericutes c_Mollicutes
## denovo4   k_Bacteria p_Proteobacteria c_Gammaproteobacteria
## denovo40  k_Bacteria p_Bacteroidetes c_Bacteroidia
##          Order       Family           Genus
## denovo604 o_Clostridiales f__ g__
## denovo495 o_Clostridiales f_Lachnospiraceae g__
## denovo88  o_Clostridiales f_Ruminococcaceae g__
## denovo165 o_Clostridiales f_Lachnospiraceae g__
## denovo8   o_Bacteroidales f_Prevotellaceae g_Prevotella
## denovo76  o_Clostridiales f_Ruminococcaceae g__
## denovo111 o_Clostridiales f_Ruminococcaceae g_Ruminococcus
## denovo173 o_RF39        f__ g__
## denovo4   o_Enterobacteriales f_Enterobacteriaceae g__
## denovo40  o_Bacteroidales f_Bacteroidaceae g_Bacteroides
##          Species    logFC   logCPM      LR     PValue      FDR
## denovo604 s__ 1.0889136 10.79897 12.828708 0.0003413414 0.01945646
## denovo495 s__ -0.9943345 10.88653 9.477717 0.0020798264 0.05927505
## denovo88  s__ -0.7623931 14.89692 3.543339 0.0597850054 0.90585455
## denovo165 s__ -0.5560401 12.80012 3.441739 0.0635687404 0.90585455
## denovo8   s_copri 0.8544375 18.74675 1.715070 0.1903288677 0.97914438
## denovo76  s__ 0.7142574 14.88601 1.602759 0.2055126174 0.97914438
## denovo111 s__ -0.4716200 13.97125 1.345434 0.2460779338 0.97914438
## denovo173 s__ 0.5744391 11.68180 1.305799 0.2531567358 0.97914438
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## denovo4      s__ 0.7545204 18.61378 1.208533 0.2716228045 0.97914438
## denovo40     s__ 0.5171439 14.99081 1.173106 0.2787638763 0.97914438

```

Income

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## Coefficient: DiscordanceLDep
##          Kingdom           Phylum           Class
## denovo400 k_Bacteria p_Firmicutes c_Erysipelotrichi
## denovo2   k_Bacteria p_Verrucomicrobia c_Verrucomicrobiae
## denovo77  k_Bacteria p_Bacteroidetes c_Bacteroidia
## denovo1750 k_Bacteria p_Firmicutes c_Clostridia
## denovo469  k_Bacteria p_Firmicutes c_Clostridia
## denovo165  k_Bacteria p_Firmicutes c_Clostridia
## denovo495  k_Bacteria p_Firmicutes c_Clostridia
## denovo22   k_Bacteria p_Actinobacteria c_Actinobacteria
## denovo99   k_Bacteria p_Firmicutes c_Clostridia
## denovo60   k_Bacteria p_Firmicutes c_Bacilli
##          Order            Family
## denovo400 o_Erysipelotrichales f_Erysipelotrichaceae
## denovo2   o_Verrucomicrobiales f_Verrucomicrobiaceae
## denovo77  o_Bacteroidales f_Prevotellaceae
## denovo1750 o_Clostridiales f_Lachnospiraceae
## denovo469  o_Clostridiales f_Ruminococcaceae
## denovo165  o_Clostridiales f_Lachnospiraceae
## denovo495  o_Clostridiales f_Lachnospiraceae
## denovo22   o_Bifidobacteriales f_Bifidobacteriaceae
## denovo99   o_Clostridiales f_Veillonellaceae
## denovo60   o_Lactobacillales f_Streptococcaceae
##          Genus            Species       logFC  logCPM
## denovo400 g_Coprobacillus          s__ 0.61071044 11.92574
## denovo2   g_Akkermansia s_muciniphila -0.98232046 20.33570
## denovo77  g_Prevotella          s__ 0.68584996 14.83980
## denovo1750 g_[Ruminococcus]    s_gnavus -0.44213558 10.86009
## denovo469 g_Faecalibacterium  s_prausnitzii 0.64753237 14.46680
## denovo165  g_                 s__ 0.36110820 14.79665
## denovo495  g_                 s__ -0.35576261 12.59660
## denovo22   g_Bifidobacterium s_adolescentis 0.21246331 18.39142
## denovo99   g_Acidaminococcus          s__ -0.14984141 15.61010
## denovo60   g_Streptococcus          s__ 0.03127444 15.41680
##          LR     PValue      FDR
## denovo400 2.898575401 0.08865787 0.4918161
## denovo2   2.214951718 0.13667934 0.4918161
## denovo77  2.097451911 0.14754484 0.4918161
## denovo1750 1.479406450 0.22386741 0.5497926

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## denovo469 1.192150139 0.27489628 0.5497926
## denovo165 0.823180827 0.36425181 0.5886087
## denovo495 0.672946809 0.41202610 0.5886087
## denovo22 0.135267296 0.71303204 0.8912901
## denovo99 0.055049374 0.81449900 0.9049989
## denovo60 0.006319754 0.93663742 0.9366374

```

IMD

```

## Coefficient: DiscordanceLDep
##                 Kingdom          Phylum          Class          Order
## denovo221 k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales
## denovo114 k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales
## denovo106 k__Bacteria     p__Firmicutes  c__Clostridia o__Clostridiales
## denovo281 k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales
## denovo91  k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales
## denovo268 k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales
## denovo958 k__Bacteria     p__Firmicutes  c__Clostridia o__Clostridiales
## denovo110 k__Bacteria     p__Firmicutes  c__Clostridia o__Clostridiales
## denovo254 k__Bacteria     p__Firmicutes  c__Clostridia o__Clostridiales
## denovo170 k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales
##                         Family          Genus          Species
## denovo221      f__Prevellaceae   g__Prevotella      s__
## denovo114      f__Bacteroidaceae g__Bacteroides s__coprophilus
## denovo106      f__Ruminococcaceae g__Ruminococcus s__
## denovo281      f__Bacteroidaceae g__Bacteroides s__
## denovo91       f__Porphyromonadaceae g__Parabacteroides s__distasonis
## denovo268      f__Rikenellaceae   g__           s__
## denovo958      f__           g__           s__
## denovo110      f__Ruminococcaceae g__           s__
## denovo254      f__           g__           s__
## denovo170      f__S24-7         g__           s__
##                 logFC    logCPM      LR      PValue      FDR
## denovo221 0.24766861 17.18822 1.2798284 0.2579309 0.9905029
## denovo114 -0.21934290 16.67888 1.0259492 0.3111120 0.9905029
## denovo106 0.21715616 16.01884 0.8628232 0.3529498 0.9905029
## denovo281 -0.17368079 16.36366 0.7054190 0.4009688 0.9905029
## denovo91 0.20900336 19.64047 0.4923223 0.4828932 0.9905029
## denovo268 0.16098626 16.59451 0.4821968 0.4874289 0.9905029
## denovo958 0.10506717 14.22086 0.2692871 0.6038104 0.9905029
## denovo110 0.15817742 17.94678 0.2309763 0.6308009 0.9905029
## denovo254 -0.10783170 15.25765 0.2270809 0.6336968 0.9905029
## denovo170 0.08645575 15.40426 0.1956921 0.6582207 0.9905029

```

Packages used

```
citation("edgeR")  
  
##  
## See Section 1.2 in the User's Guide for more detail about how to  
## cite the different edgeR pipelines.  
##  
## Robinson MD, McCarthy DJ and Smyth GK (2010). edgeR: a  
## Bioconductor package for differential expression analysis of  
## digital gene expression data. Bioinformatics 26, 139-140  
##  
## McCarthy DJ, Chen Y and Smyth GK (2012). Differential expression  
## analysis of multifactor RNA-Seq experiments with respect to  
## biological variation. Nucleic Acids Research 40, 4288-4297  
##  
## To see these entries in BibTeX format, use 'print(<citation>,  
## bibtex=TRUE)', 'toBibtex(.)', or set  
## 'options(citation.bibtex.max=999)'.  
  
citation("phyloseq")  
  
##  
## To cite phyloseq in publications, or otherwise credit, please use:  
##  
## phyloseq: An R package for reproducible interactive analysis and  
## graphics of microbiome census data. Paul J. McMurdie and Susan  
## Holmes (2013) PLoS ONE 8(4):e61217.  
##  
## A BibTeX entry for LaTeX users is  
##  
## @Article{,  
##   author = {Paul J. McMurdie and Susan Holmes},  
##   journal = {PLoS ONE},  
##   pages = {e61217},  
##   title = {phyloseq: An R package for reproducible interactive analysis and graphics of m},  
##   volume = {8},  
##   number = {4},  
##   year = {2013},  
##   url = {http://dx.plos.org/10.1371/journal.pone.0061217},  
## }  
  
citation("ape")  
  
##
```

```

## To cite ape in a publication use:
##
## Paradis E. & Schliep K. 2018. ape 5.0: an environment for modern
## phylogenetics and evolutionary analyses in R. Bioinformatics xx:
## xxx-xxx.
##
## A BibTeX entry for LaTeX users is
##
## @Article{,
##   title = {ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R},
##   author = {E. Paradis and K. Schliep},
##   journal = {Bioinformatics},
##   year = {2018},
##   volume = {xx},
##   pages = {xxx-xxx},
## }
##
## As ape is evolving quickly, you may want to cite also its version
## number (found with 'library(help = ape)' or
## 'packageVersion("ape")').
citation("data.table")

##
## To cite package 'data.table' in publications use:
##
## Matt Dowle and Arun Srinivasan (2018). data.table: Extension of
## `data.frame`. R package version 1.11.8.
## https://CRAN.R-project.org/package=data.table
##
## A BibTeX entry for LaTeX users is
##
## @Manual{,
##   title = {data.table: Extension of `data.frame`},
##   author = {Matt Dowle and Arun Srinivasan},
##   year = {2018},
##   note = {R package version 1.11.8},
##   url = {https://CRAN.R-project.org/package=data.table},
## }
citation("knitr")

##
## To cite the 'knitr' package in publications use:
##
## Yihui Xie (2018). knitr: A General-Purpose Package for Dynamic

```

```

## Report Generation in R. R package version 1.20.
##
## Yihui Xie (2015) Dynamic Documents with R and knitr. 2nd
## edition. Chapman and Hall/CRC. ISBN 978-1498716963
##
## Yihui Xie (2014) knitr: A Comprehensive Tool for Reproducible
## Research in R. In Victoria Stodden, Friedrich Leisch and Roger
## D. Peng, editors, Implementing Reproducible Computational
## Research. Chapman and Hall/CRC. ISBN 978-1466561595
##
## To see these entries in BibTeX format, use 'print(<citation>,
## bibtex=TRUE)', 'toBibtex(.)', or set
## 'options(citation.bibtex.max=999)'.

citation("rmarkdown")

##
## To cite package 'rmarkdown' in publications use:
##
## JJ Allaire, Yihui Xie, Jonathan McPherson, Javier Luraschi,
## Kevin Ushey, Aron Atkins, Hadley Wickham, Joe Cheng and Winston
## Chang (2018). rmarkdown: Dynamic Documents for R. R package
## version 1.10. https://CRAN.R-project.org/package=rmarkdown
##
## A BibTeX entry for LaTeX users is
##
## @Manual{,
##   title = {rmarkdown: Dynamic Documents for R},
##   author = {JJ Allaire and Yihui Xie and Jonathan McPherson and Javier Luraschi and Kevin
##             Chang},
##   year = {2018},
##   note = {R package version 1.10},
##   url = {https://CRAN.R-project.org/package=rmarkdown},
## }
citation("base")

##
## To cite R in publications use:
##
## R Core Team (2018). R: A language and environment for
## statistical computing. R Foundation for Statistical Computing,
## Vienna, Austria. URL https://www.R-project.org/.
##
## A BibTeX entry for LaTeX users is
##
## @Manual{,
```

```
##   title = {R: A Language and Environment for Statistical Computing},
##   author = {{R Core Team}},
##   organization = {R Foundation for Statistical Computing},
##   address = {Vienna, Austria},
##   year = {2018},
##   url = {https://www.R-project.org/},
## }
##
## We have invested a lot of time and effort in creating R, please
## cite it when using it for data analysis. See also
## 'citation("pkgname")' for citing R packages.
```