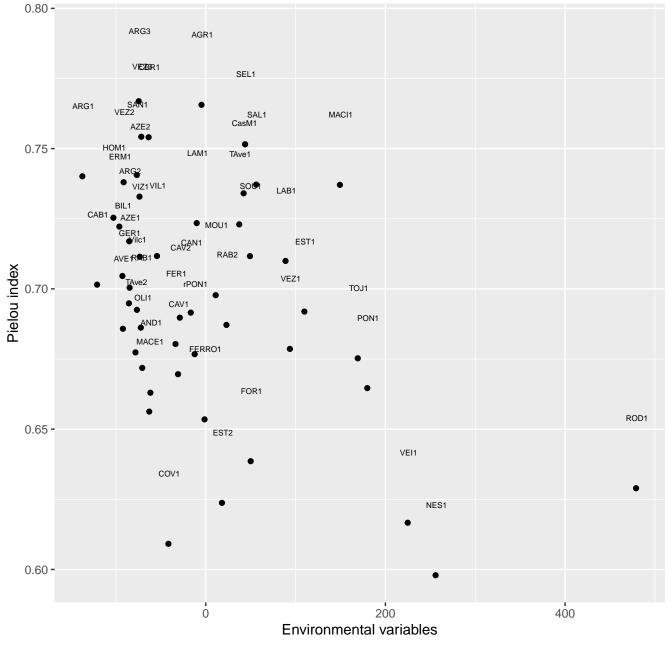
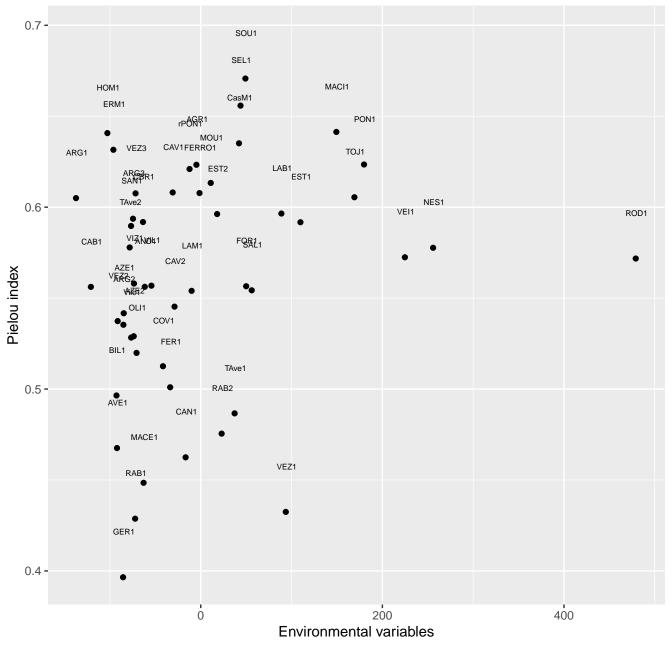
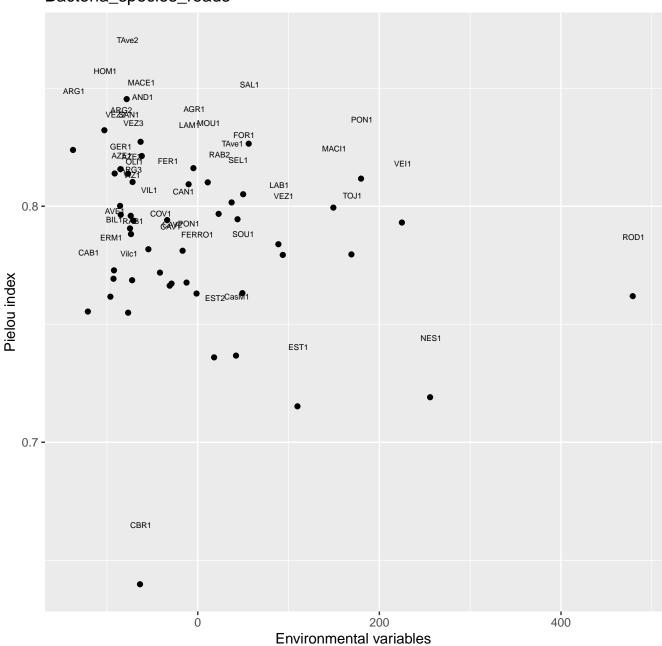
Bacteria_genus_reads



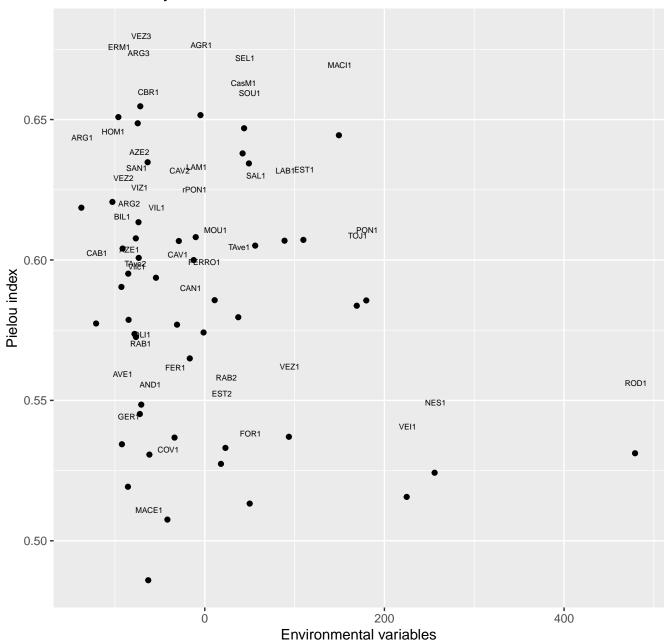
Bacteria_order_reads



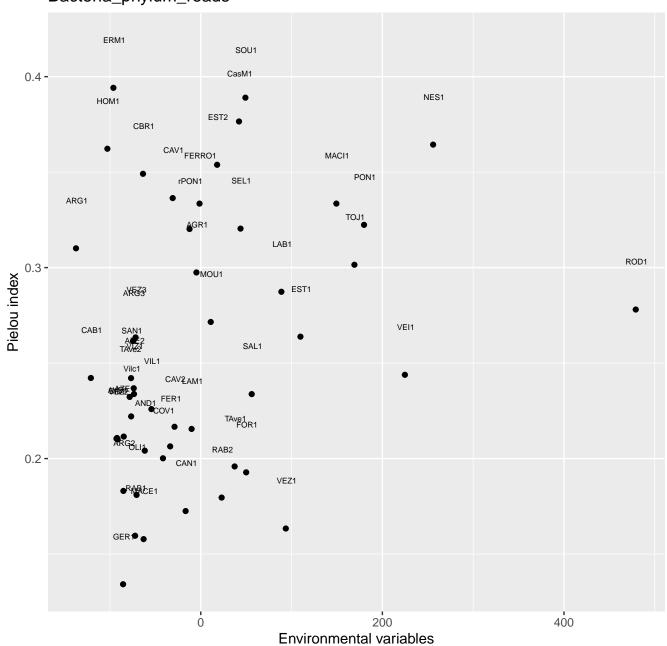
Bacteria_species_reads



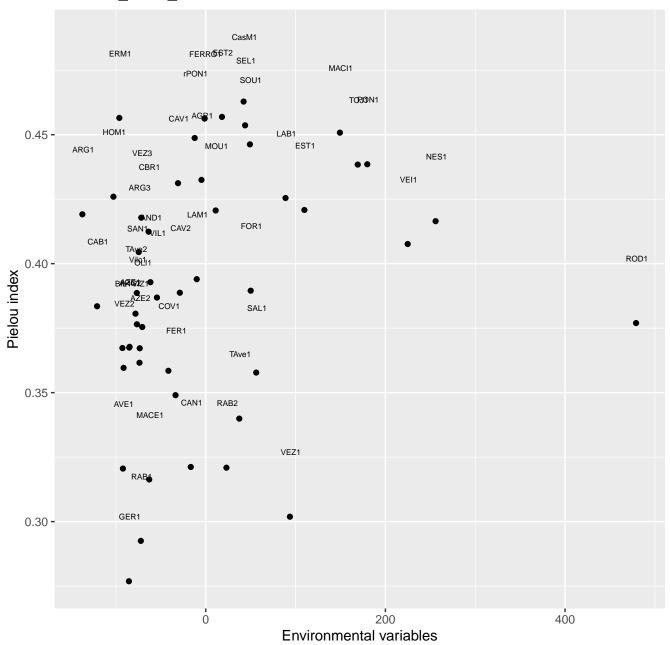
Bacteria_family_reads



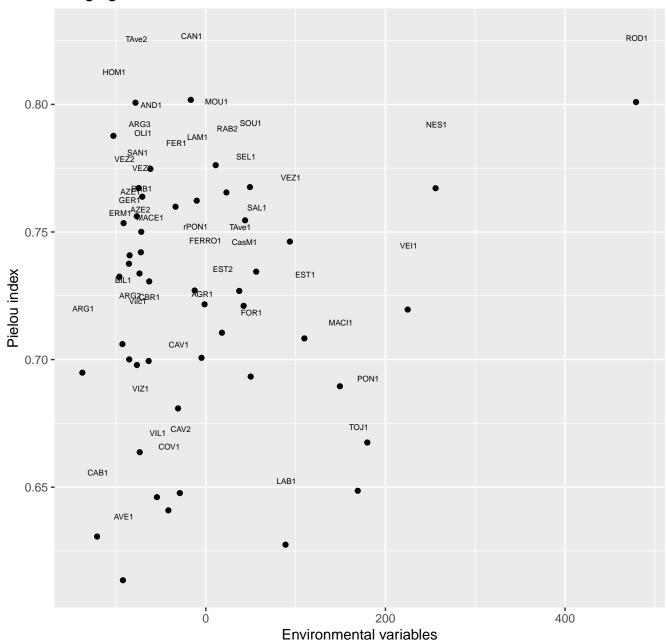
Bacteria_phylum_reads



Bacteria_class_reads



Fungi_genus_reads

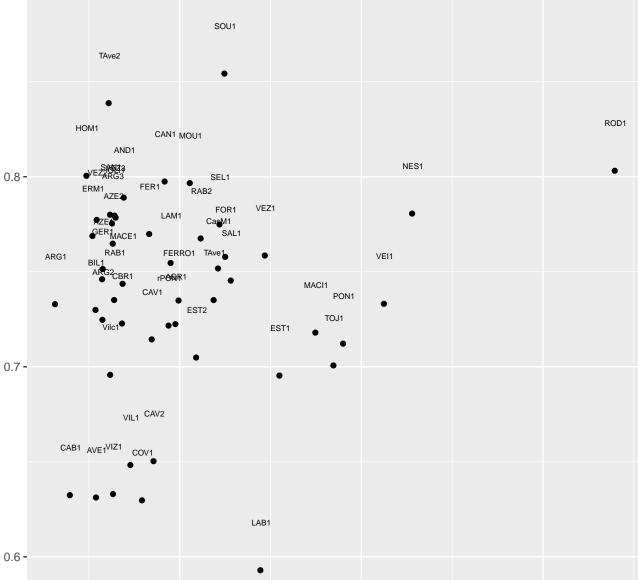


Fungi_order_reads ROD1 0.8 -VEI1 VIZ1 0.7 -ERMTAVE21 RAB2 SOU1 PON1 Pielou index MANGE1 HOM1 MACITOJ1 ARG1 SAL1 0.6 -CÆ1FERRŒ6T2 FOR1 CasM1 SAN1 NES1 CAB1 0.5 -VIL1 SEL1 ARYGIZ1 CBR1 AGR1

0.4 ö 200 400 Environmental variables

Fungi_species_reads TAve2

Pielou index



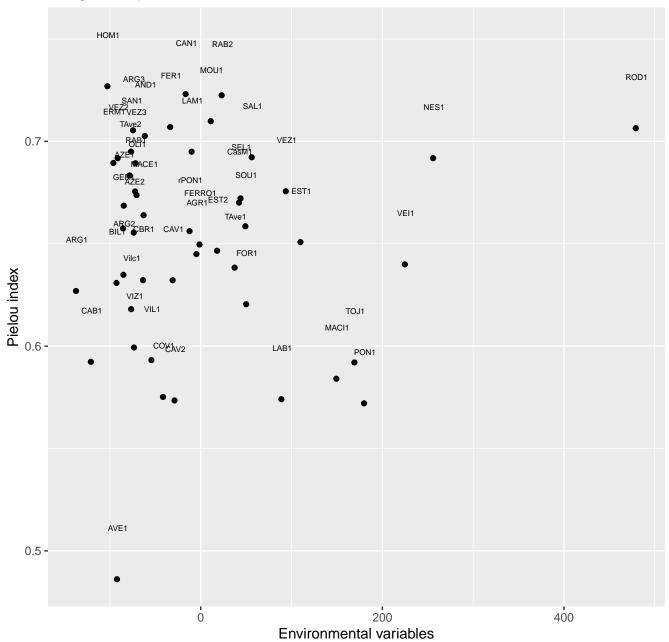
200

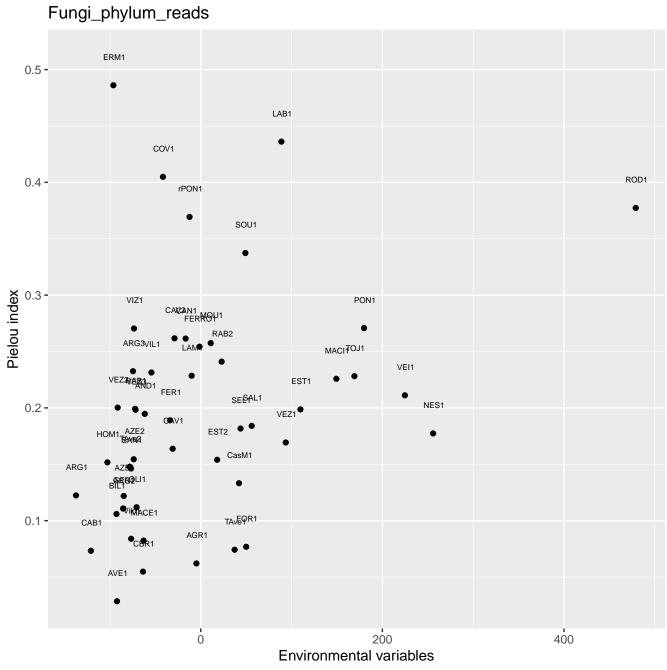
Environmental variables

0

400

Fungi_family_reads





Fungi_class_reads

