

JOB : tex_test_mix_sp_read_0
READ ID : Streptococcus

2022-06-03

Abstract

Sample has been splitted in 500 distinct lectures over 20220 sequenced nucleotides.

Explored hypothesis are all above 10 percent of attributed reads.

All explorations have been made within a significance range of $[0, 0.1[$.

This report was produced with WISP version 0.0.1+0.g8ad307b.dirty.

You may get source code from <https://github.com/Tharos-ux/wisp>

window_size	10000
sampling_objective	500
domain_ref	[4, 50, '1111']
phylum_ref	[4, 100, '1111']
group_ref	[4, 500, '1111']
order_ref	[4, 400, '1111']
family_ref	[4, 200, '1111']
merged_ref	[4, 50, '1111']
domain_sample	[4, '1111']
phylum_sample	[4, '1111']
group_sample	[4, '1111']
order_sample	[4, '1111']
family_sample	[4, '1111']
merged_sample	[4, '1111']
input_train	genomes/train/
input_unk	genomes/unk/
database_output	data/
reports_output	output/
threshold	0.1
nb_boosts	10
tree_depth	10
full_test_set	False
reads_th	0.1
selection_mode	delta_mean
force_model_rebuild	False
single_way	True
targeted_level	family
levels_list	['domain', 'phylum', 'group', 'order', 'family']
abundance_threshold	0.25

Algorithm parameters

Raw reads predictions for tex_test_mix_sp_read_0

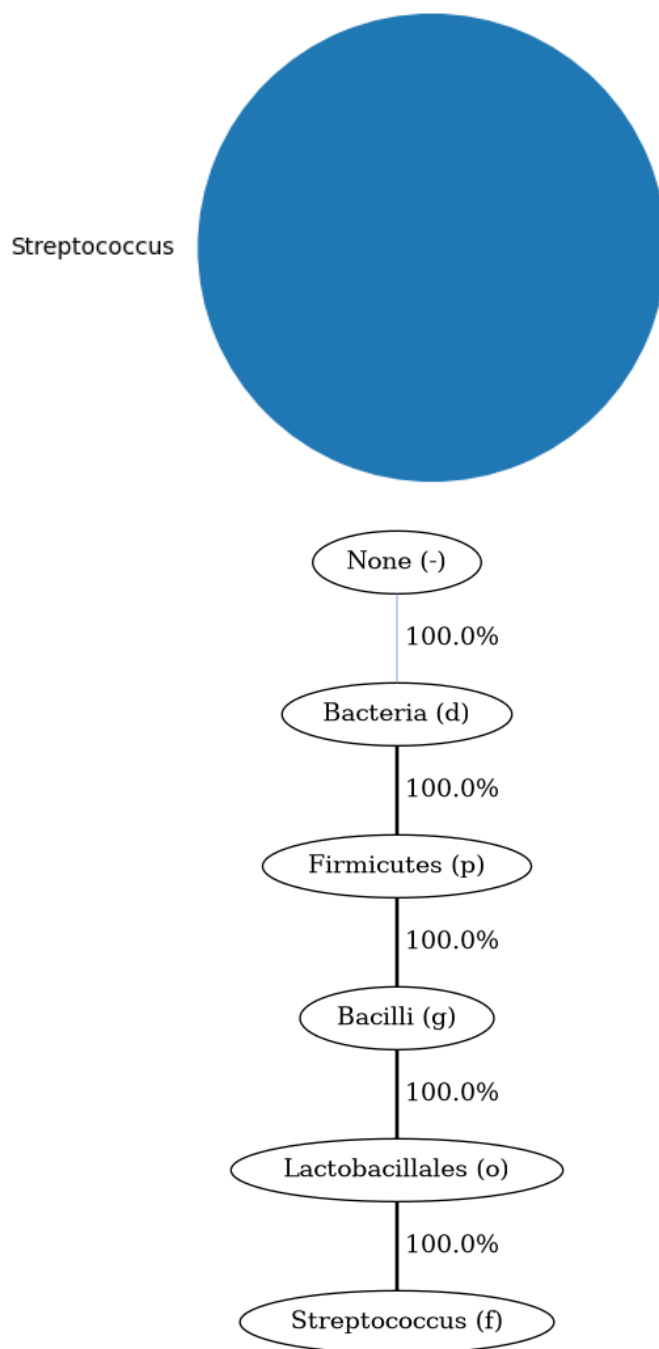


Figure 1: Global data for tex_test_mix_sp_read_0

Level domain

accuracy : 0.9937106918238994

macro avg : 'precision': 0.99, 'recall': 0.96, 'f1-score': 0.98, 'support': 1113

weighted avg : 'precision': 0.99, 'recall': 0.99, 'f1-score': 0.99, 'support': 1113

Bacteria : 'precision': 0.99, 'recall': 1.0, 'f1-score': 1.0, 'support': 1028

Archaea : 'precision': 0.99, 'recall': 0.93, 'f1-score': 0.96, 'support': 85

Estimators for None

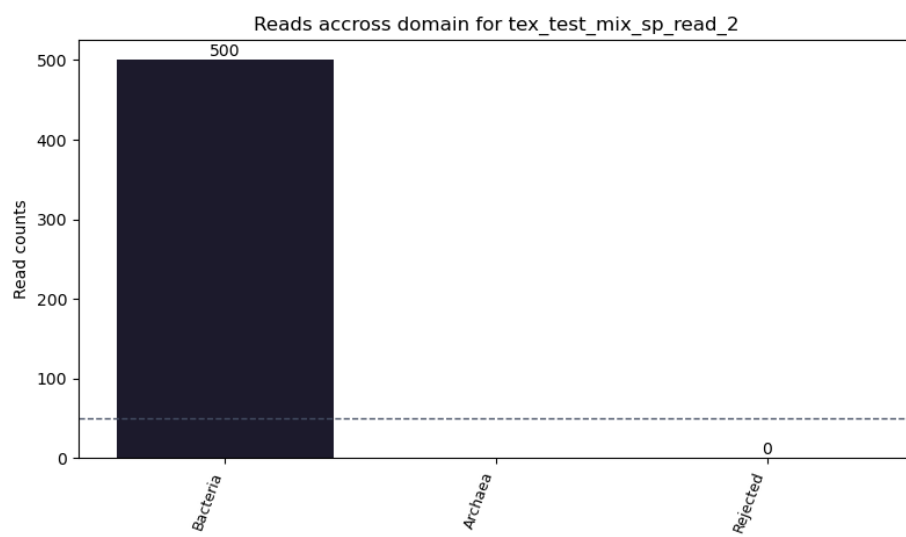
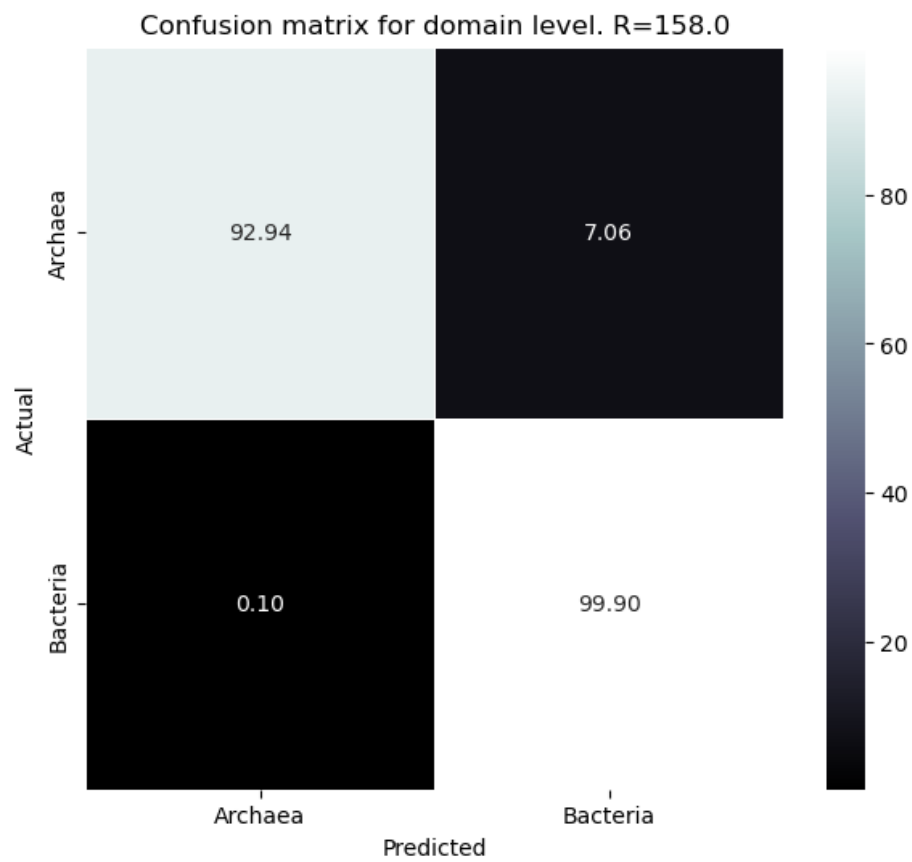


Figure 2: Level domain

Level phylum for hypothesis Bacteria

accuracy : 0.9778365347227622
macro avg : 'precision': 0.99, 'recall': 0.95, 'f1-score': 0.97, 'support': 25718
weighted avg : 'precision': 0.98, 'recall': 0.98, 'f1-score': 0.98, 'support': 25718
Dictyoglomi : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 75
Verrucomicrobia : 'precision': 0.97, 'recall': 0.89, 'f1-score': 0.93, 'support': 75
Aquificae : 'precision': 1.0, 'recall': 0.99, 'f1-score': 1.0, 'support': 374
Spirochaetes : 'precision': 0.98, 'recall': 0.98, 'f1-score': 0.98, 'support': 1873
Planctomycetes : 'precision': 0.99, 'recall': 0.97, 'f1-score': 0.98, 'support': 450
Chlamydiae : 'precision': 0.99, 'recall': 0.98, 'f1-score': 0.99, 'support': 300
Chlorobi : 'precision': 0.98, 'recall': 0.79, 'f1-score': 0.87, 'support': 75
Firmicutes : 'precision': 0.96, 'recall': 0.97, 'f1-score': 0.96, 'support': 3824
Deinococcus-Thermus : 'precision': 1.0, 'recall': 0.99, 'f1-score': 0.99, 'support': 449
Fusobacteria : 'precision': 0.99, 'recall': 0.93, 'f1-score': 0.96, 'support': 150
Actinobacteria : 'precision': 0.98, 'recall': 0.98, 'f1-score': 0.98, 'support': 2925
Thermotogae : 'precision': 0.99, 'recall': 0.97, 'f1-score': 0.98, 'support': 150
Acidobacteria : 'precision': 1.0, 'recall': 0.83, 'f1-score': 0.91, 'support': 75
Tenericutes : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 75
Deferribacteres : 'precision': 0.98, 'recall': 0.91, 'f1-score': 0.94, 'support': 150
Synergistetes : 'precision': 1.0, 'recall': 0.98, 'f1-score': 0.99, 'support': 449
Chloroflexi : 'precision': 1.0, 'recall': 0.93, 'f1-score': 0.97, 'support': 75
Cyanobacteria : 'precision': 0.99, 'recall': 0.9, 'f1-score': 0.94, 'support': 450
Thermodesulfobacteria : 'precision': 0.99, 'recall': 1.0, 'f1-score': 0.99, 'support': 75
Calditrichaeota : 'precision': 1.0, 'recall': 0.92, 'f1-score': 0.96, 'support': 75
Proteobacteria : 'precision': 0.98, 'recall': 0.99, 'f1-score': 0.99, 'support': 10950
Bacteroidetes : 'precision': 0.97, 'recall': 0.97, 'f1-score': 0.97, 'support': 2624

Estimators for Bacteria

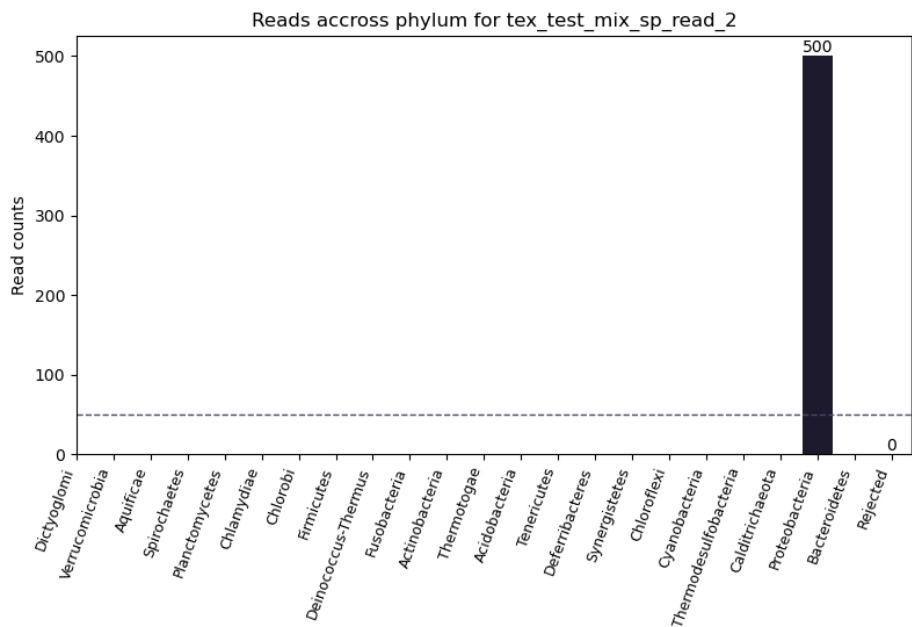
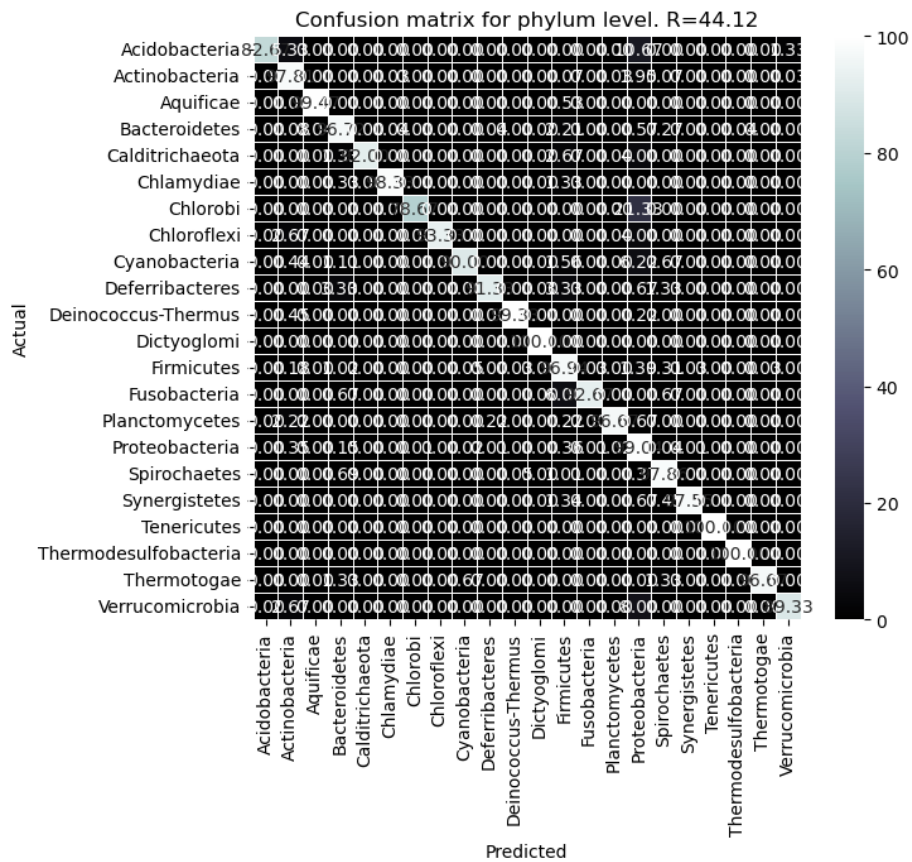


Figure 3: Level phylum for hypothesis Bacteria

Level group for hypothesis Firmicutes

accuracy : 0.9950300810881507

macro avg : 'precision': 1.0, 'recall': 0.99, 'f1-score': 0.99, 'support': 3823

weighted avg : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 3823

Negativicutes : 'precision': 1.0, 'recall': 0.98, 'f1-score': 0.99, 'support': 223

Clostridia : 'precision': 0.99, 'recall': 0.99, 'f1-score': 0.99, 'support': 1125

Bacilli : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 2475

Estimators for Firmicutes

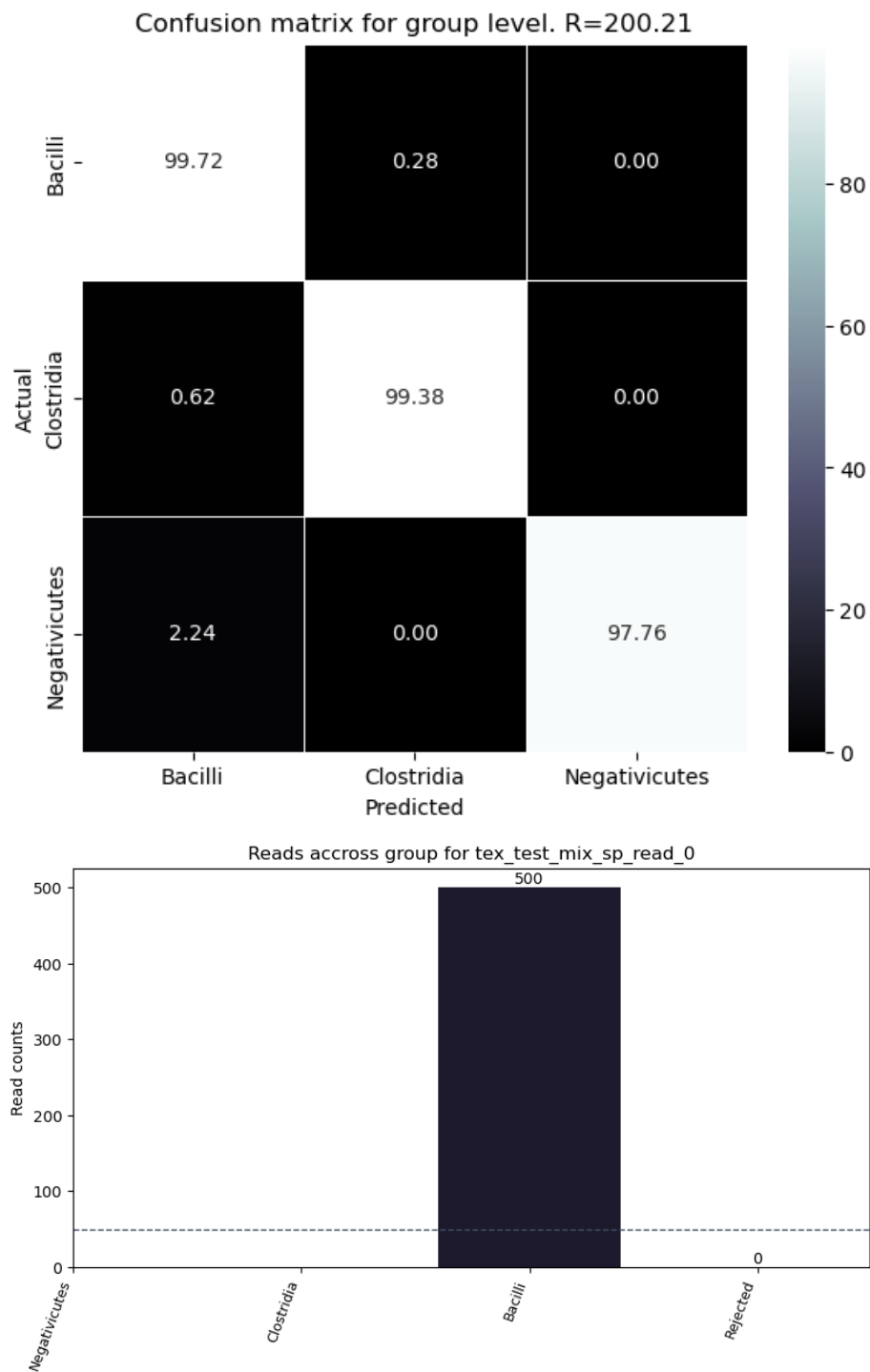


Figure 4: Level group for hypothesis Firmicutes

Level order for hypothesis Bacilli

accuracy : 0.989010989010989

macro avg : 'precision': 0.99, 'recall': 0.99, 'f1-score': 0.99, 'support': 1638

weighted avg : 'precision': 0.99, 'recall': 0.99, 'f1-score': 0.99, 'support': 1638

Bacillales : 'precision': 0.99, 'recall': 0.98, 'f1-score': 0.98, 'support': 491

Lactobacillales : 'precision': 0.99, 'recall': 0.99, 'f1-score': 0.99, 'support': 1147

Estimators for Bacilli

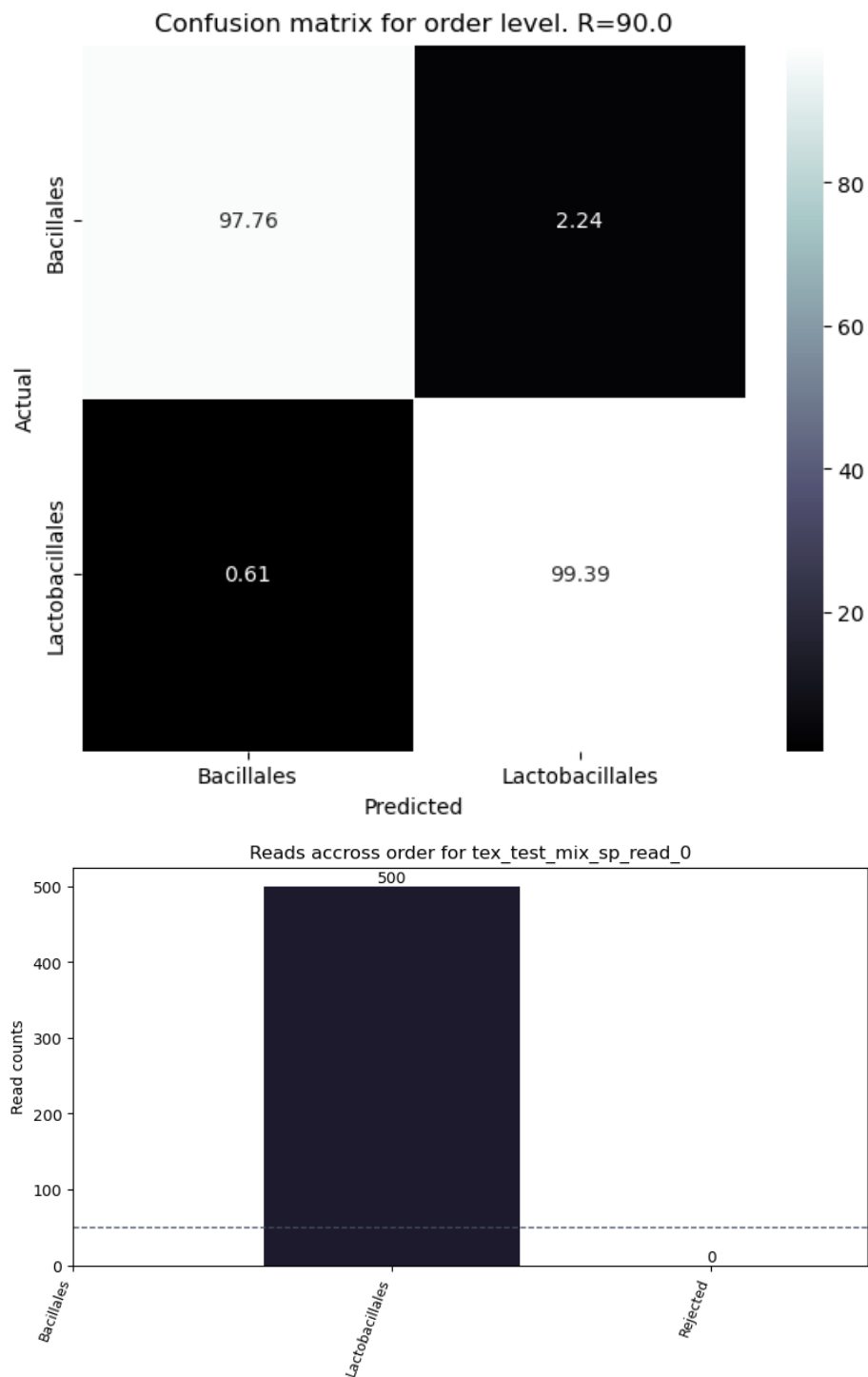


Figure 5: Level order for hypothesis Bacilli

Level family for hypothesis Lactobacillales

accuracy : 0.9754816112084063
macro avg : 'precision': 0.98, 'recall': 0.97, 'f1-score': 0.97, 'support': 571
weighted avg : 'precision': 0.98, 'recall': 0.98, 'f1-score': 0.98, 'support': 571
Weissella : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 25
Enterococcus : 'precision': 0.94, 'recall': 0.99, 'f1-score': 0.96, 'support': 74
Lactobacillus : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 24
Lactiplantibacillus : 'precision': 0.96, 'recall': 0.98, 'f1-score': 0.97, 'support': 50
Atopococcus : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 25
Aerococcus : 'precision': 0.96, 'recall': 0.96, 'f1-score': 0.96, 'support': 24
Streptococcus : 'precision': 0.99, 'recall': 0.99, 'f1-score': 0.99, 'support': 150
Lactococcus : 'precision': 1.0, 'recall': 0.96, 'f1-score': 0.98, 'support': 25
Convivina : 'precision': 0.95, 'recall': 0.84, 'f1-score': 0.89, 'support': 25
Lacticaseibacillus : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 24
Pediococcus : 'precision': 0.96, 'recall': 0.92, 'f1-score': 0.94, 'support': 25
Vagococcus : 'precision': 0.96, 'recall': 1.0, 'f1-score': 0.98, 'support': 25
Leuconostoc : 'precision': 1.0, 'recall': 1.0, 'f1-score': 1.0, 'support': 25
Facklamia : 'precision': 0.98, 'recall': 0.96, 'f1-score': 0.97, 'support': 50

Estimators for Lactobacillales

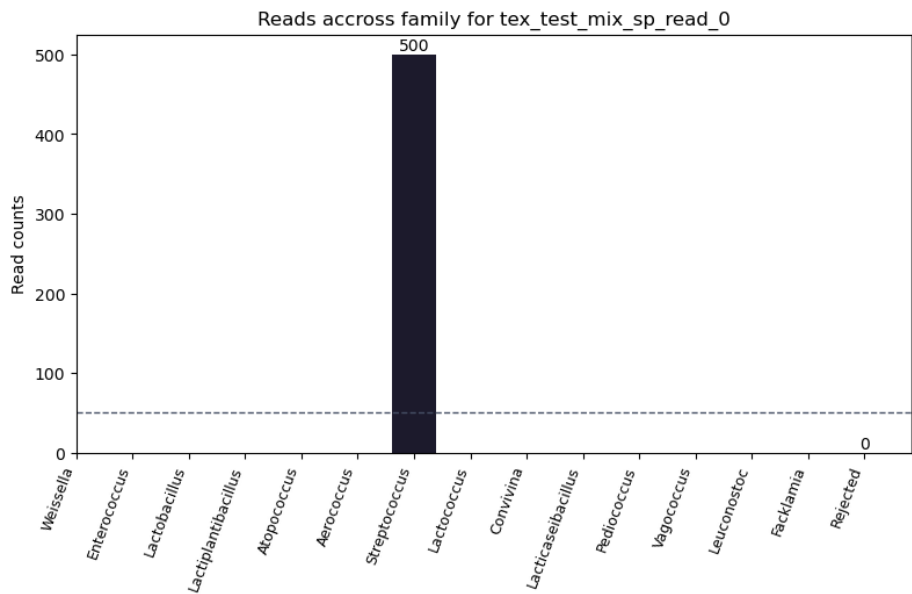
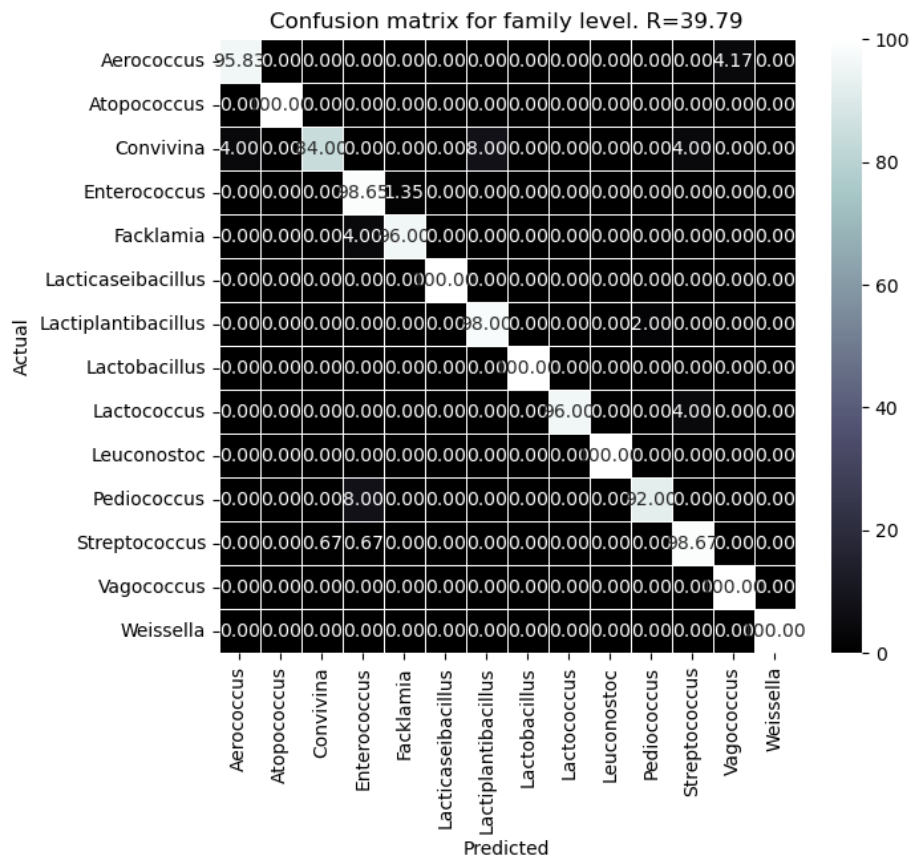


Figure 6: Level family for hypothesis Lactobacillales