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Ramirez, KS, Knight, CG, de Hollander, M, Brearley, FQ, Constantinides, B, Cotton, A, Creer, S, Crowther, TW, Davison, J, Delgado-Baquerizo, M, Dorrepaal, E, Elliott, DR, Fox, G, Griffiths, RI, Hale, C, Hartman, K, Houlden, A, Jones, DL, Krab, EJ, Maestre, FT, McGuire, KL, Monteux, S, Orr, CH, van der Putten, WH, Roberts, IS, Robinson, DA, Rocca, JD, Rowntree, J, Schlaeppi, K, Shepherd, M, Singh, BK, Straathof, AL, Bhatnagar, JM, Thion, C, van der Heijden, MGA and de Vries, FT (2018) Detecting macroecological patterns in bacterial communities across independent studies of global soils. Nature Microbiology, 3 (2). pp. 189-196. ISSN 2058-5276

DOI: https://doi.org/10.1038/s41564-017-0062-x

Publisher: Nature Publishing Group

Version: Supplemental Material

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Supplementary Information Guide

Detecting macroecological patterns in bacterial communities across independent studies of global soils

1. Supplementary Tables and Figures (Ramirez_etal_SupplementaryInfo.docx) (790KB)
2. Summary Datasets: Description of all datasets used - summary_datsets.csv (475KF)
3. Figure generation code: R code to generate figures – Ramirez_etal_final.R (12KB)
4. Figure generation data: Data used to generate figures – Ramirez_etal_data.csv (2MB)
5. 'Sequence-matched' sequence merging (De Hollander 2016): Script to combine subset of datasets using sequence data - https://gitlab.bioinf.nioo.knaw.nl/amplicon-metagenomics/meta-16S
6. Name-Based merged OTU table: (Rameriz_etal_NameMatched.csv.zip) (6.7MB)
7. Sequence-Based merged OTU table: (Rameriz_etal_SeqMatched.csv.zip) (12MB)