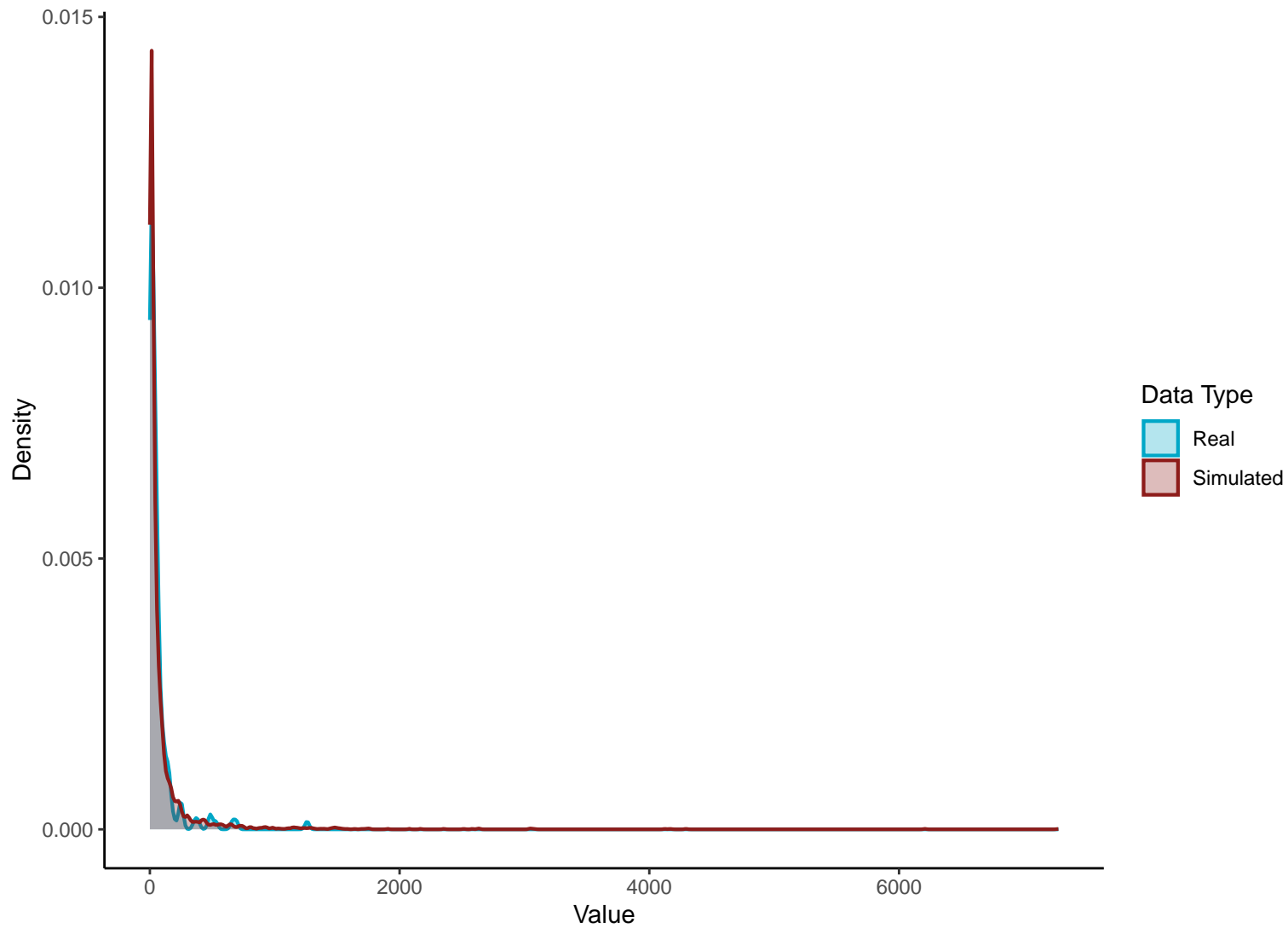
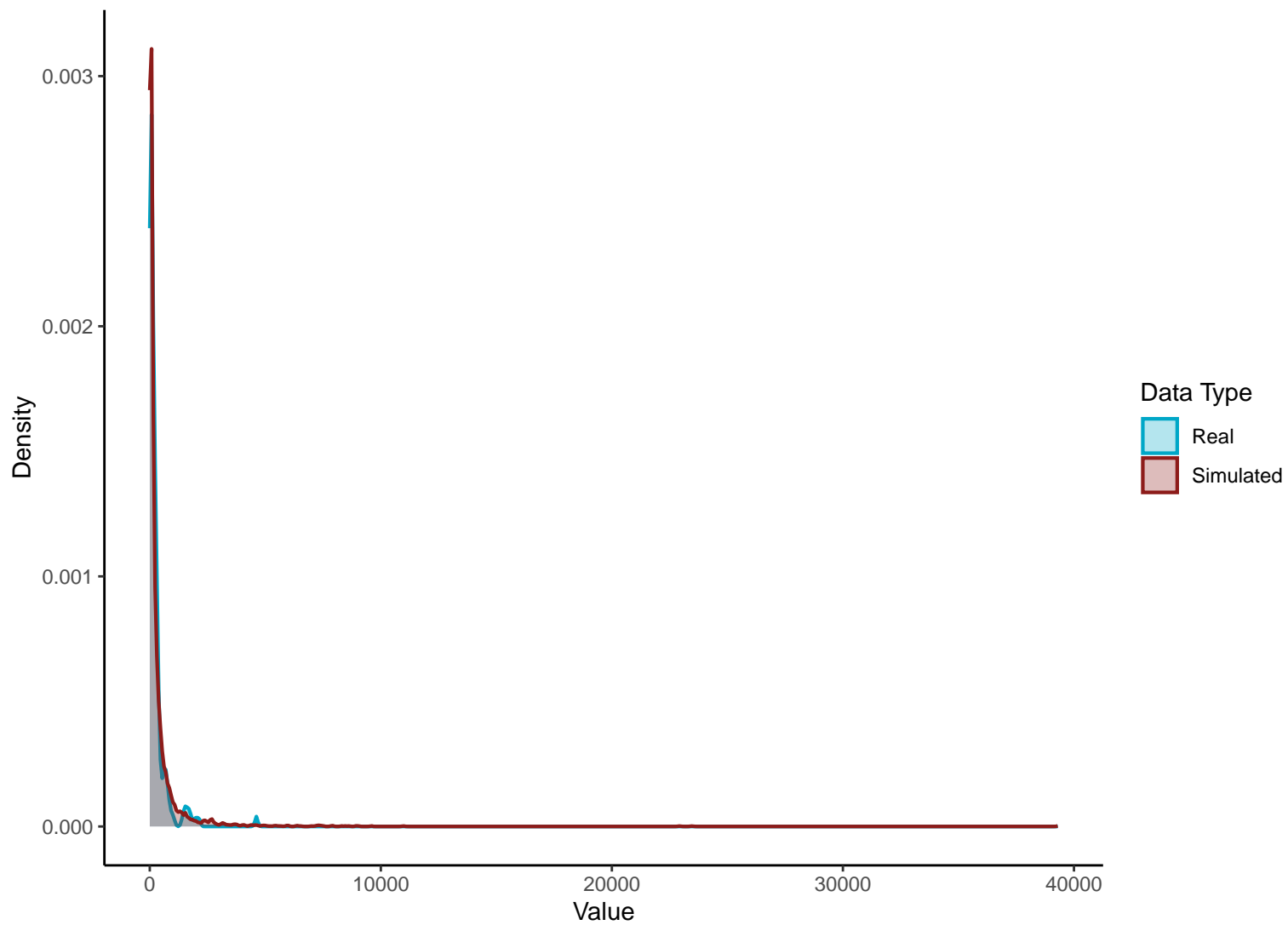


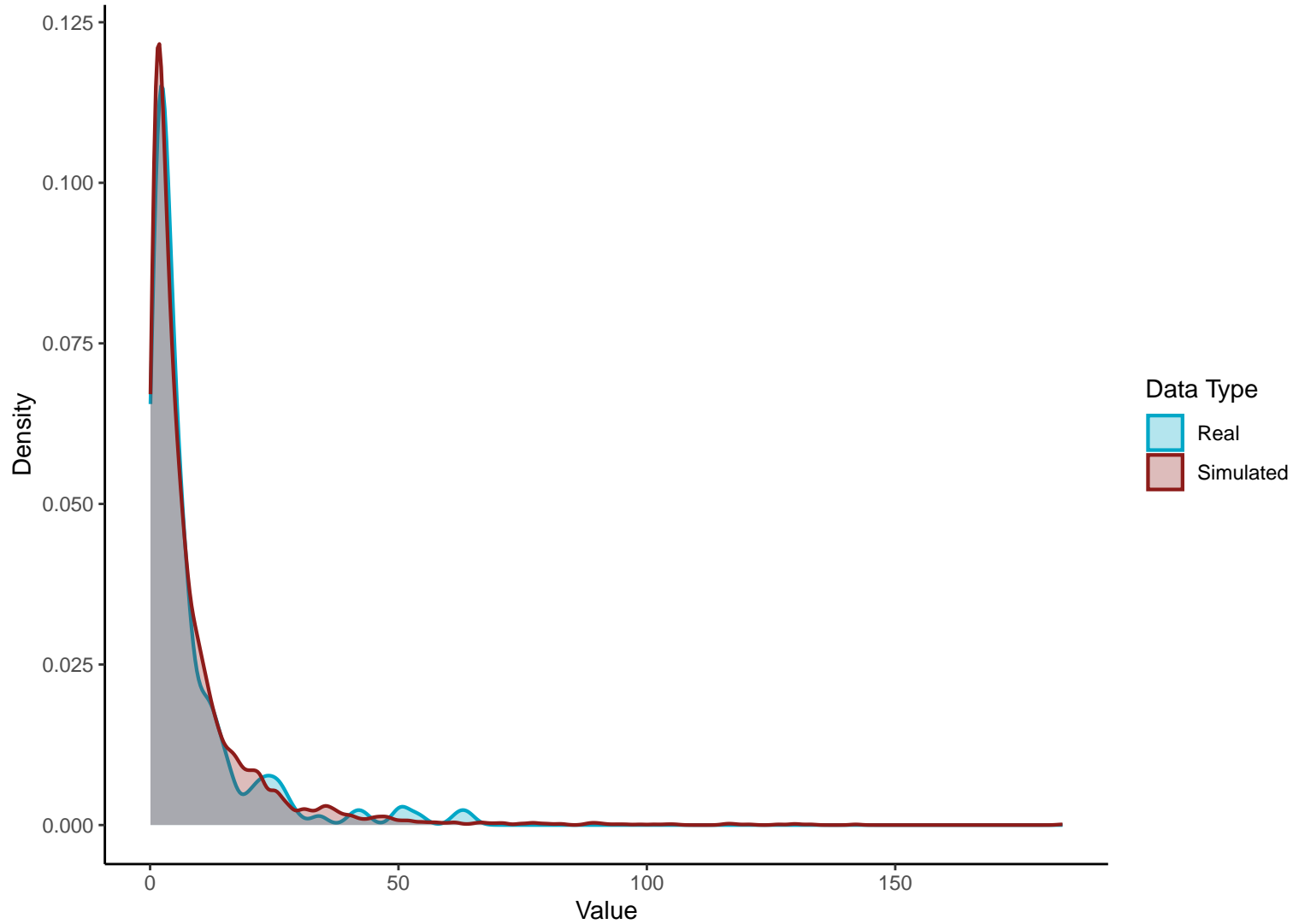
Prevotellaceae.UCG.003



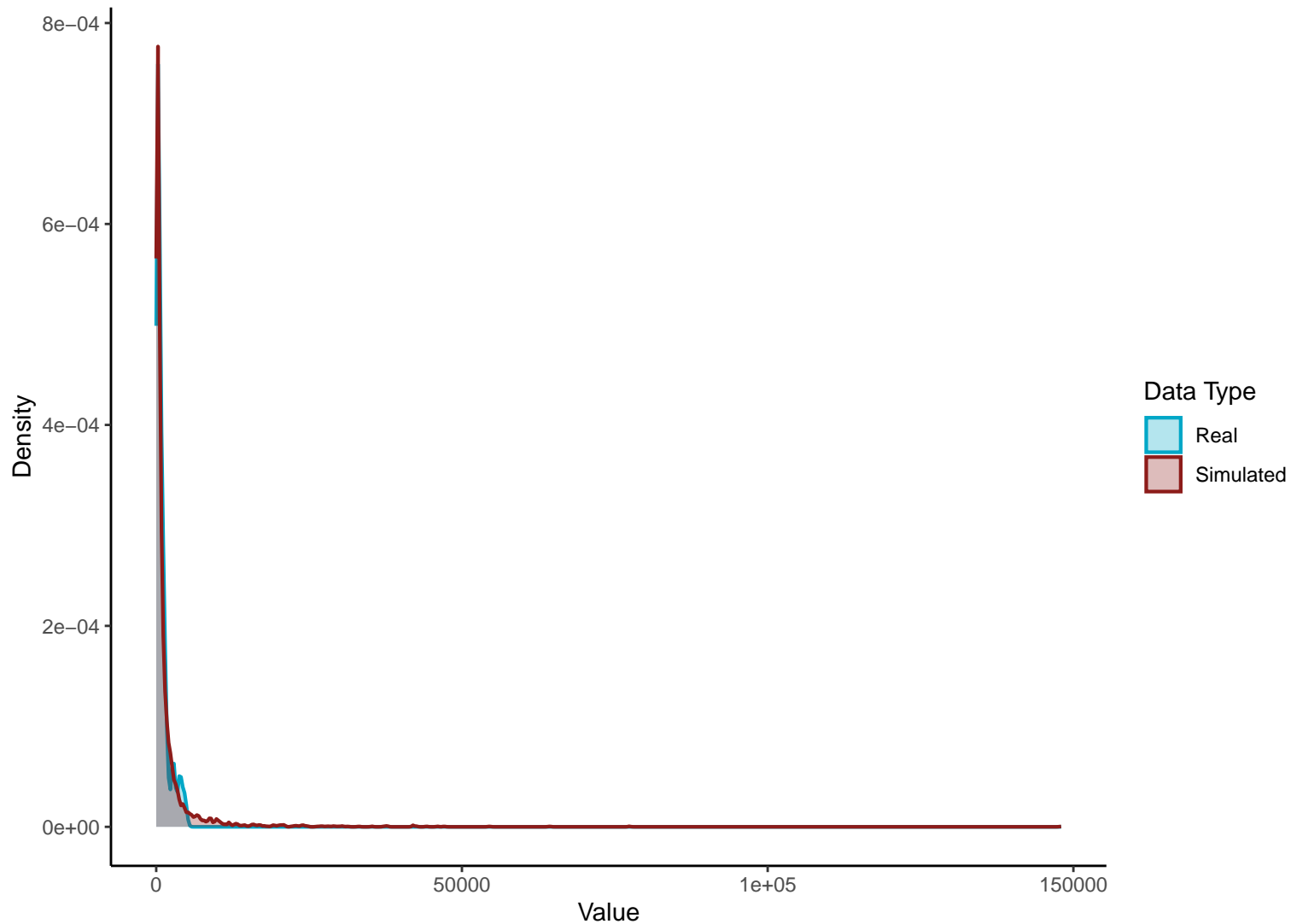
Prevotellaceae.NK3B31.group



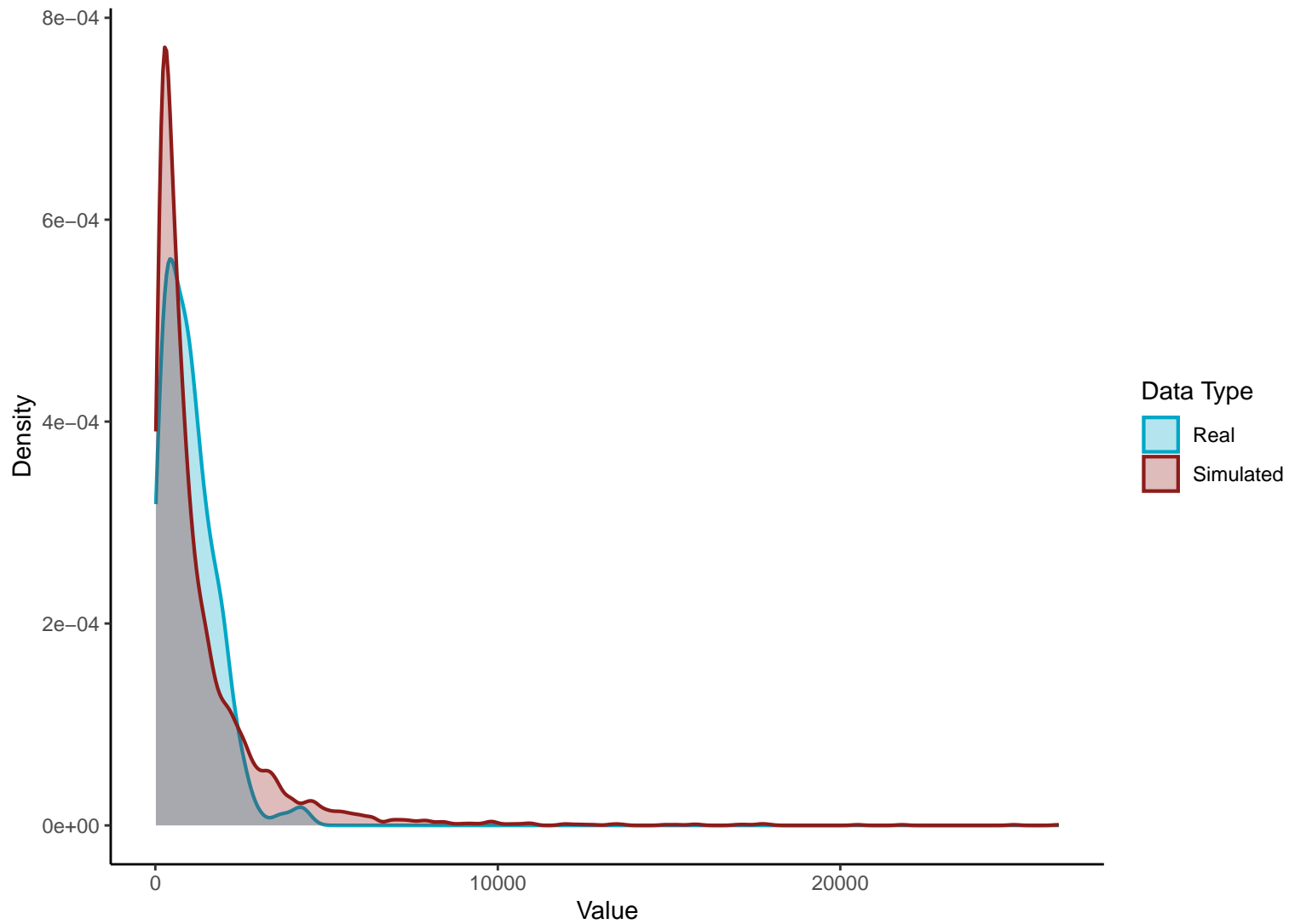
Sutterella



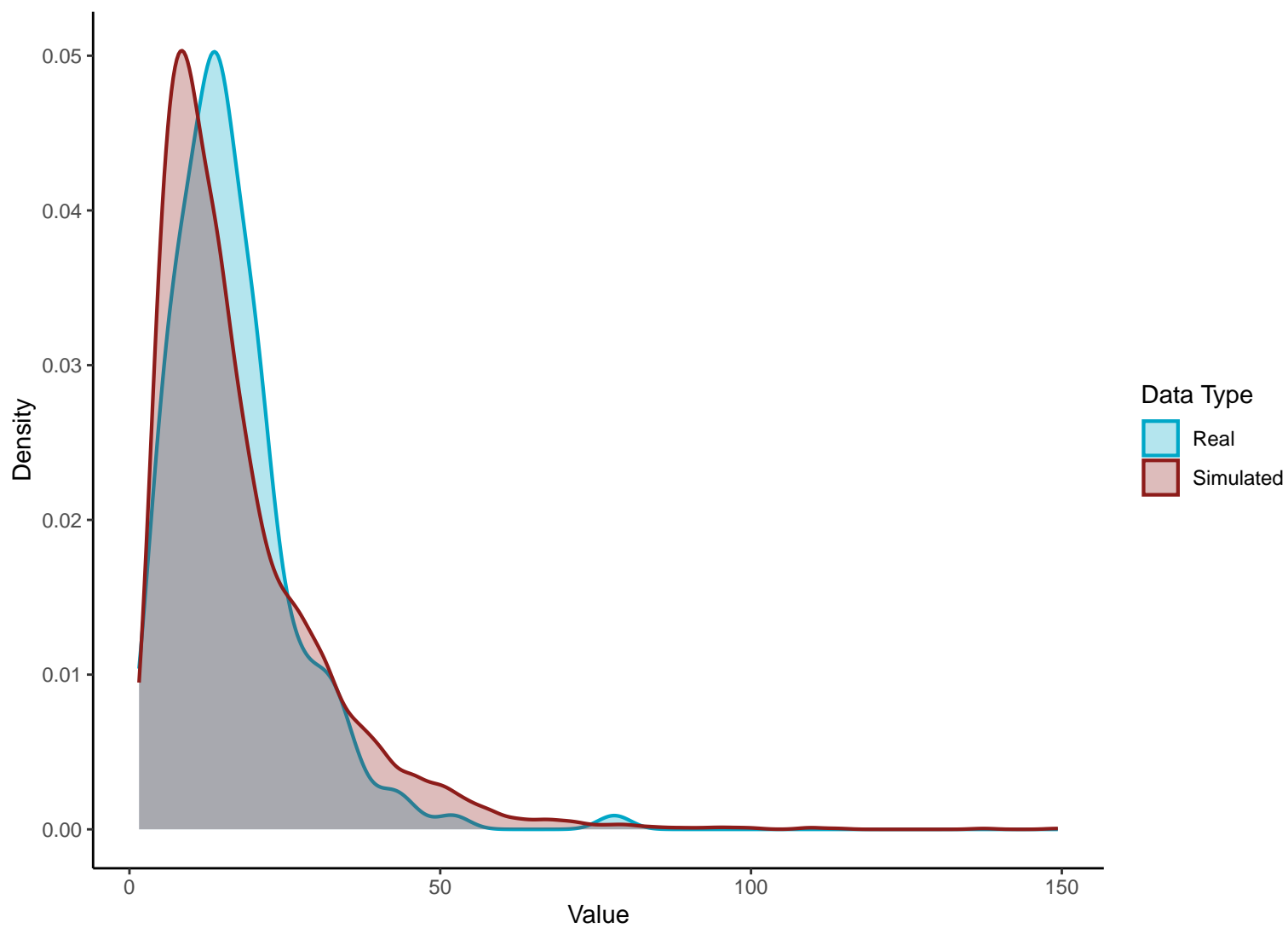
Christensenellaceae.R.7.group



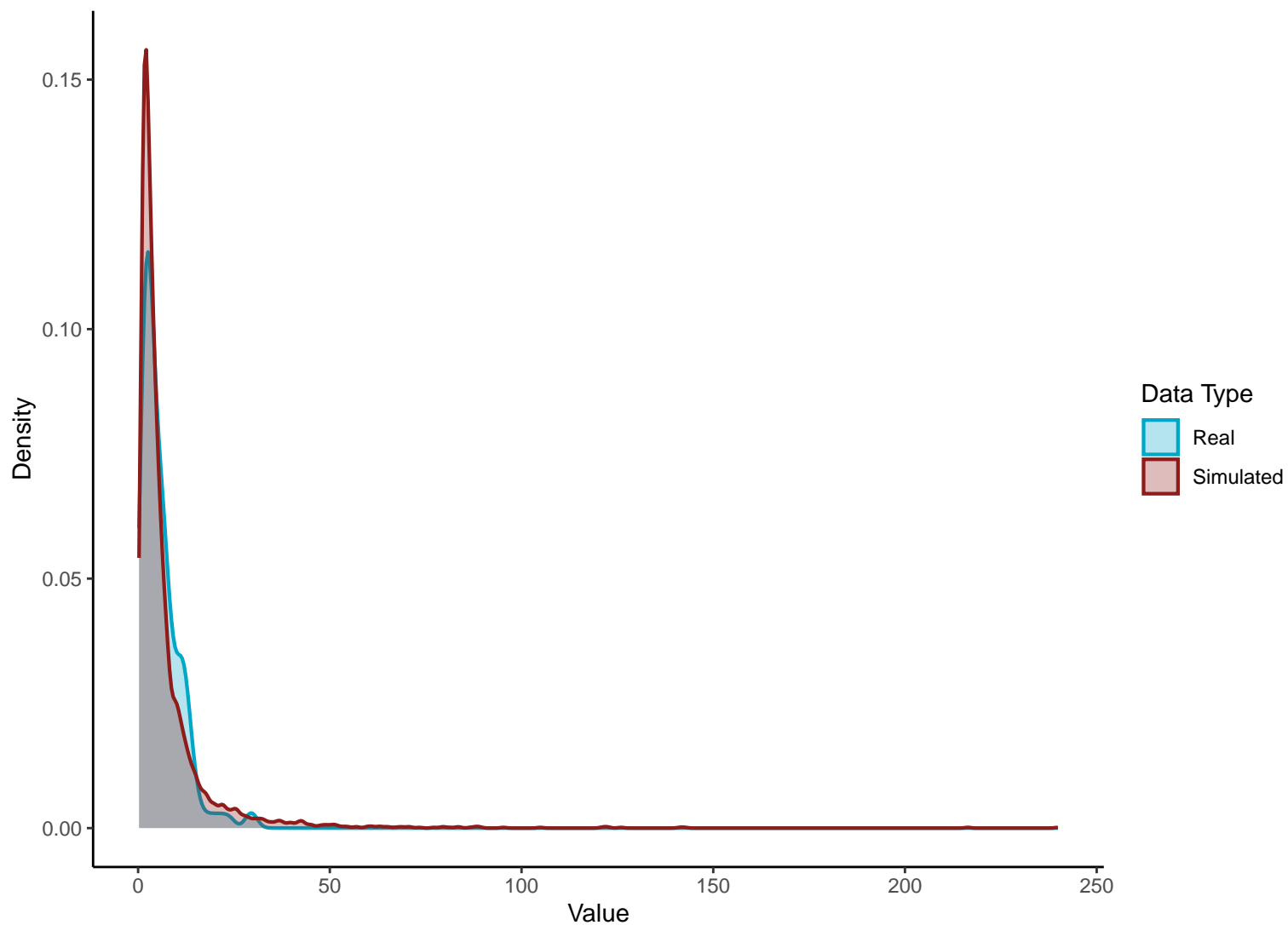
UCG.005



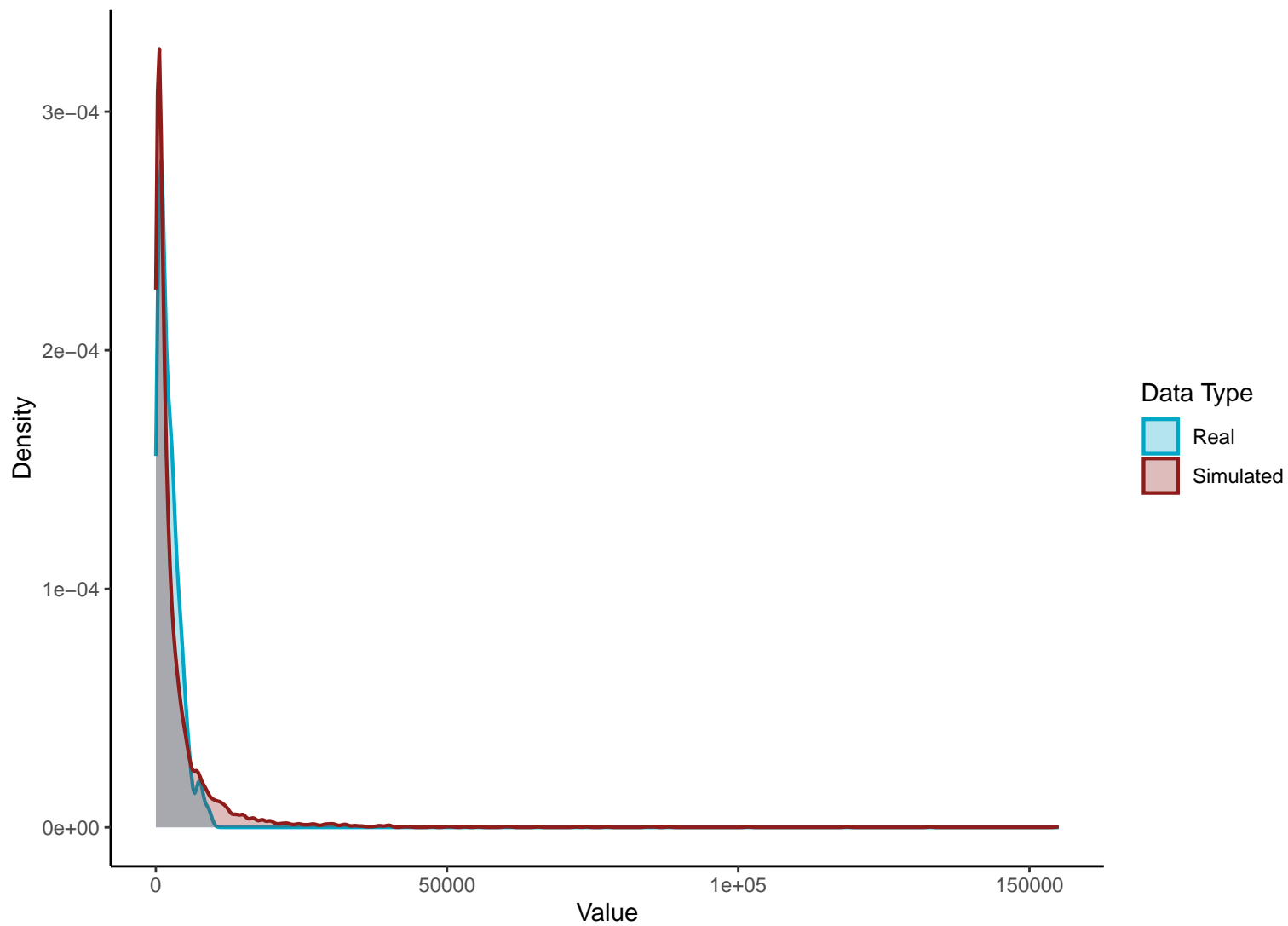
Slackia



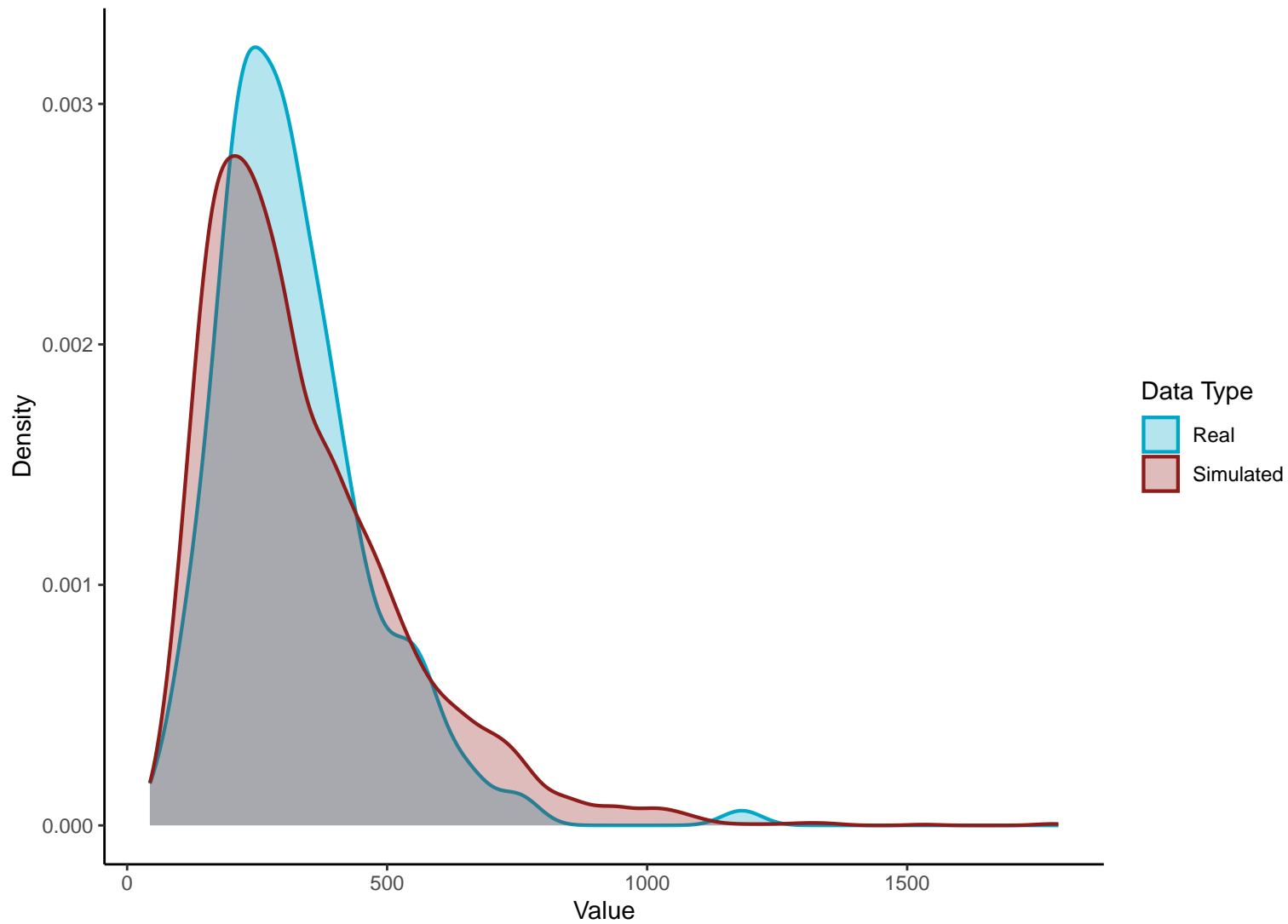
UCG.007



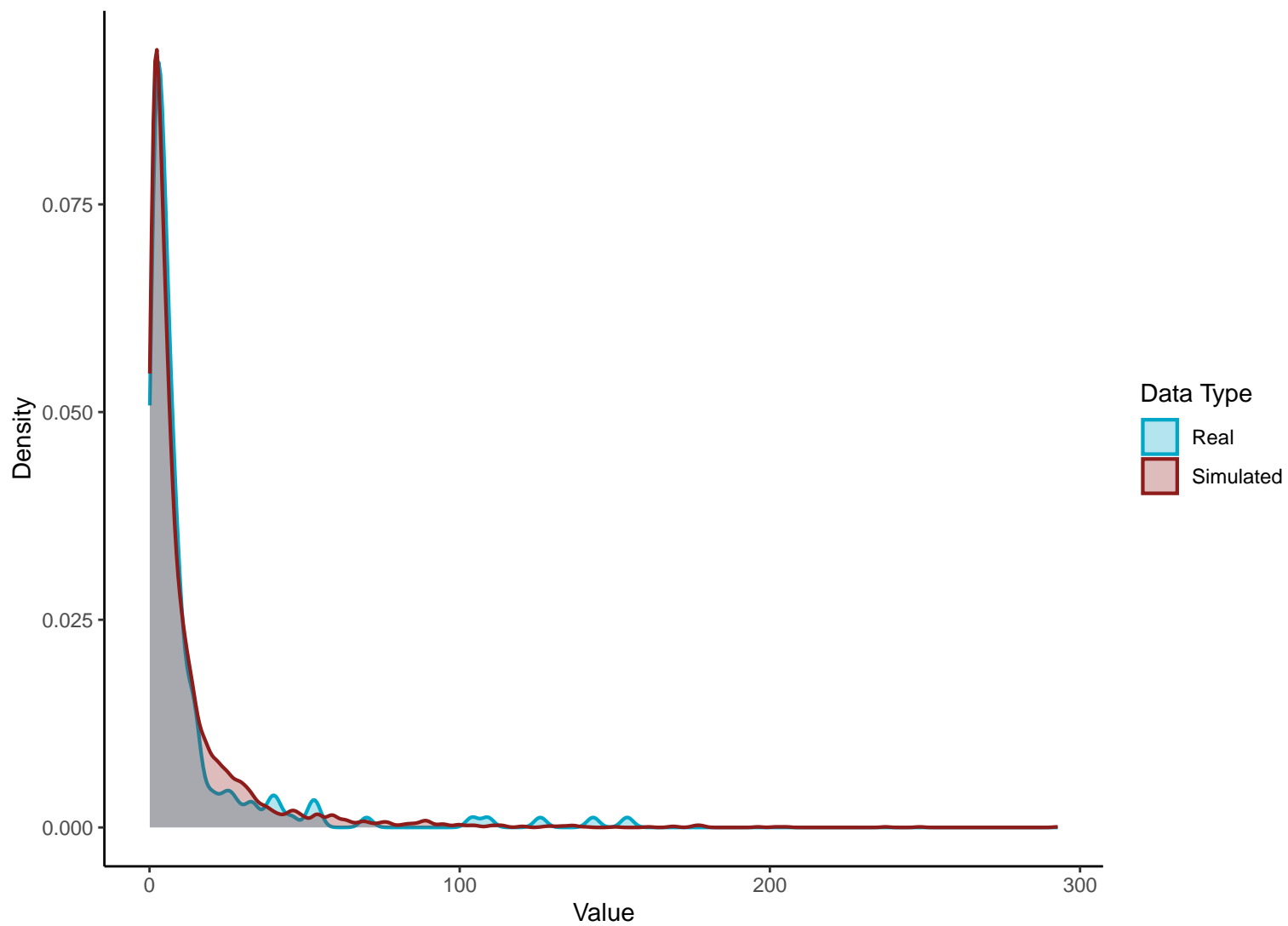
Terrisporobacter



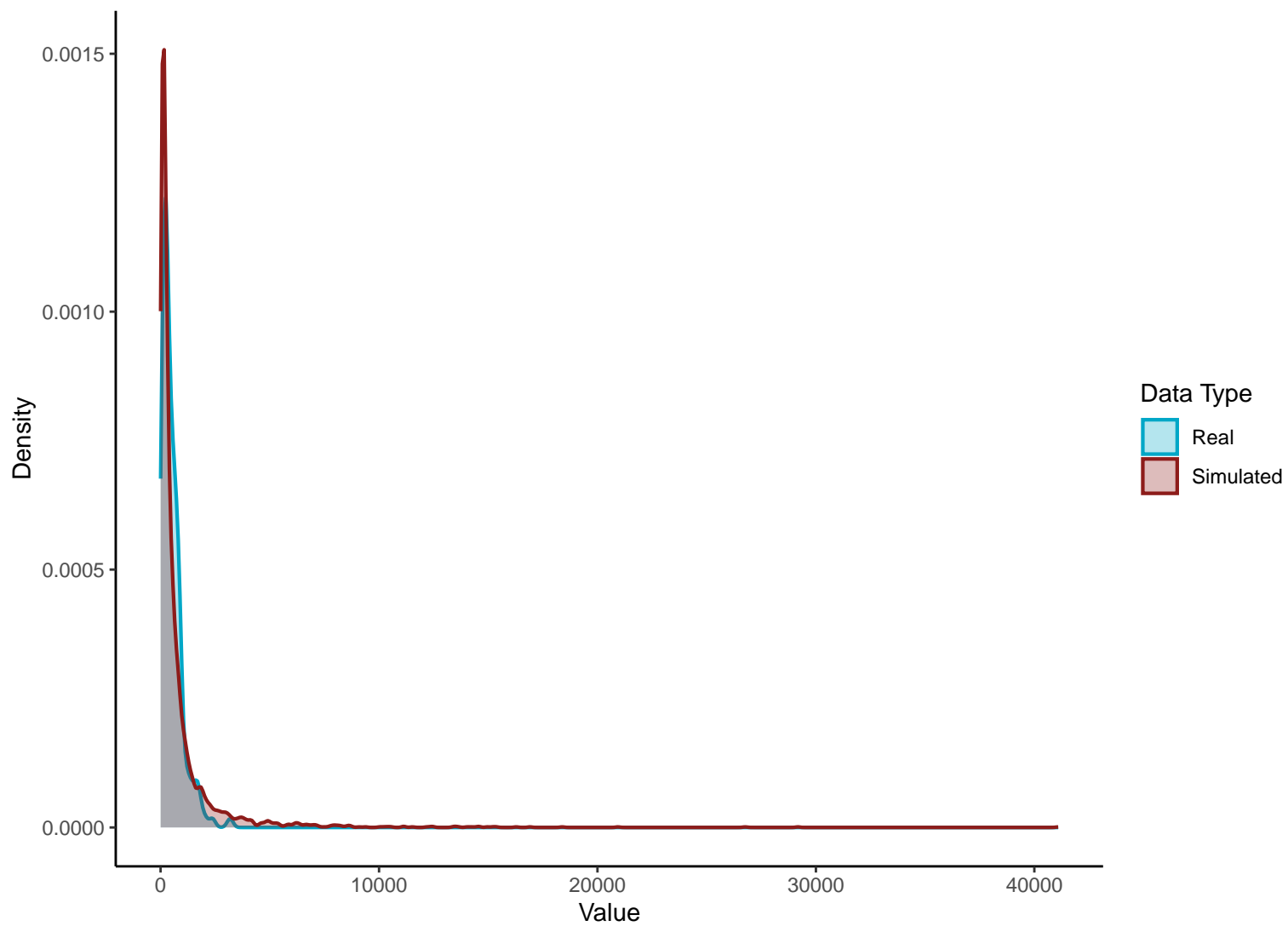
X.Eubacterium..hallii.group



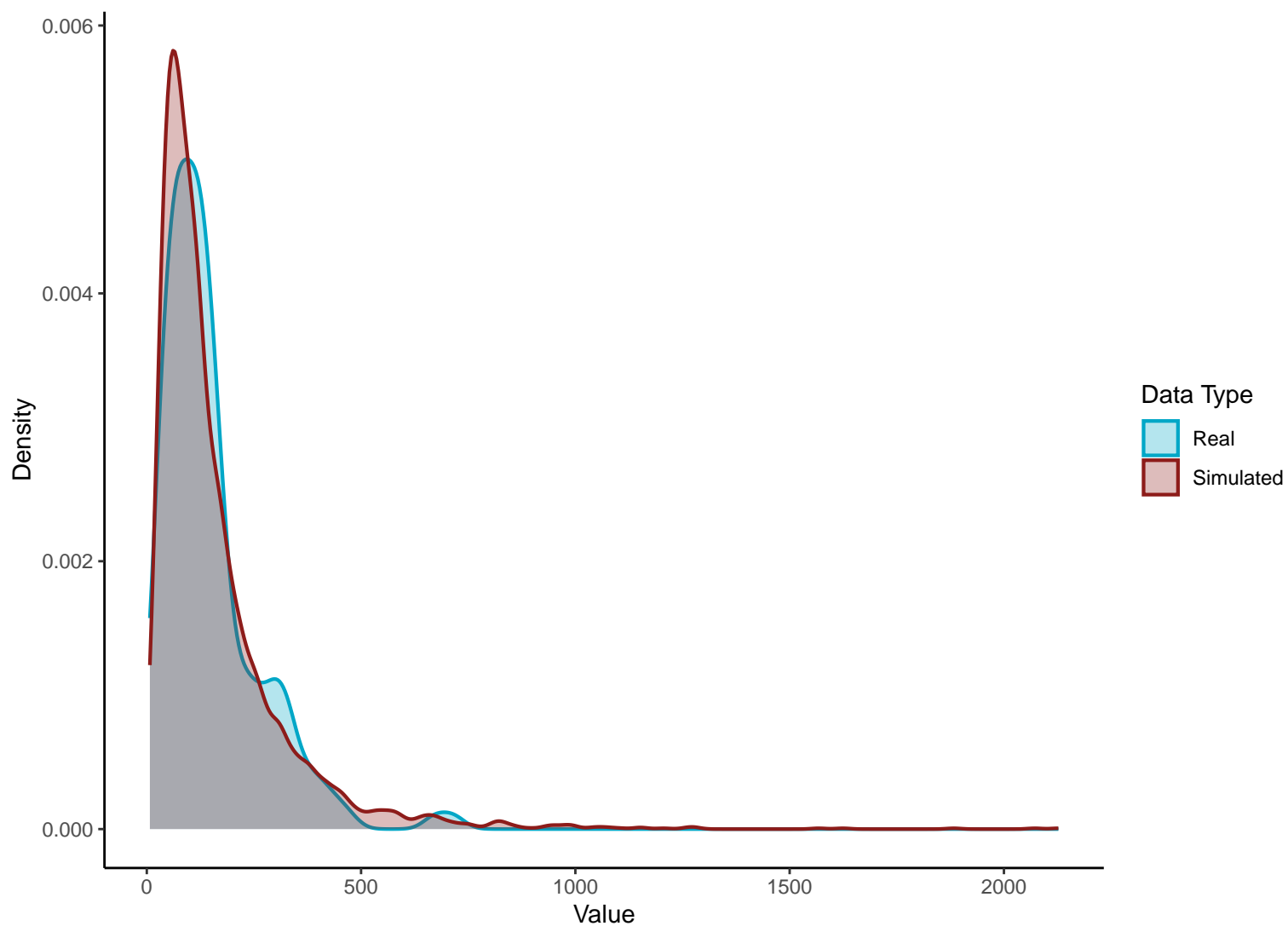
UCG.004



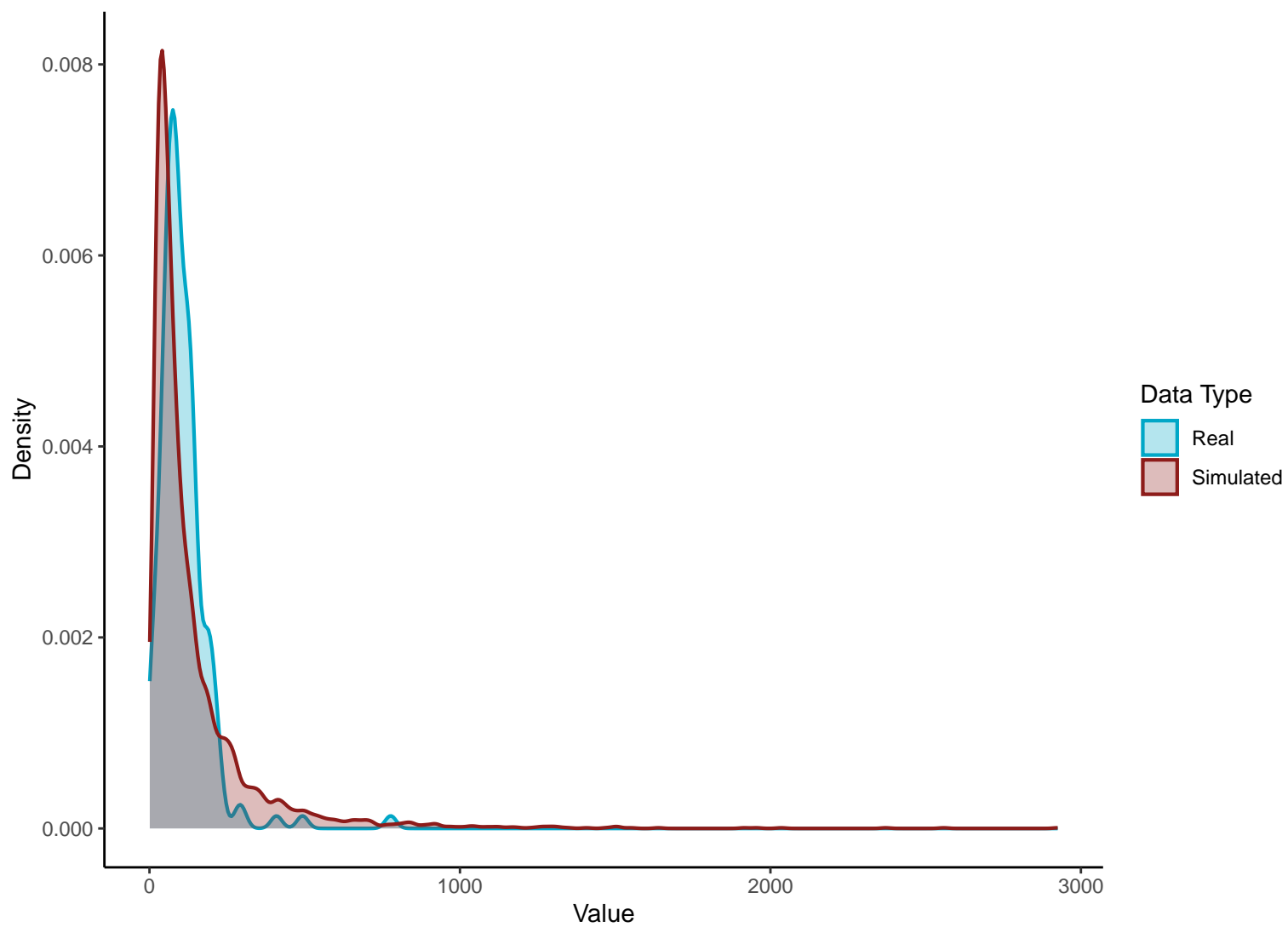
NK4A214.group



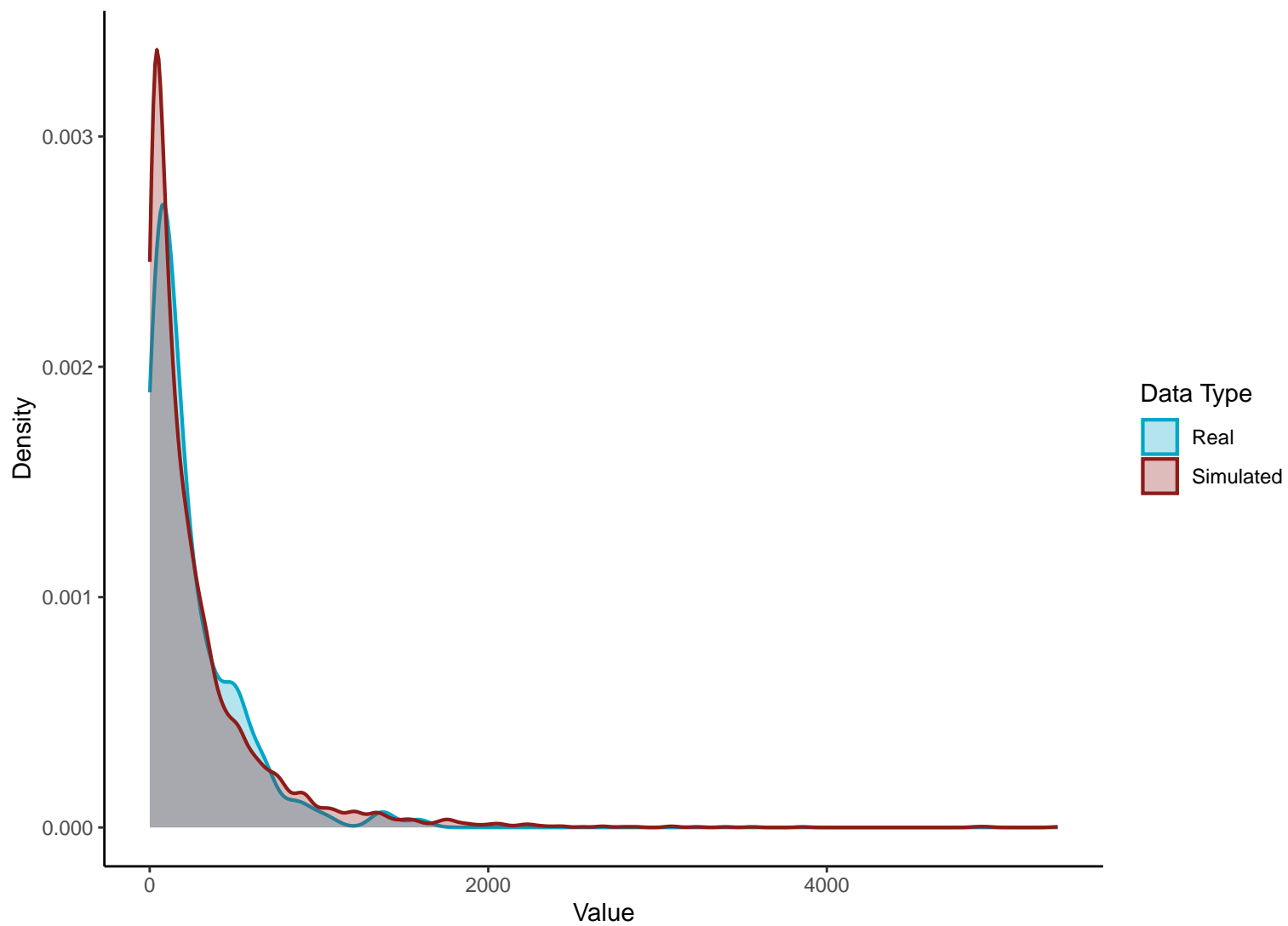
Lachnospiraceae.NK4A136.group



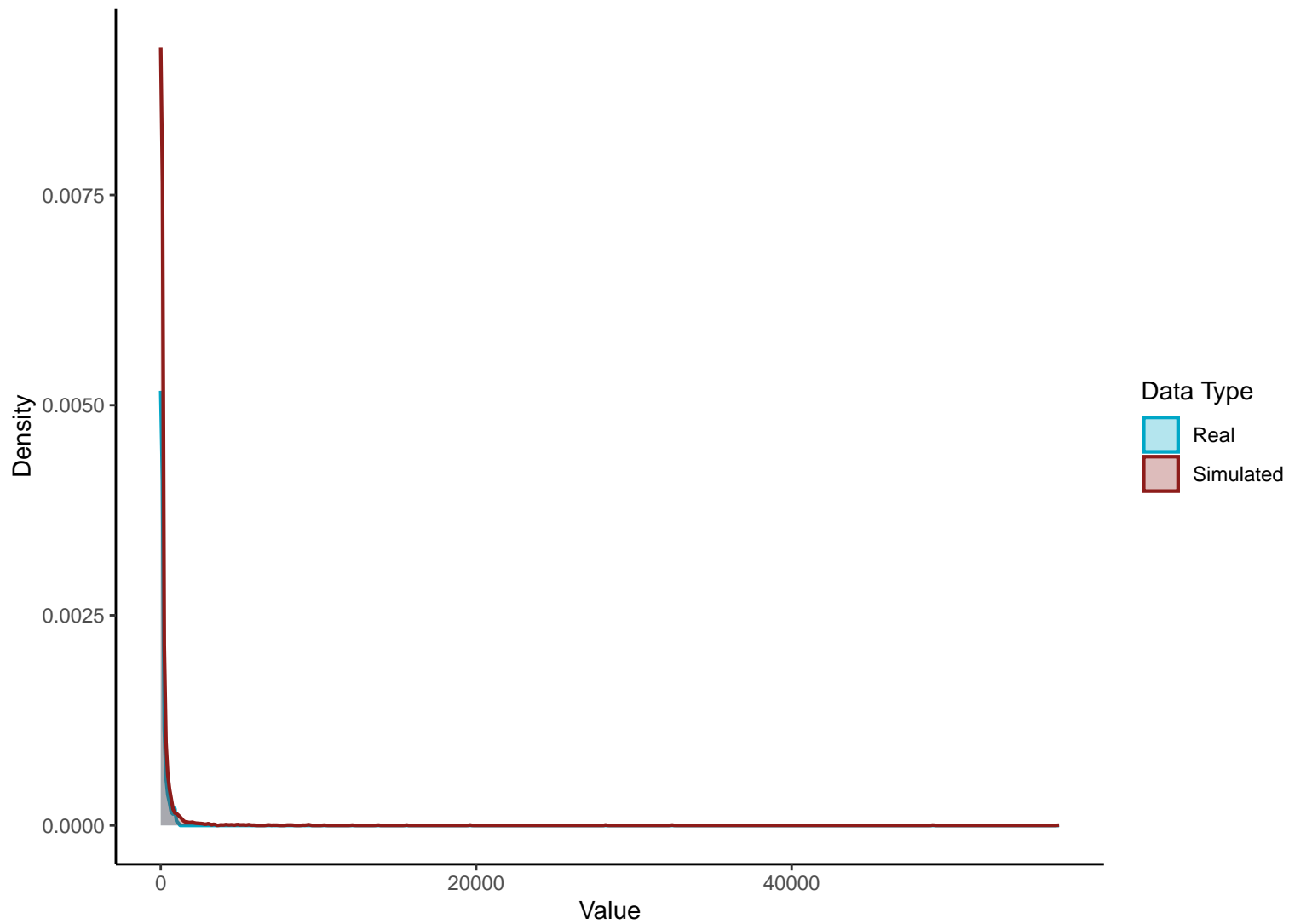
Monoglobus



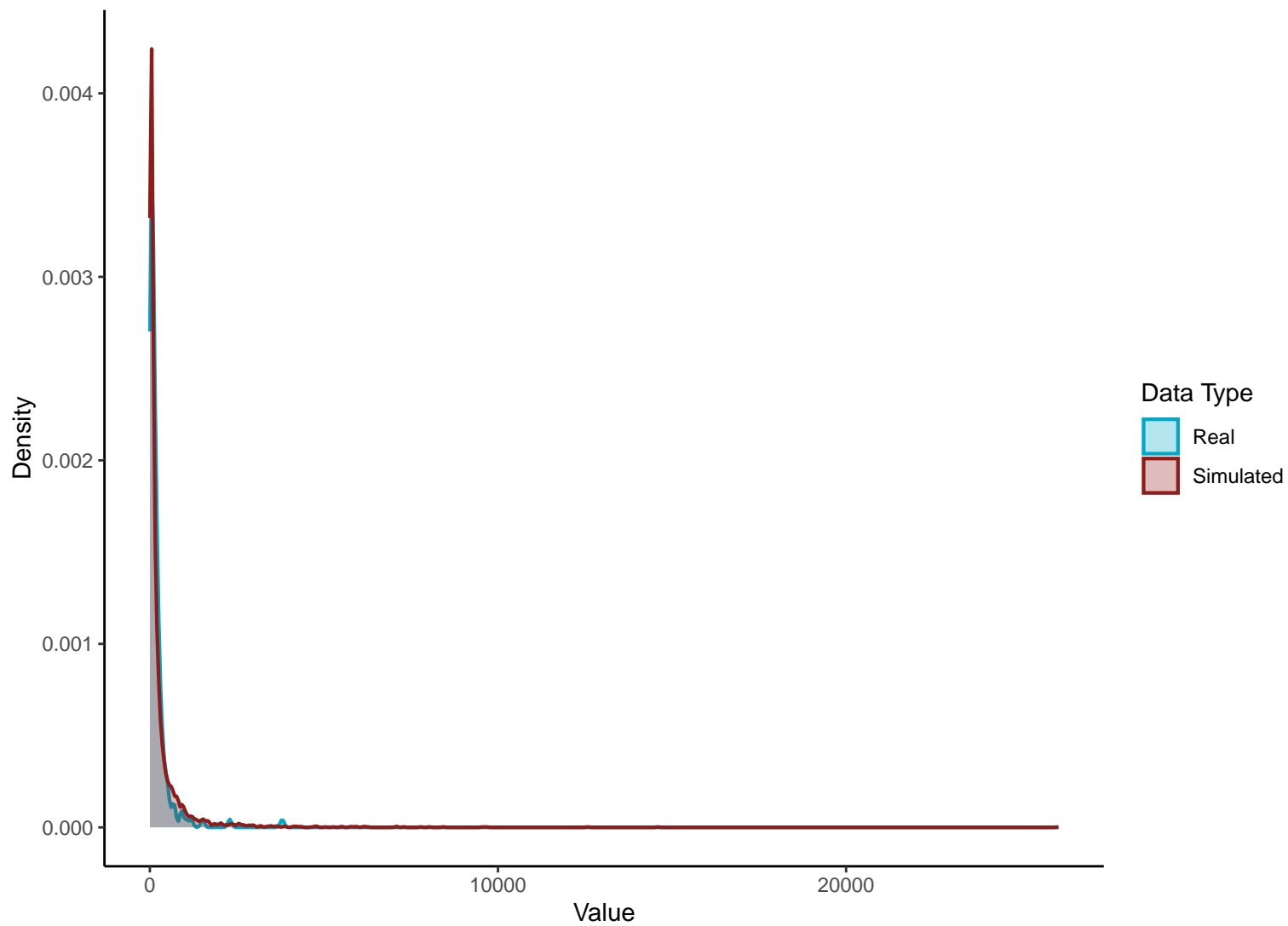
Prevotella



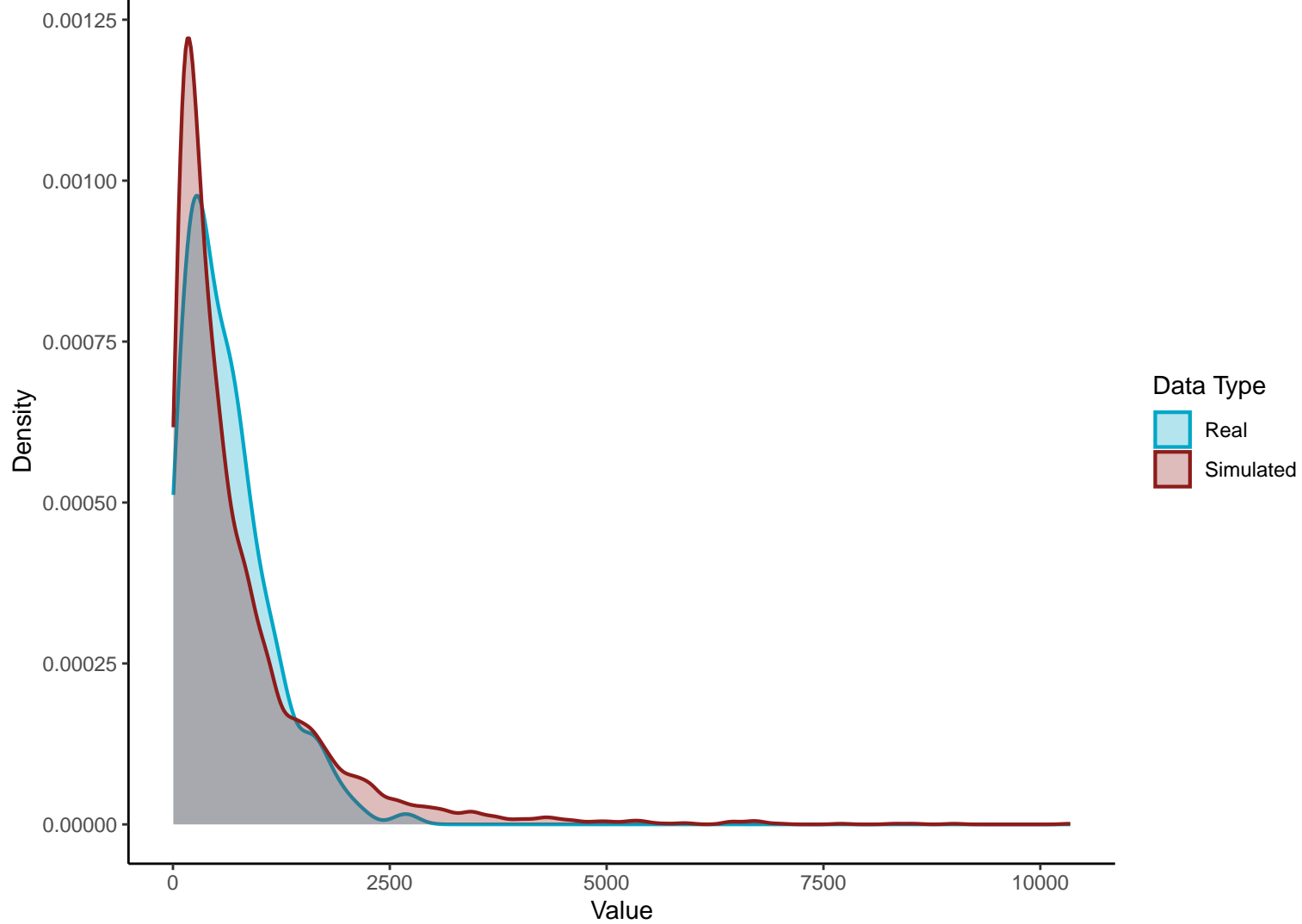
Treponema



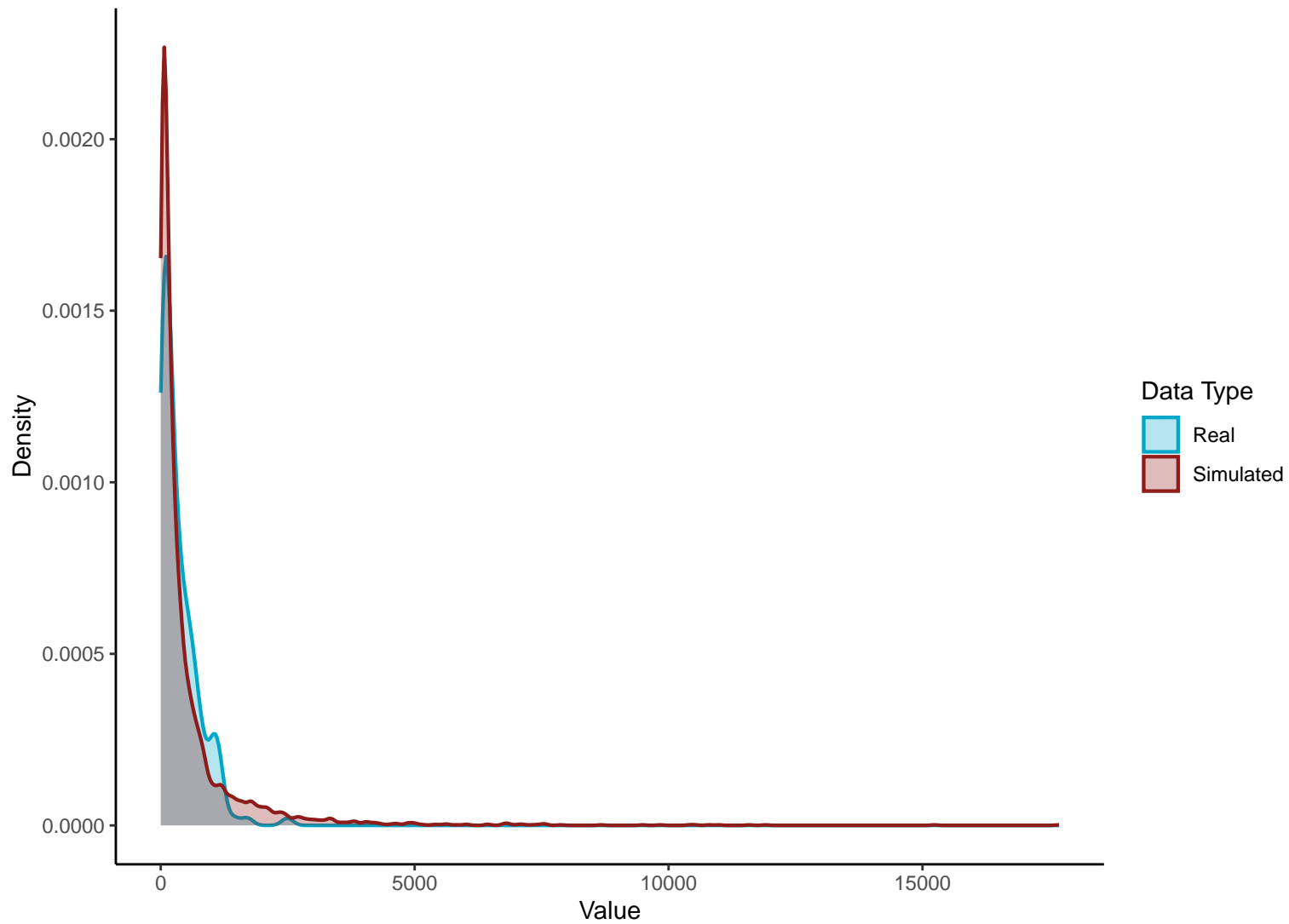
Rikenellaceae.RC9.gut.group



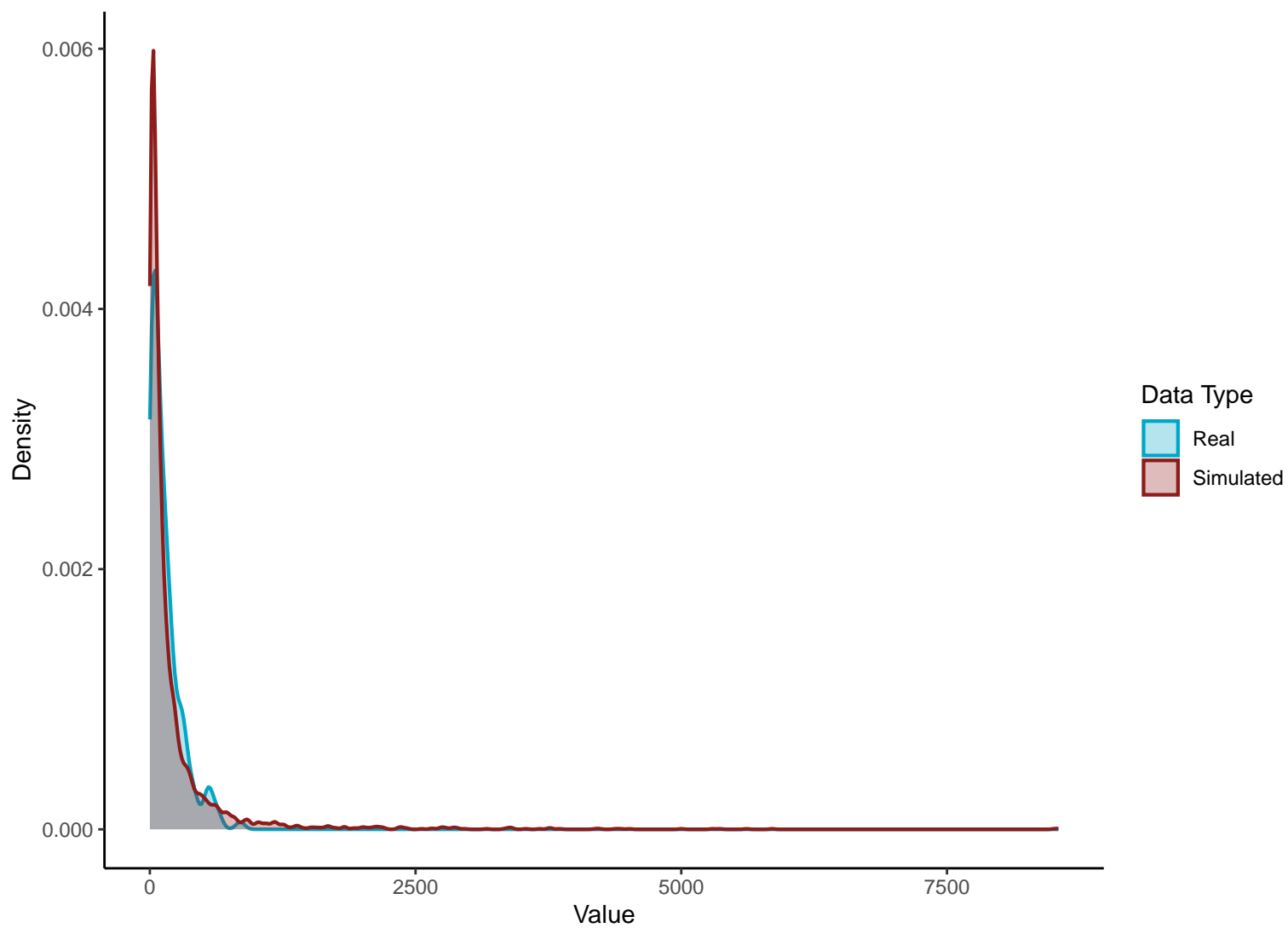
Faecalibacterium



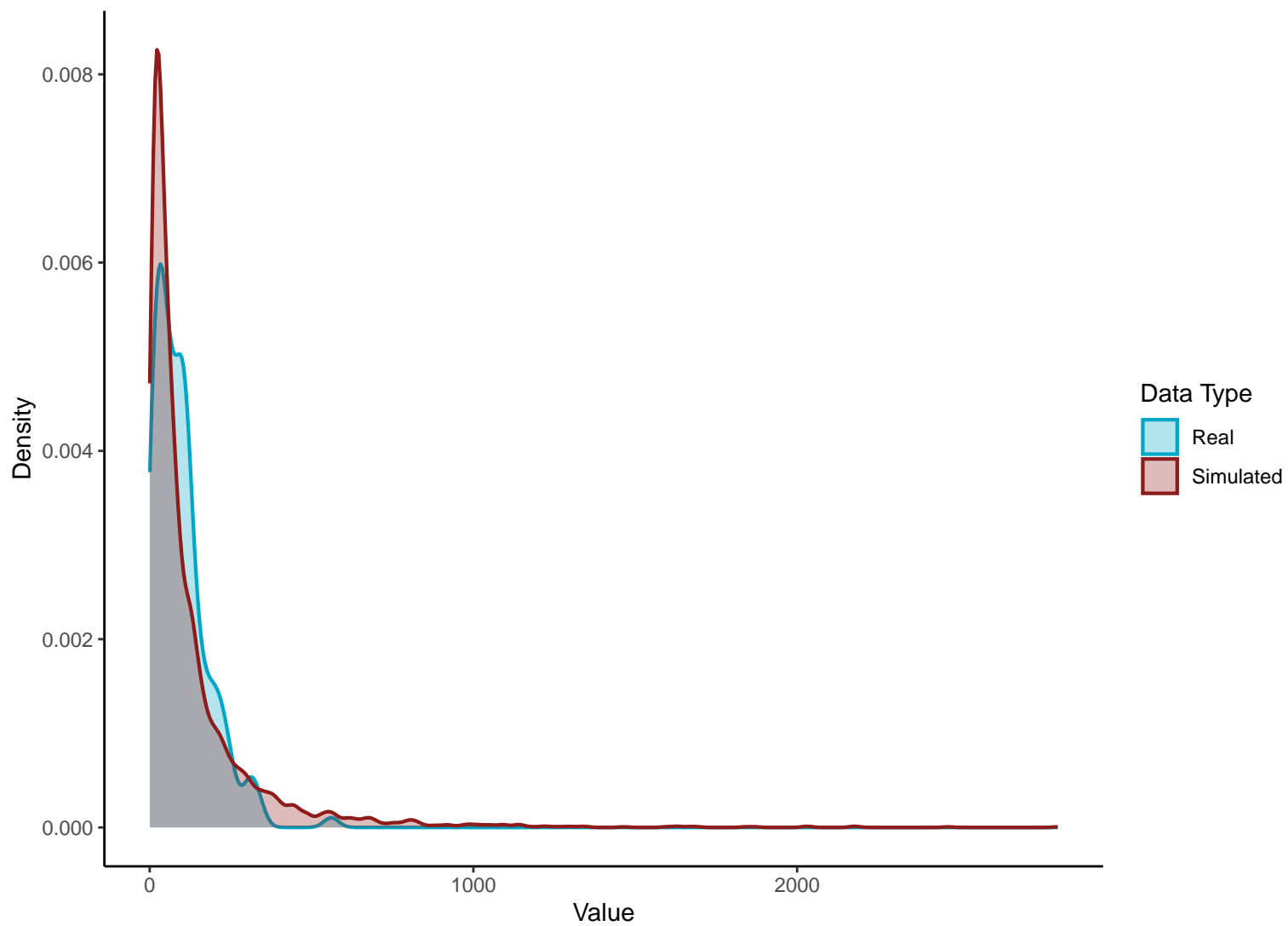
Anaerovibrio



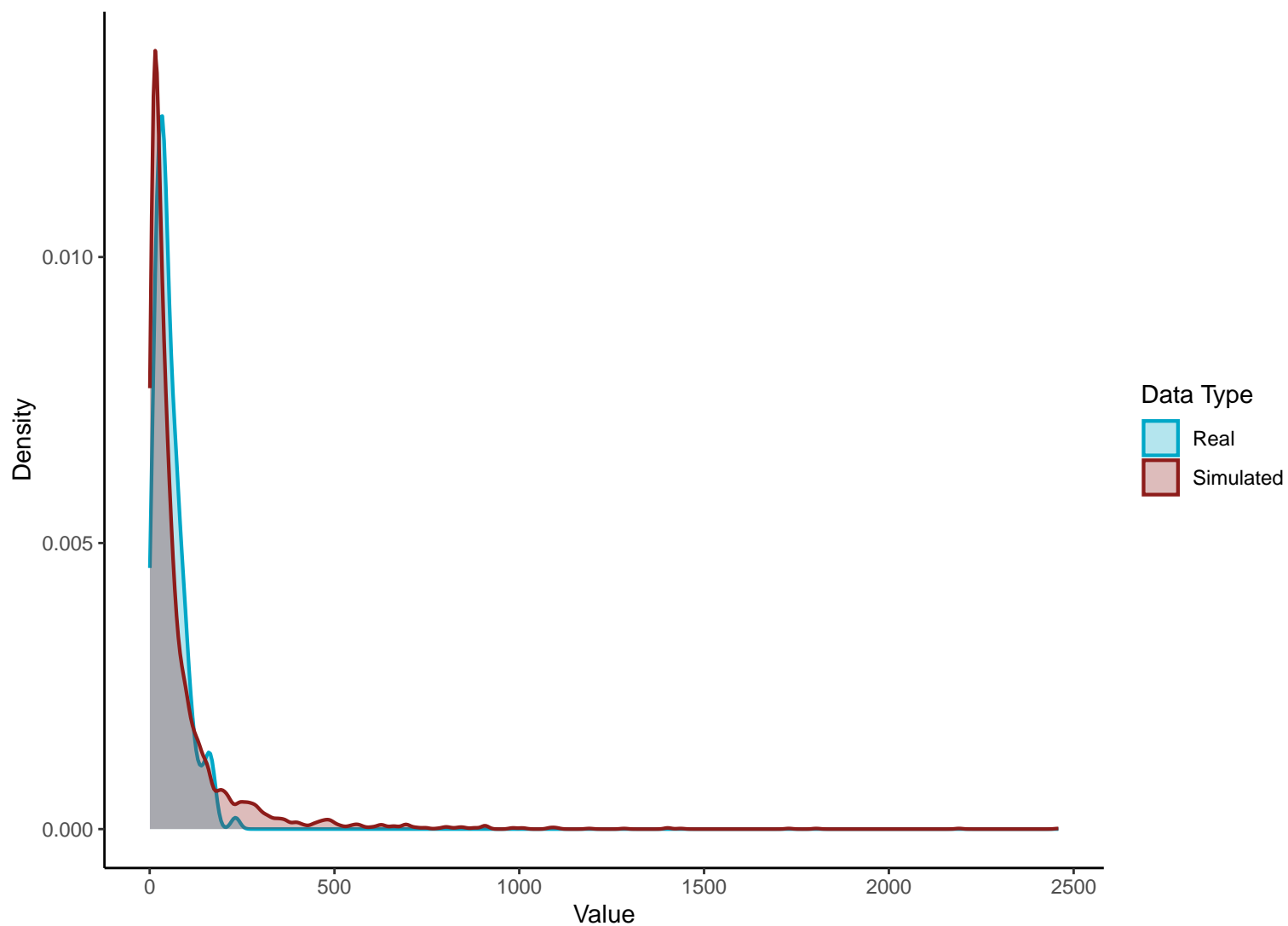
X.Eubacterium..xylanophilum.group



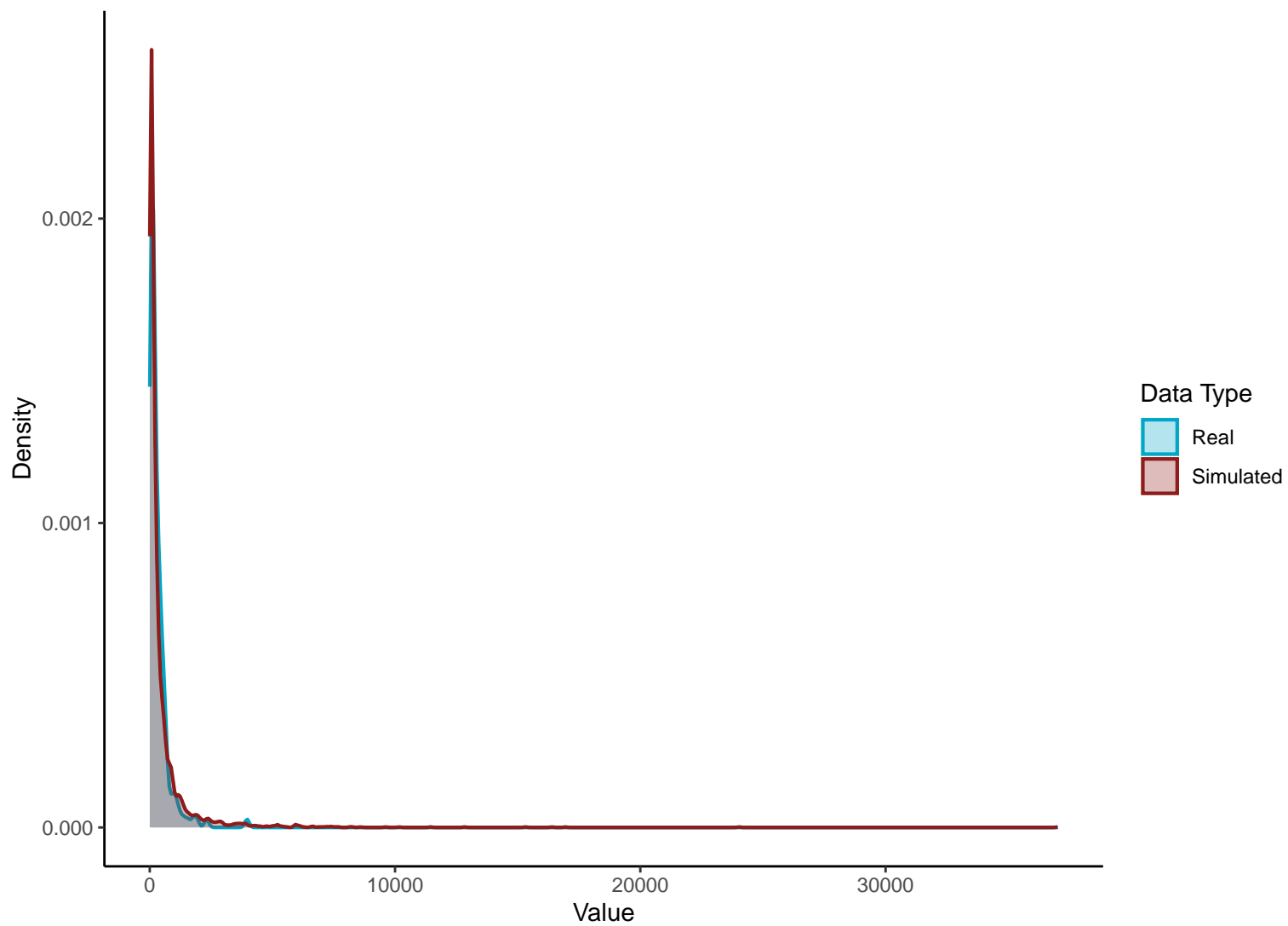
X.Ruminococcus..torques.group



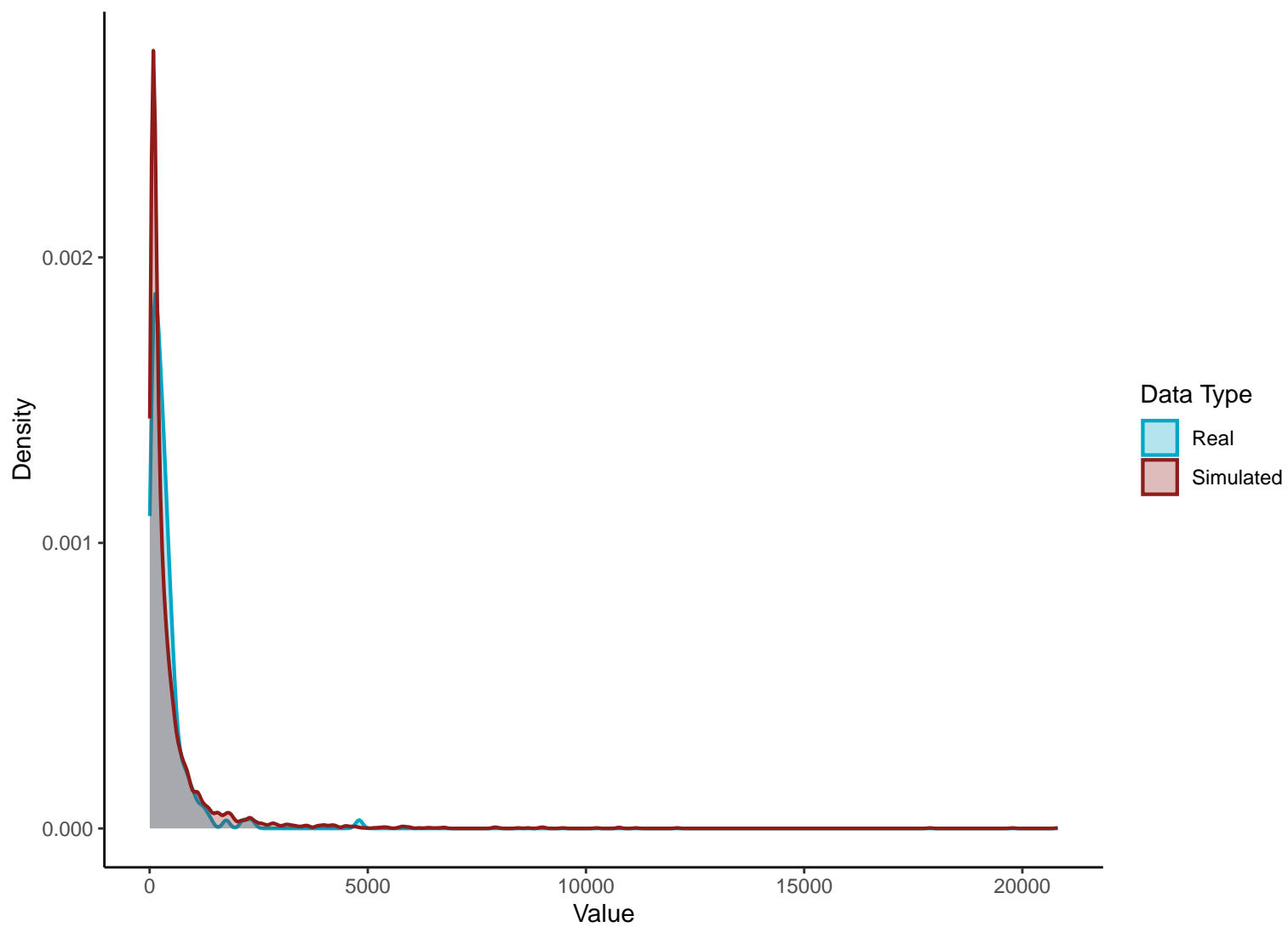
X.Eubacterium..siraeum.group



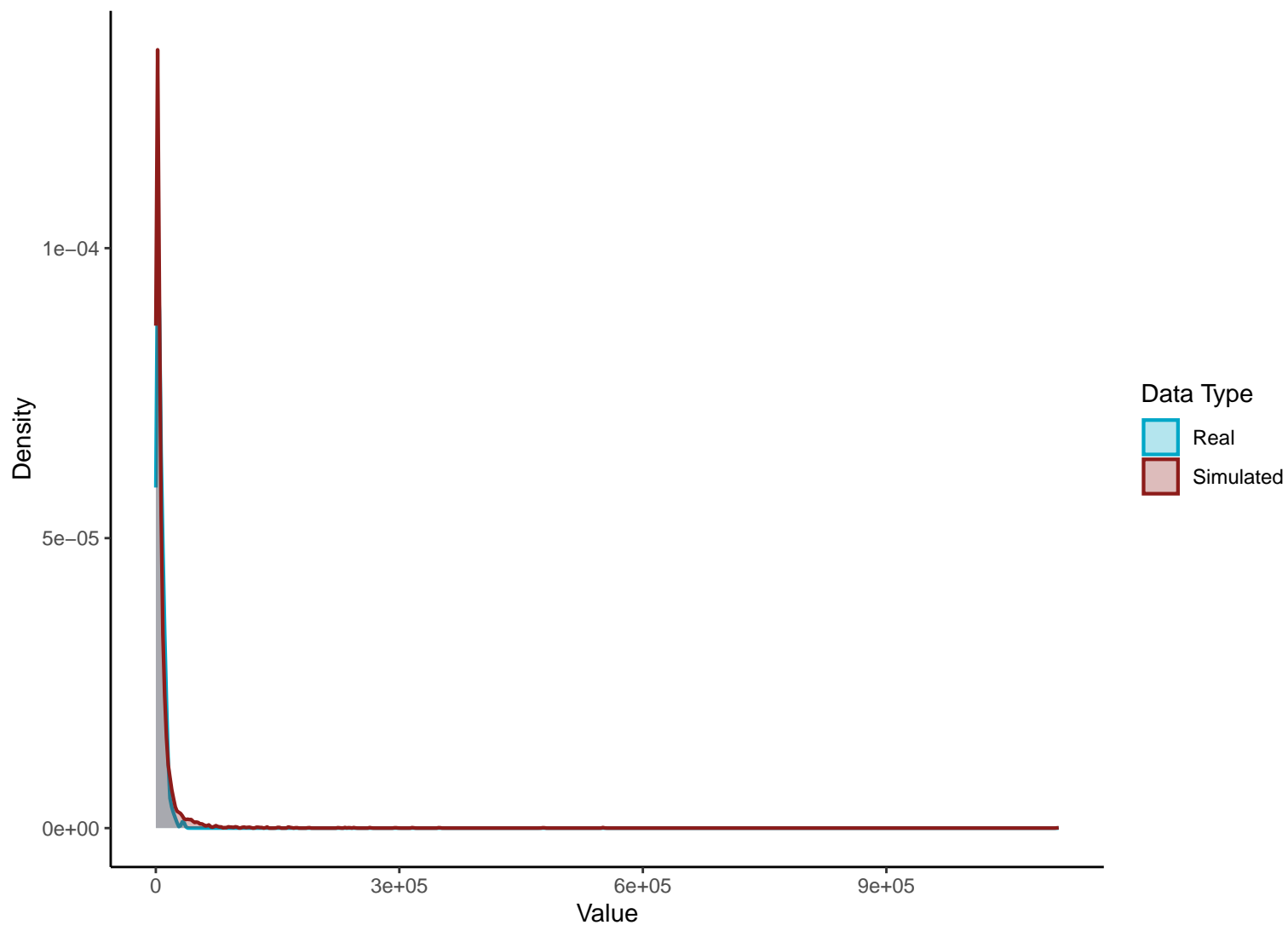
Alloprevotella



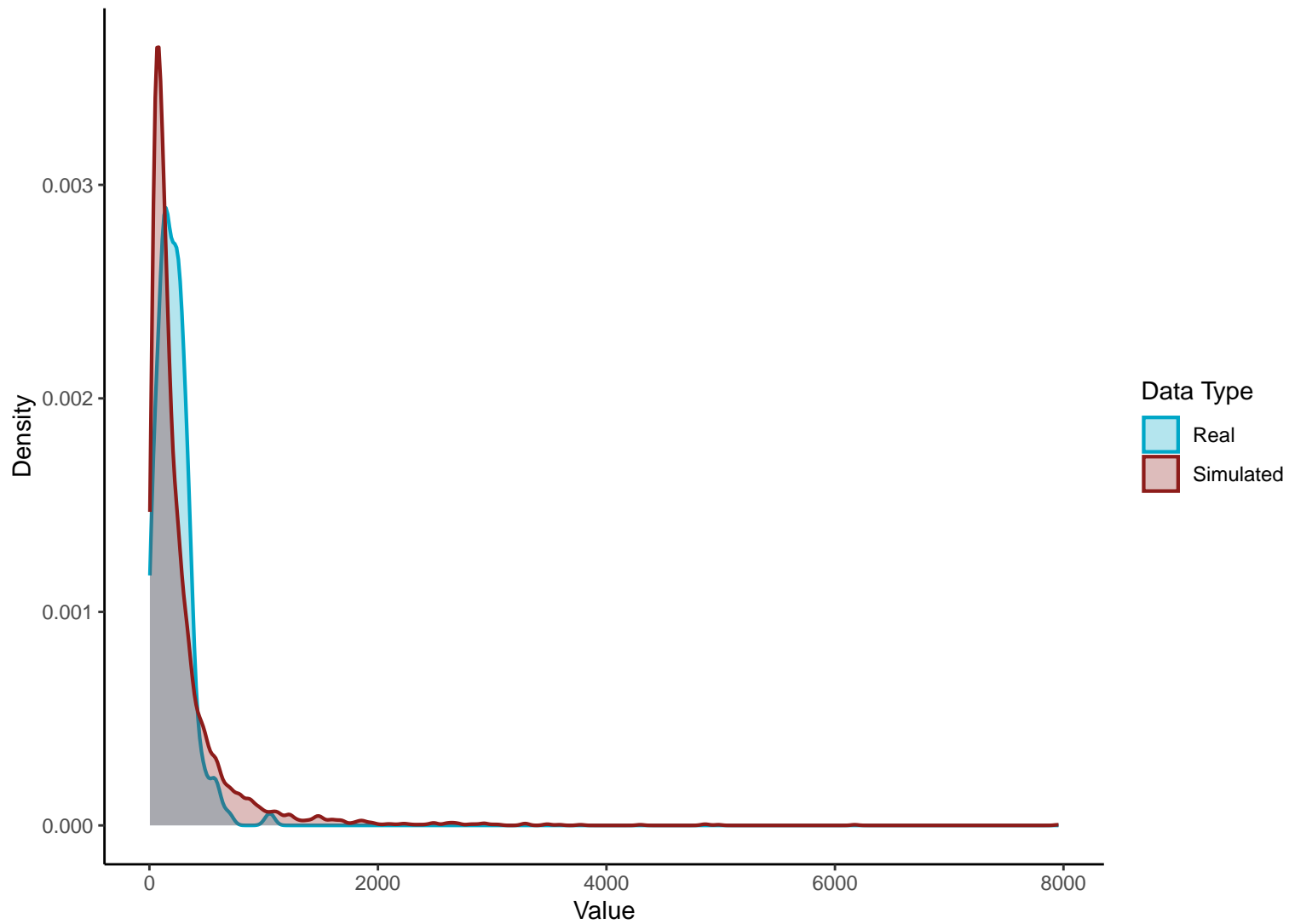
Catenibacterium



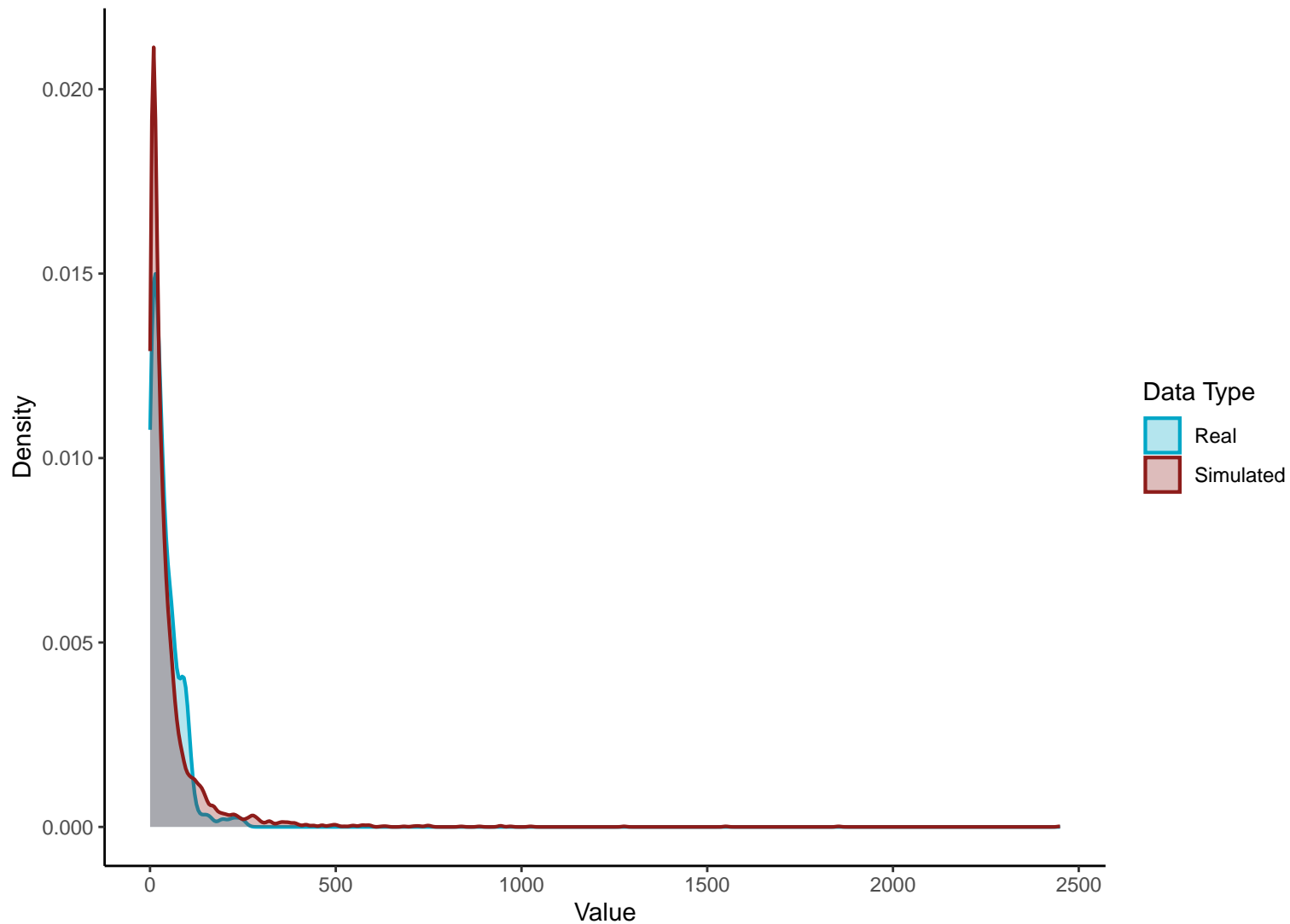
Clostridium.sensu.stricto.1



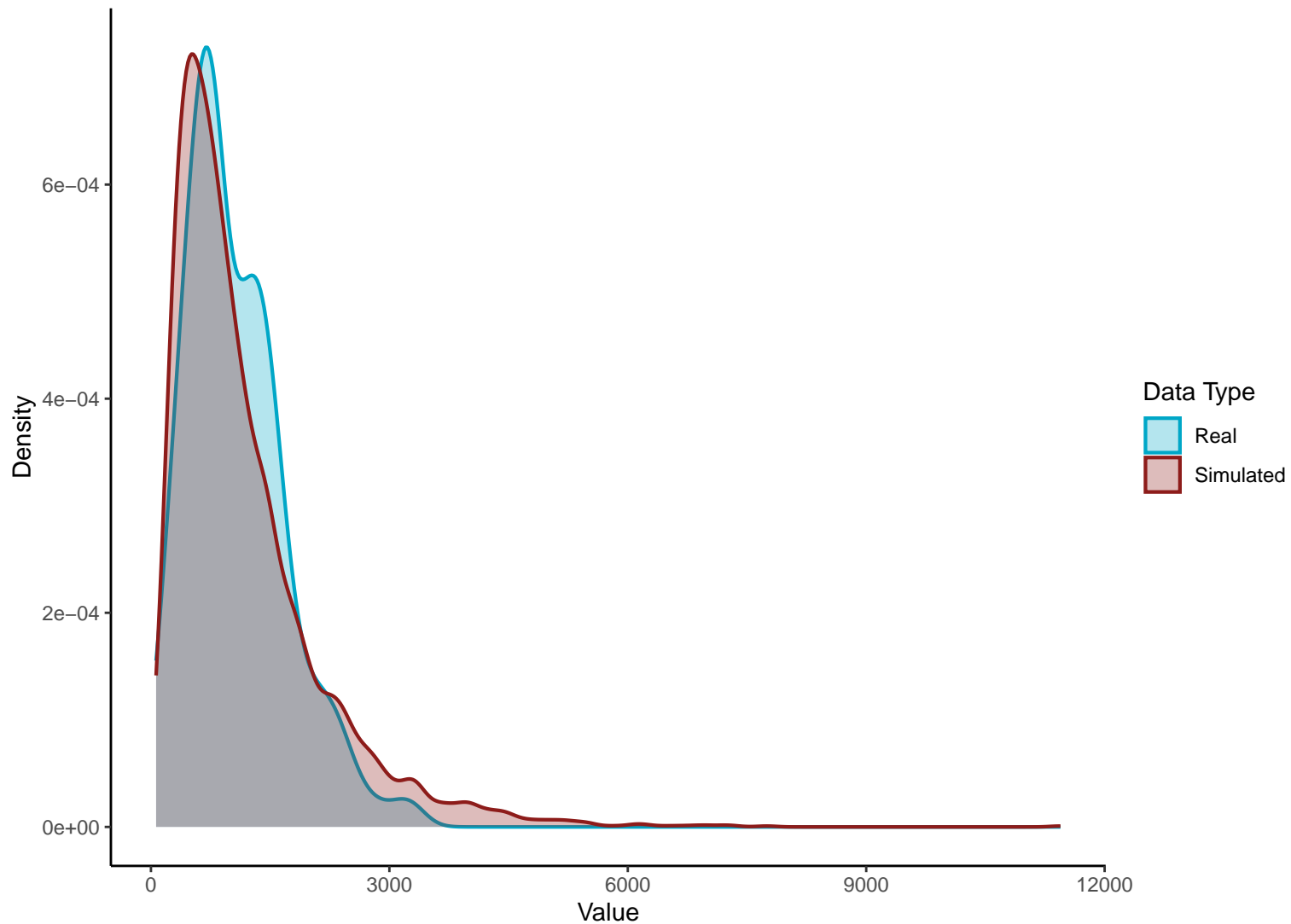
Butyrificoccus



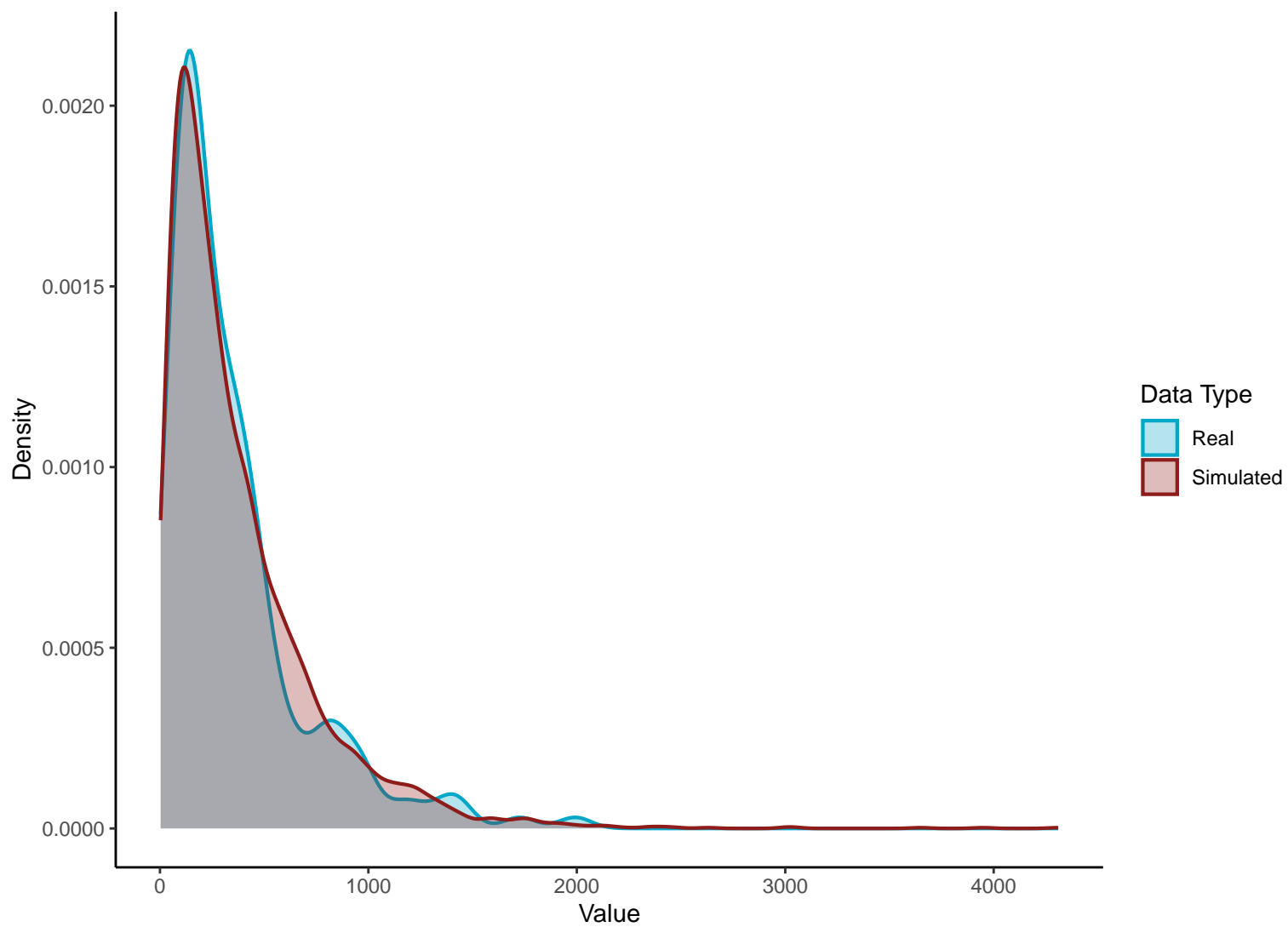
Intestinimonas



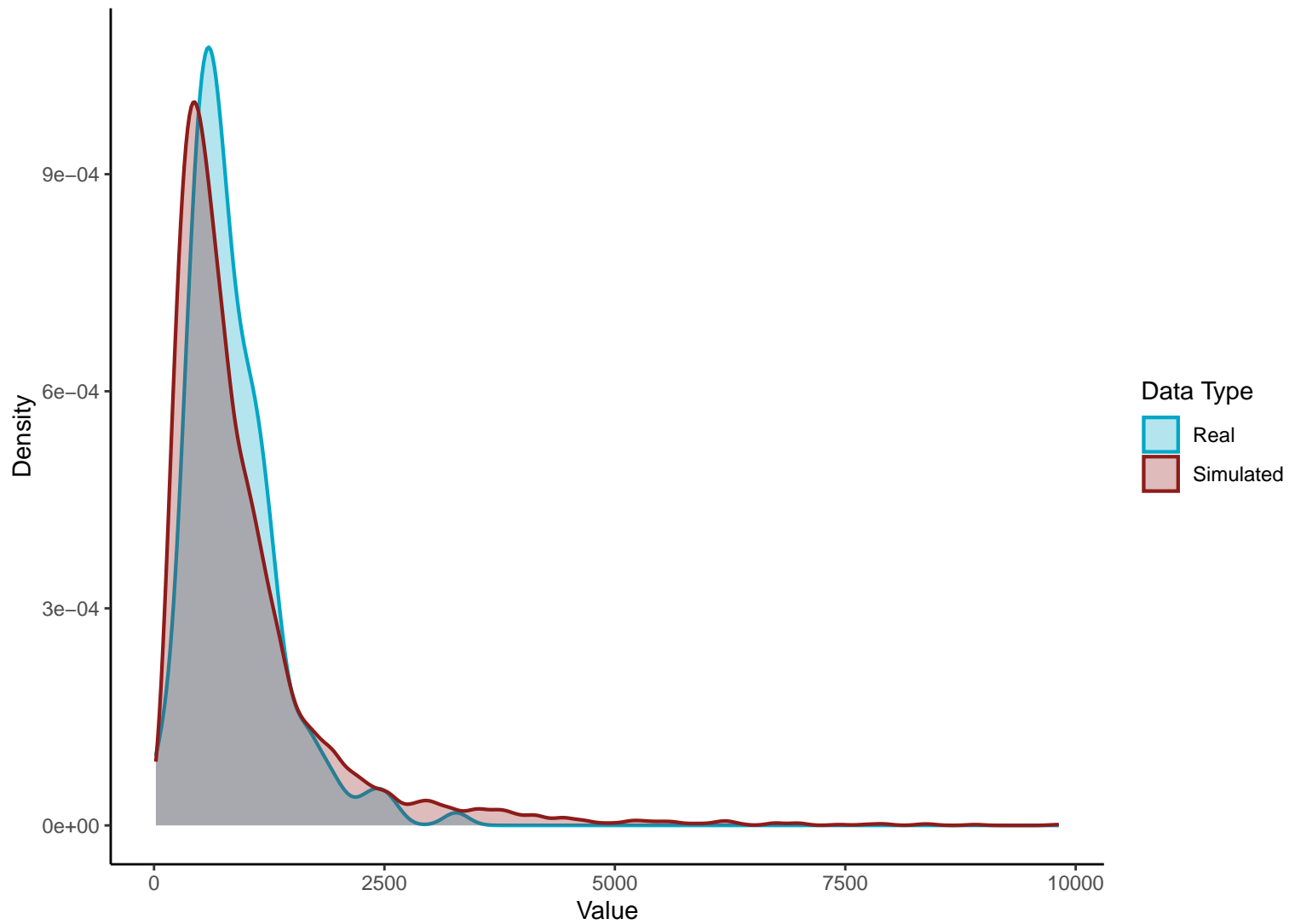
Subdoligranulum



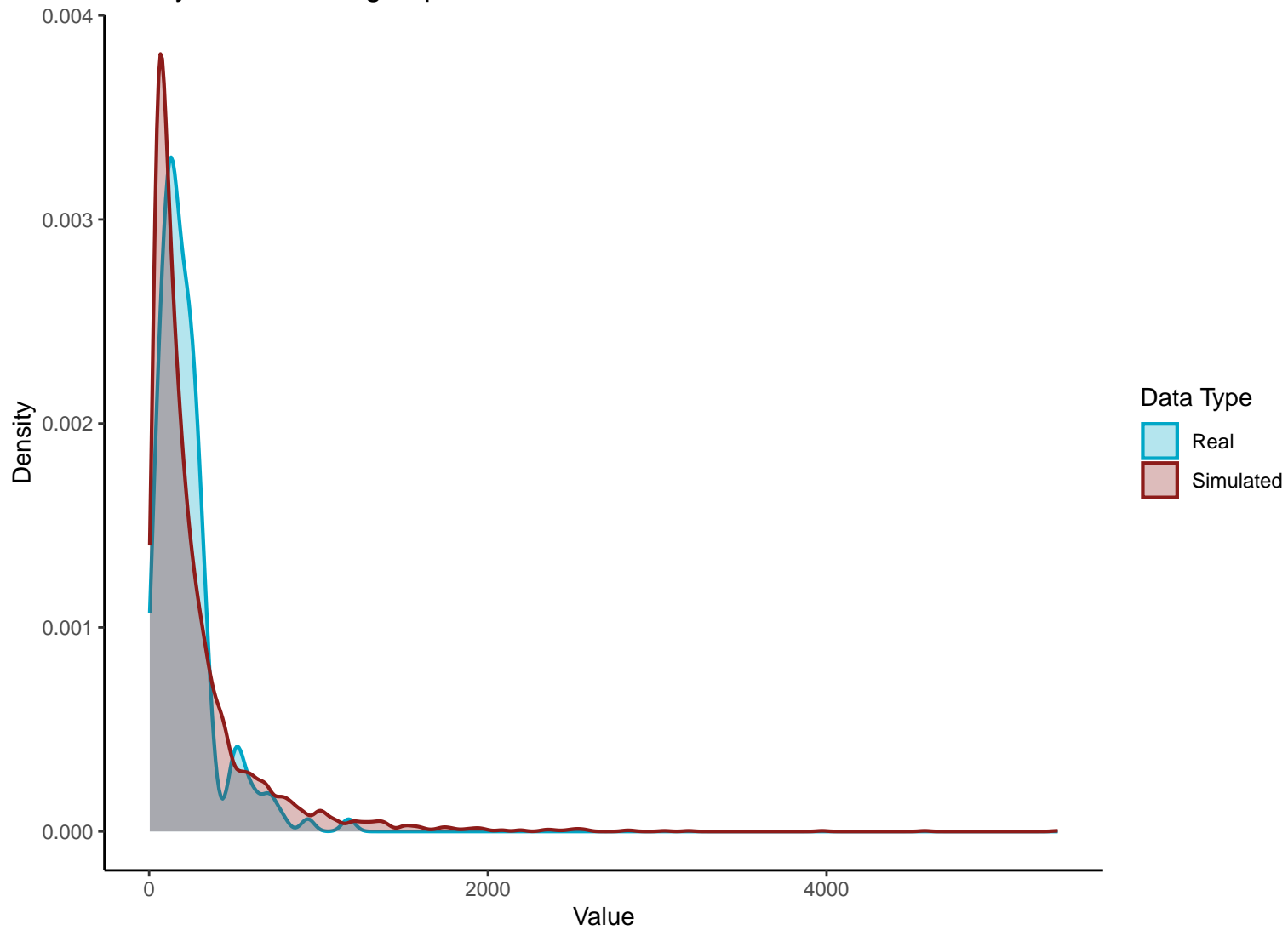
Roseburia



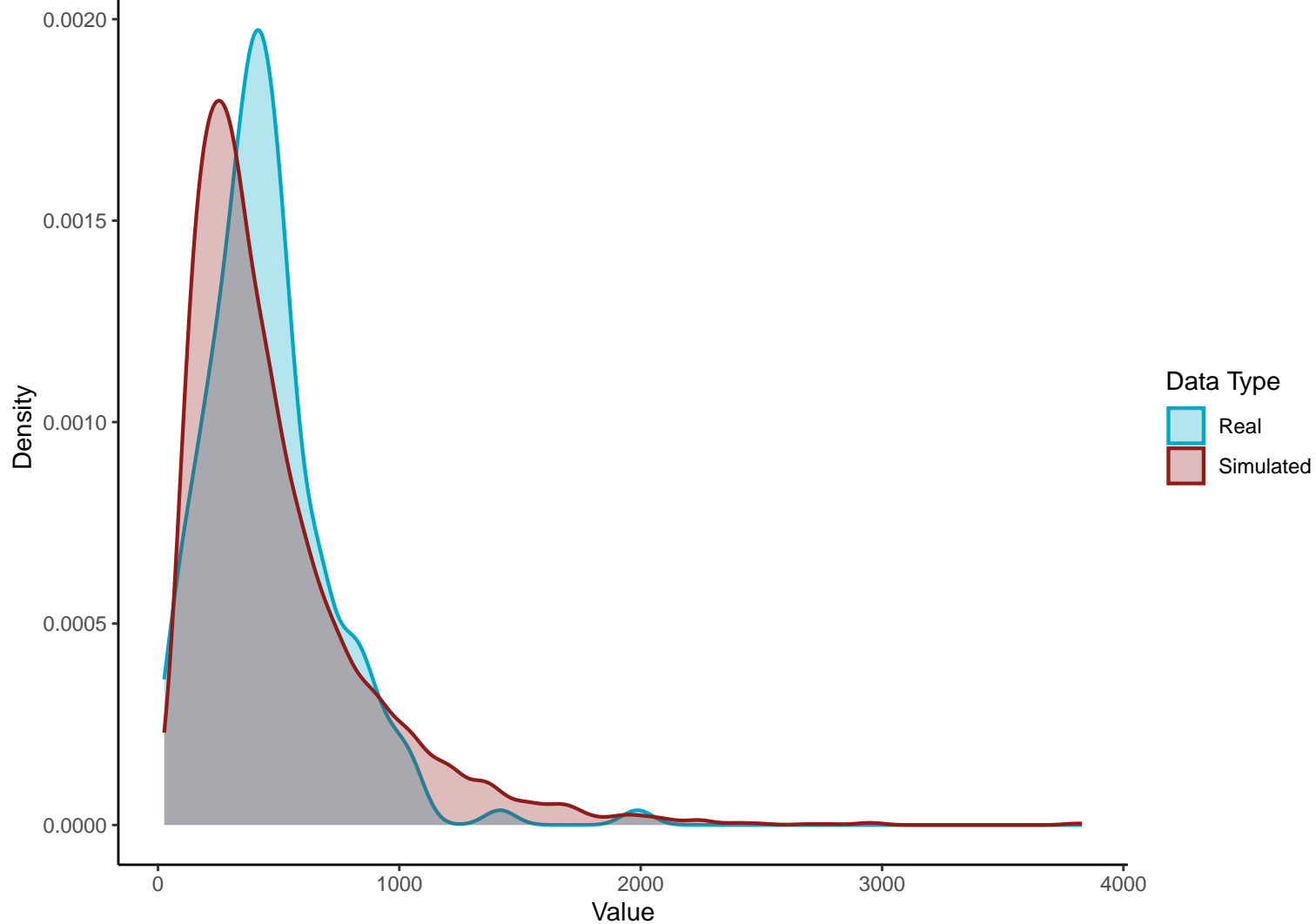
Ruminococcus



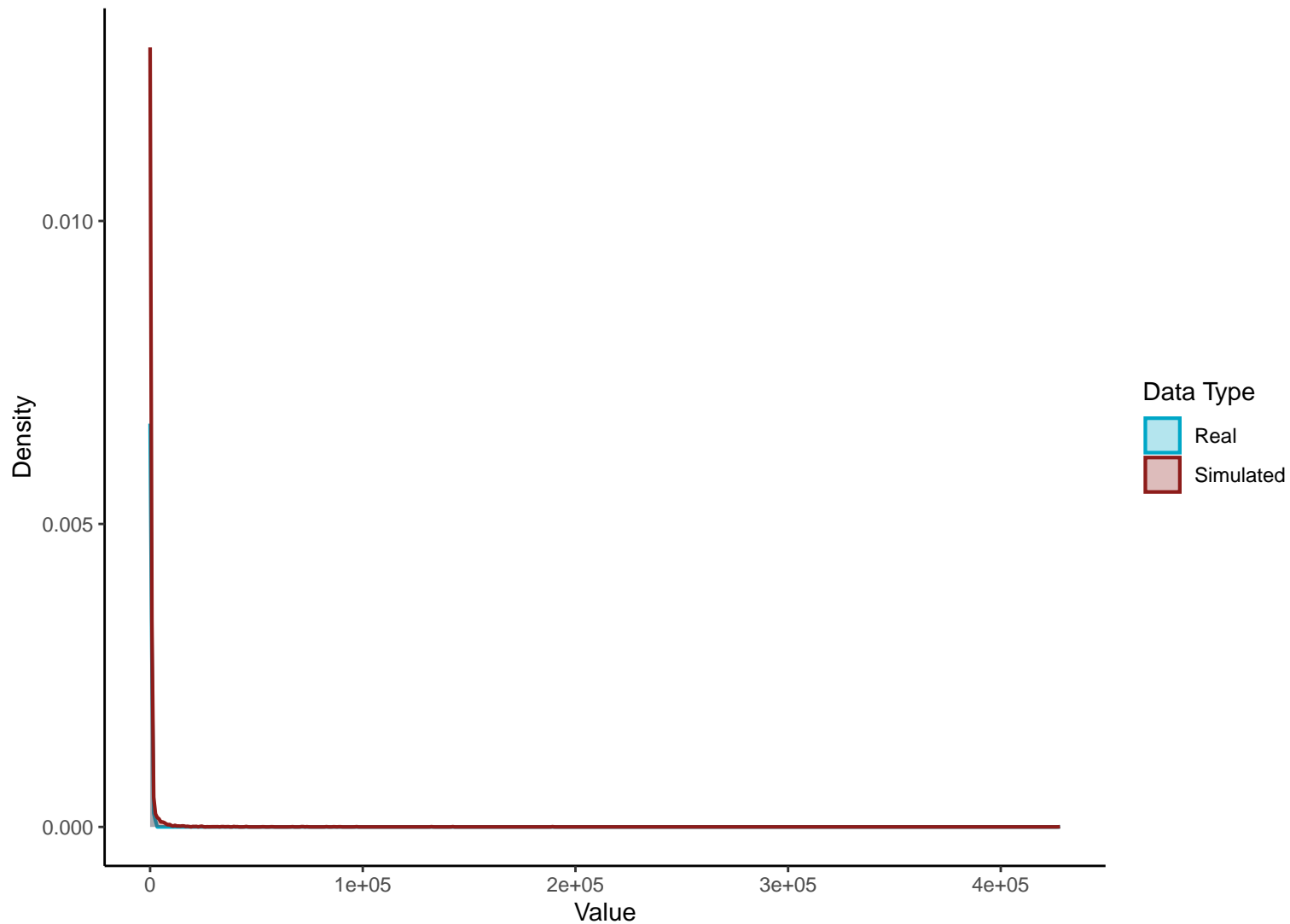
Family.XIII.AD3011.group



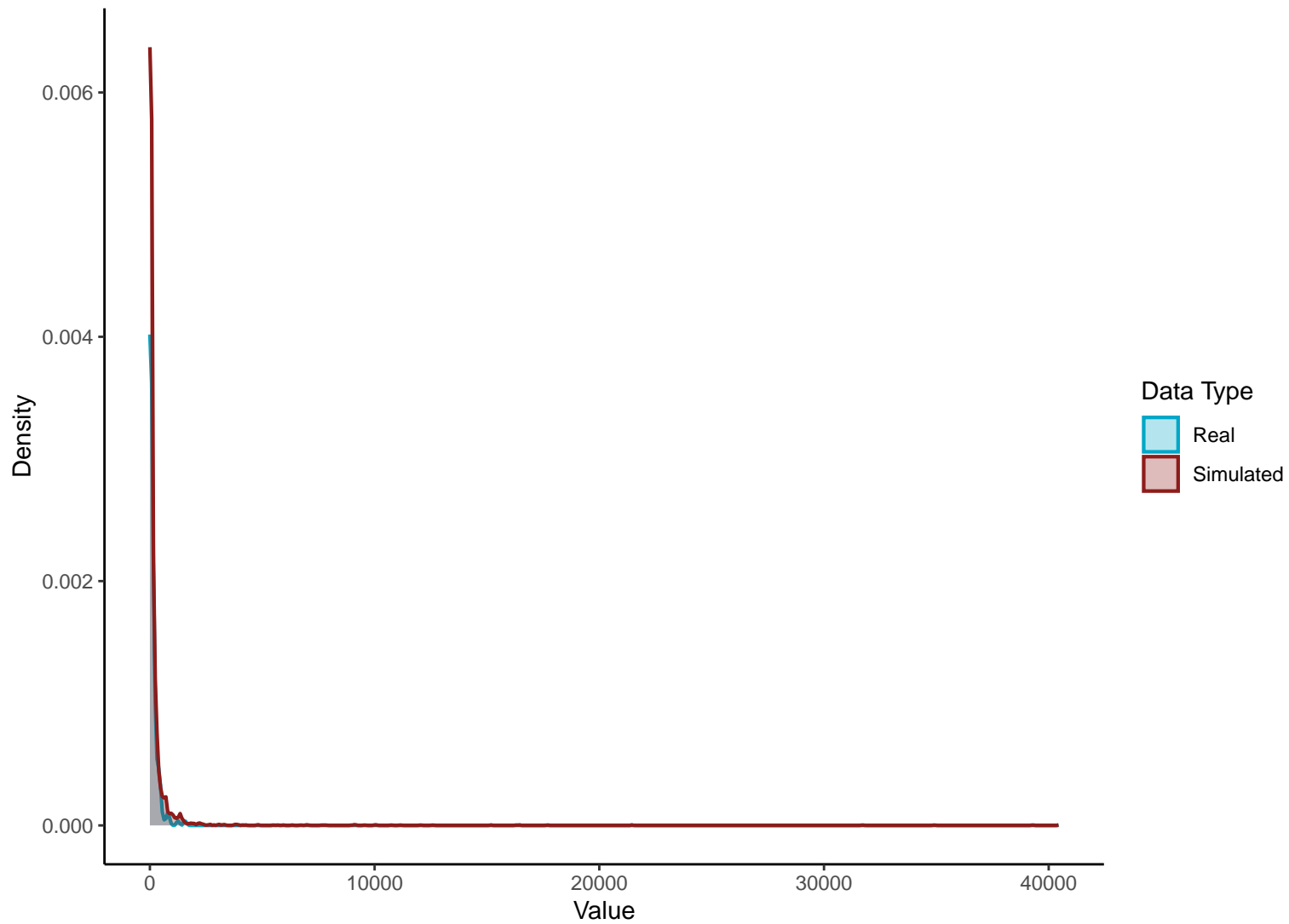
Solobacterium



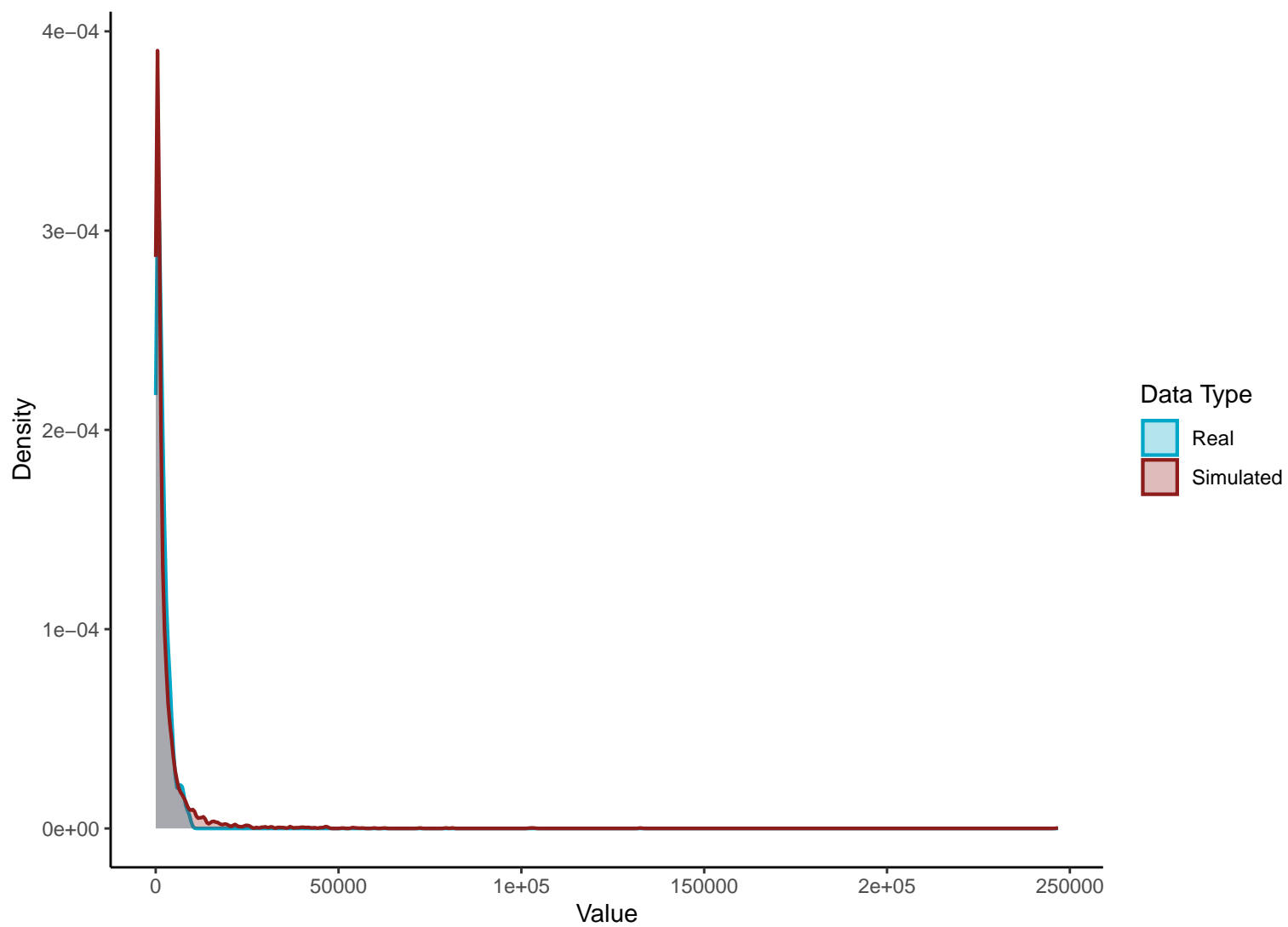
Lachnospiraceae.XPB1014.group



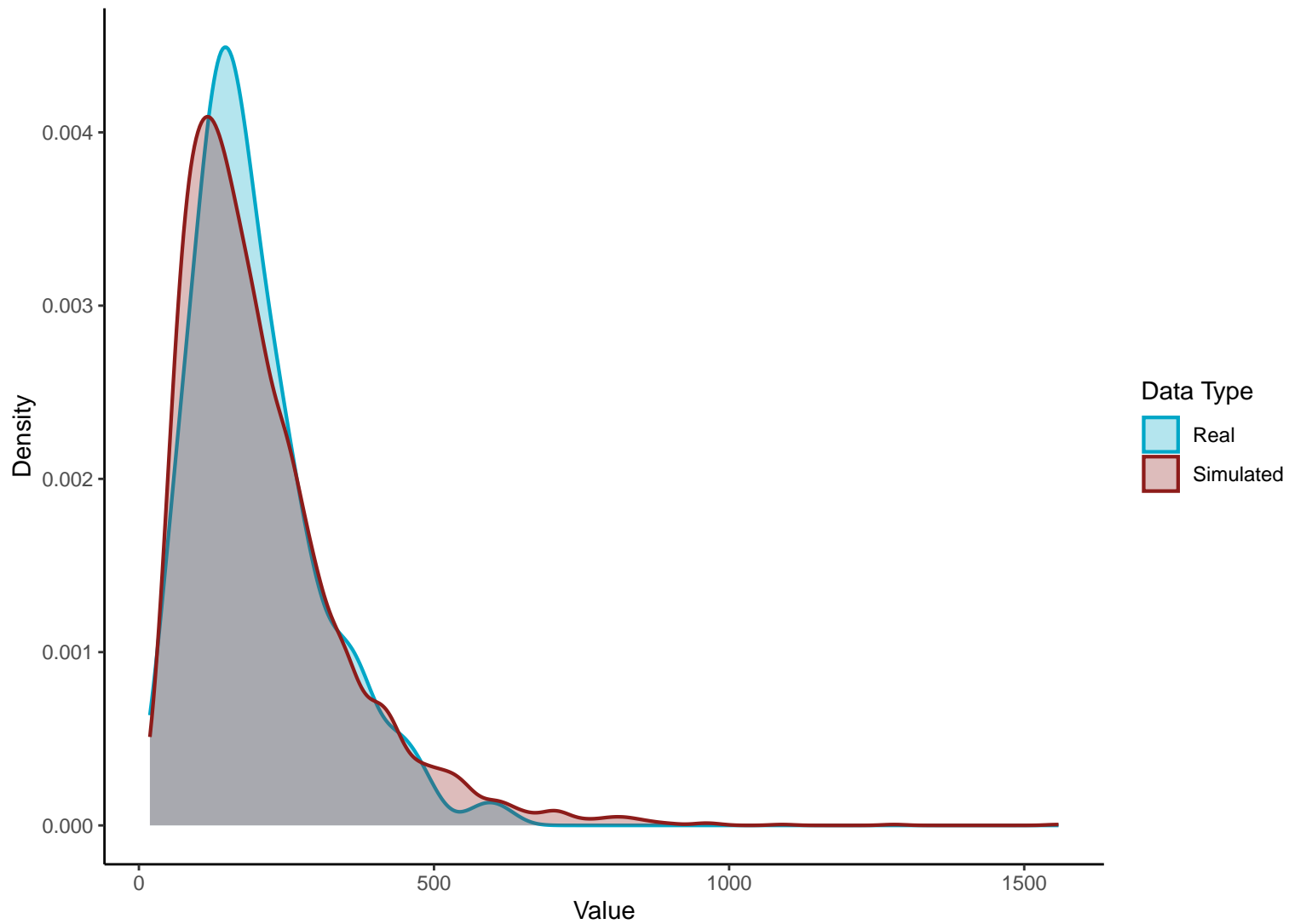
Prevotella_7



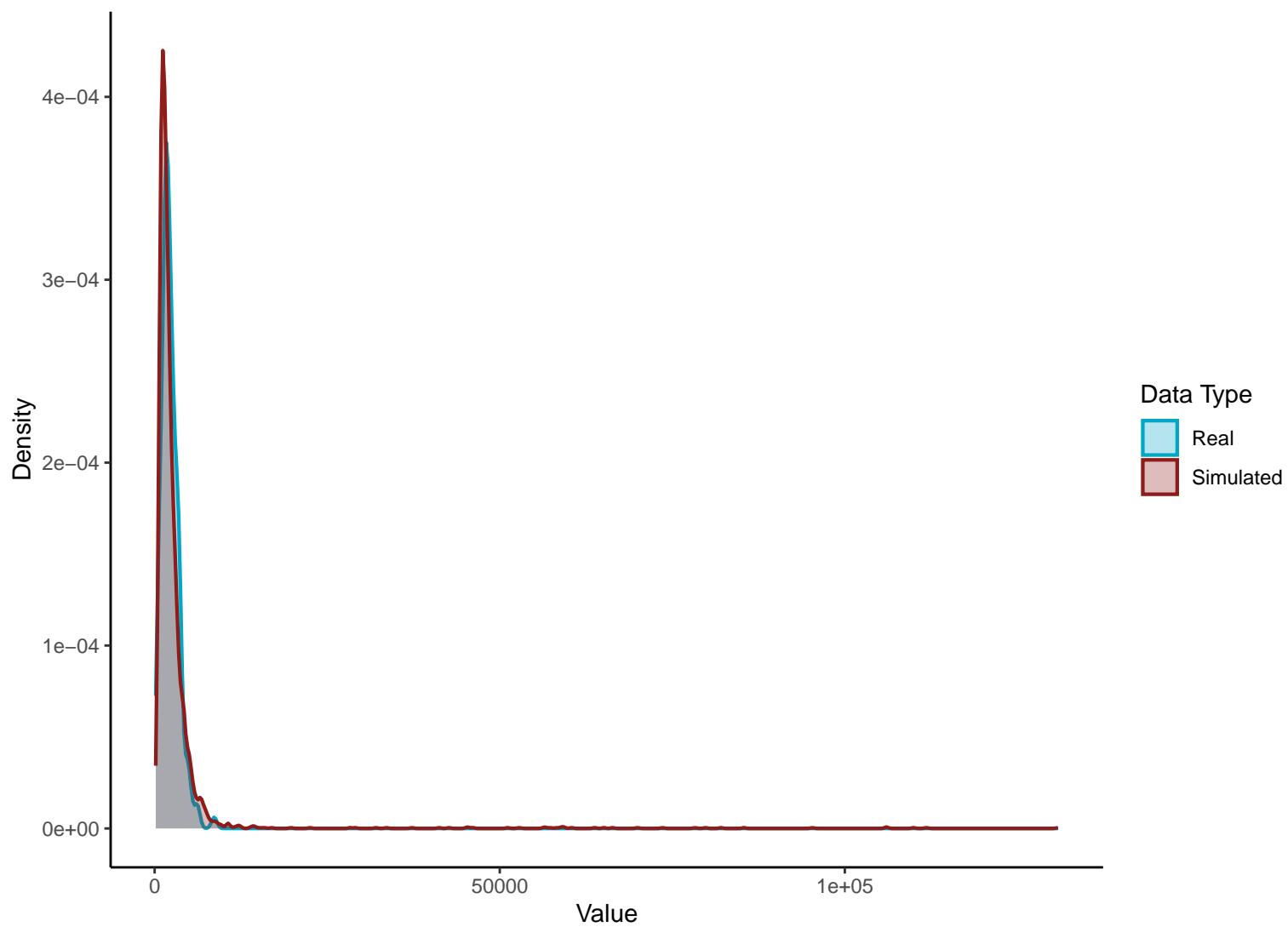
Prevotella_9



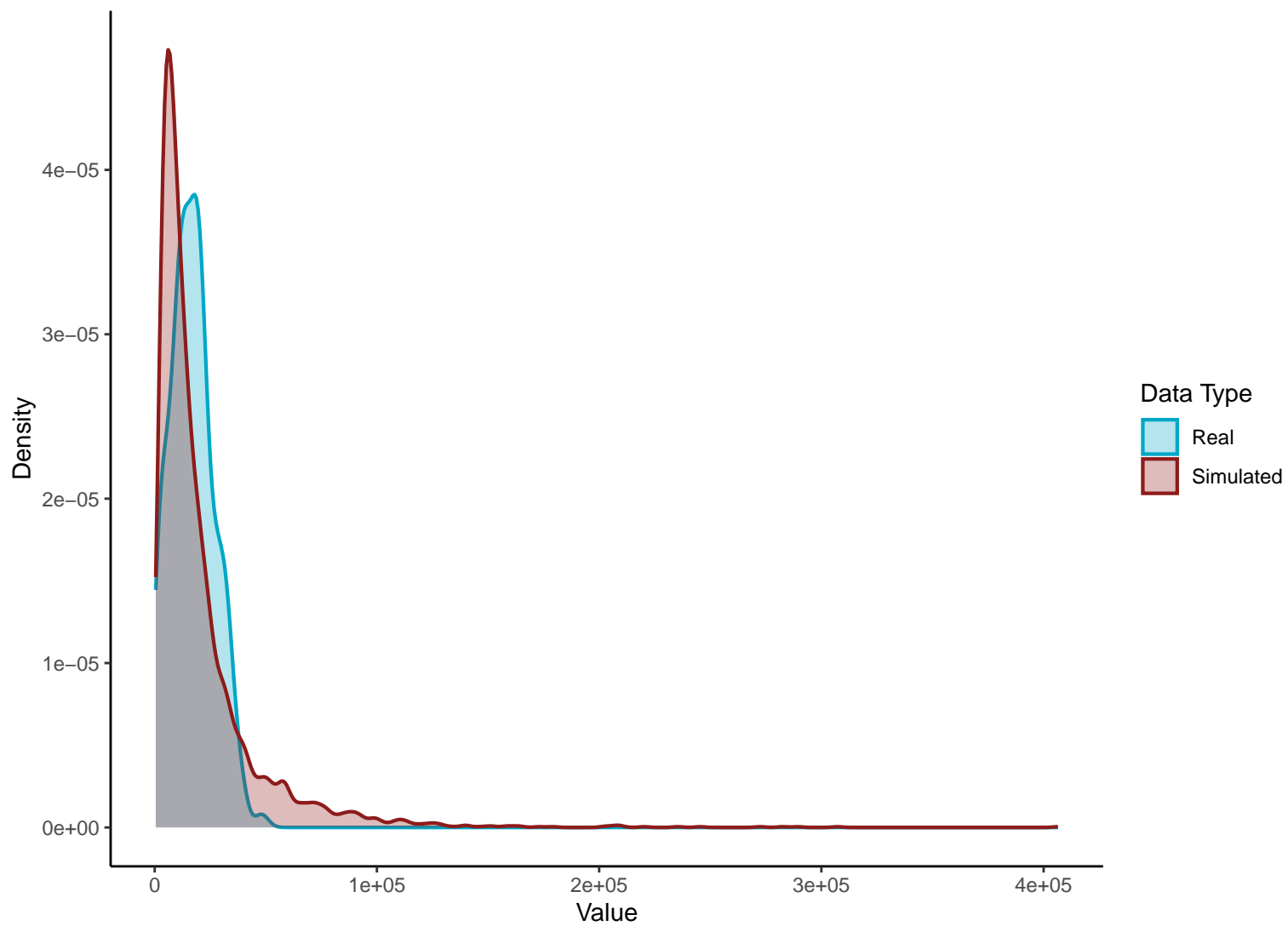
Lachnospiraceae.ND3007.group



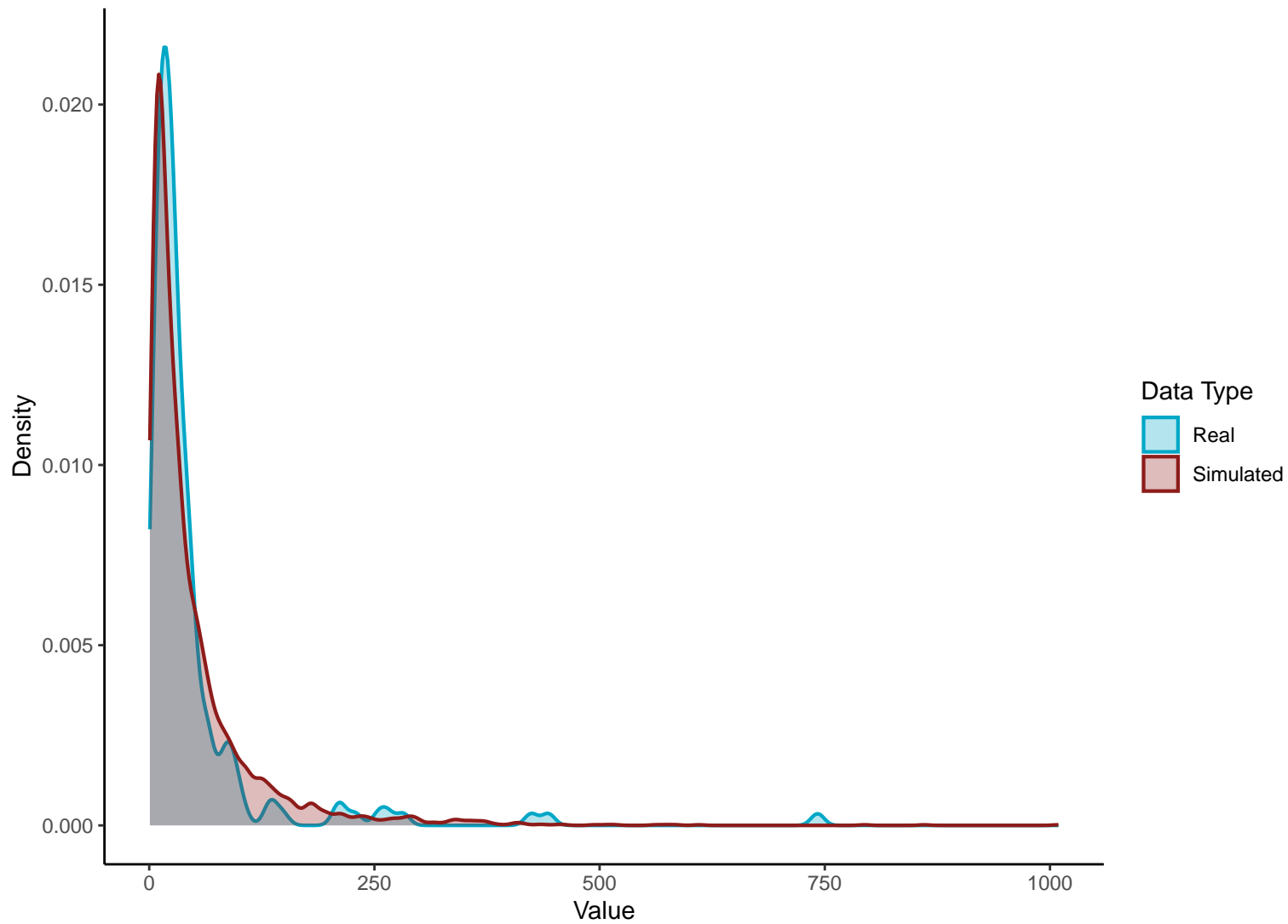
Coproccoccus



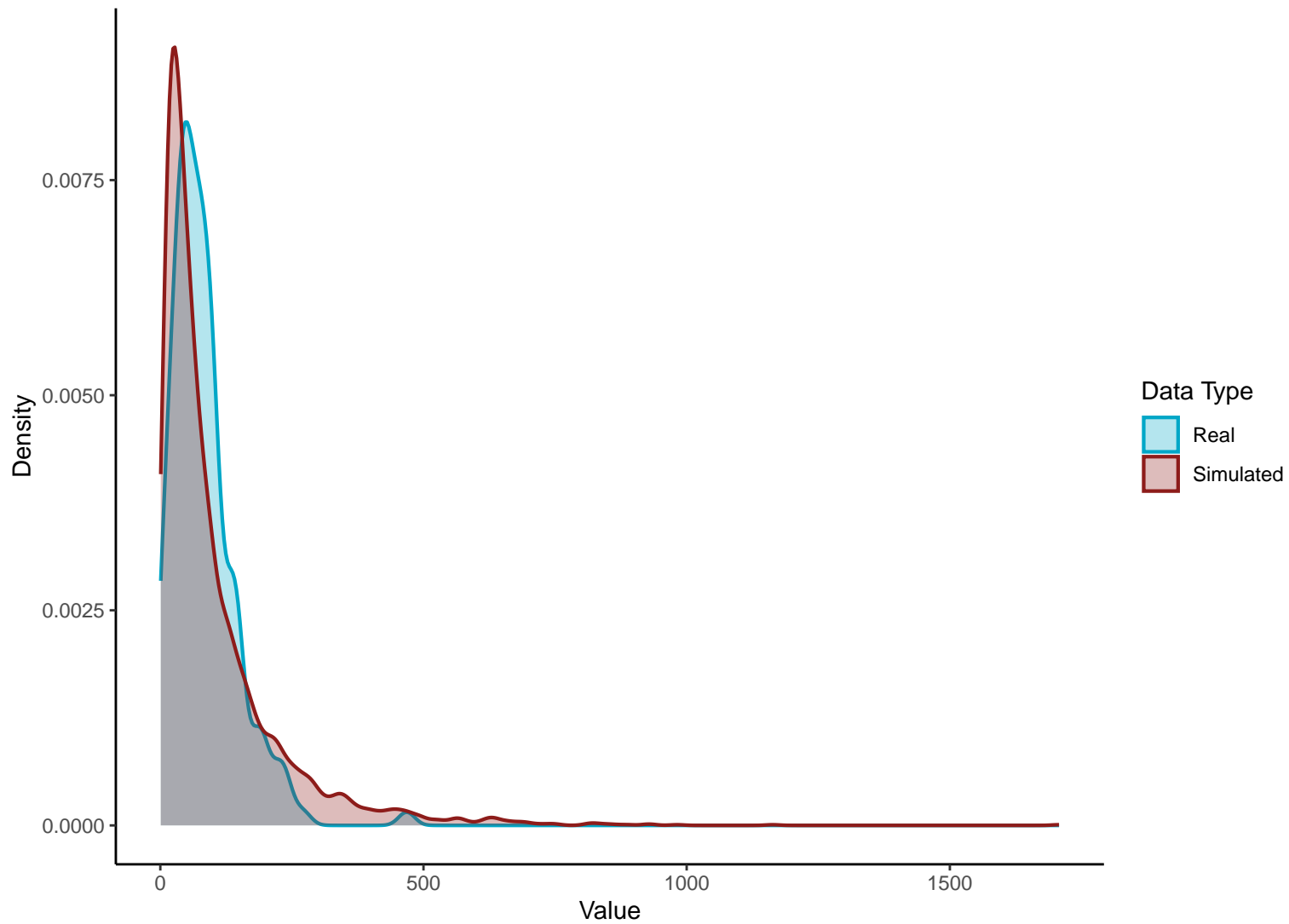
Lactobacillus



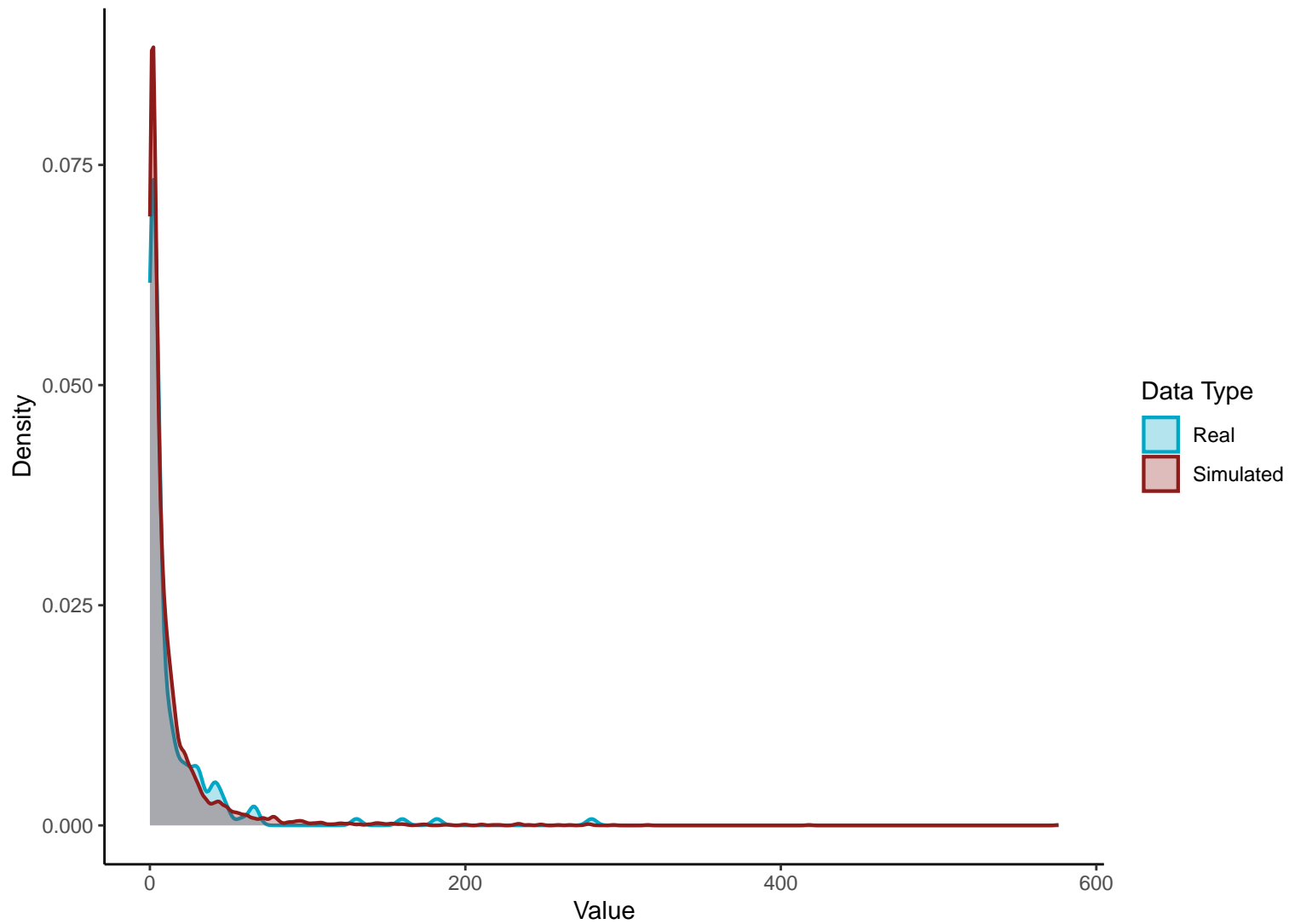
UCG.009



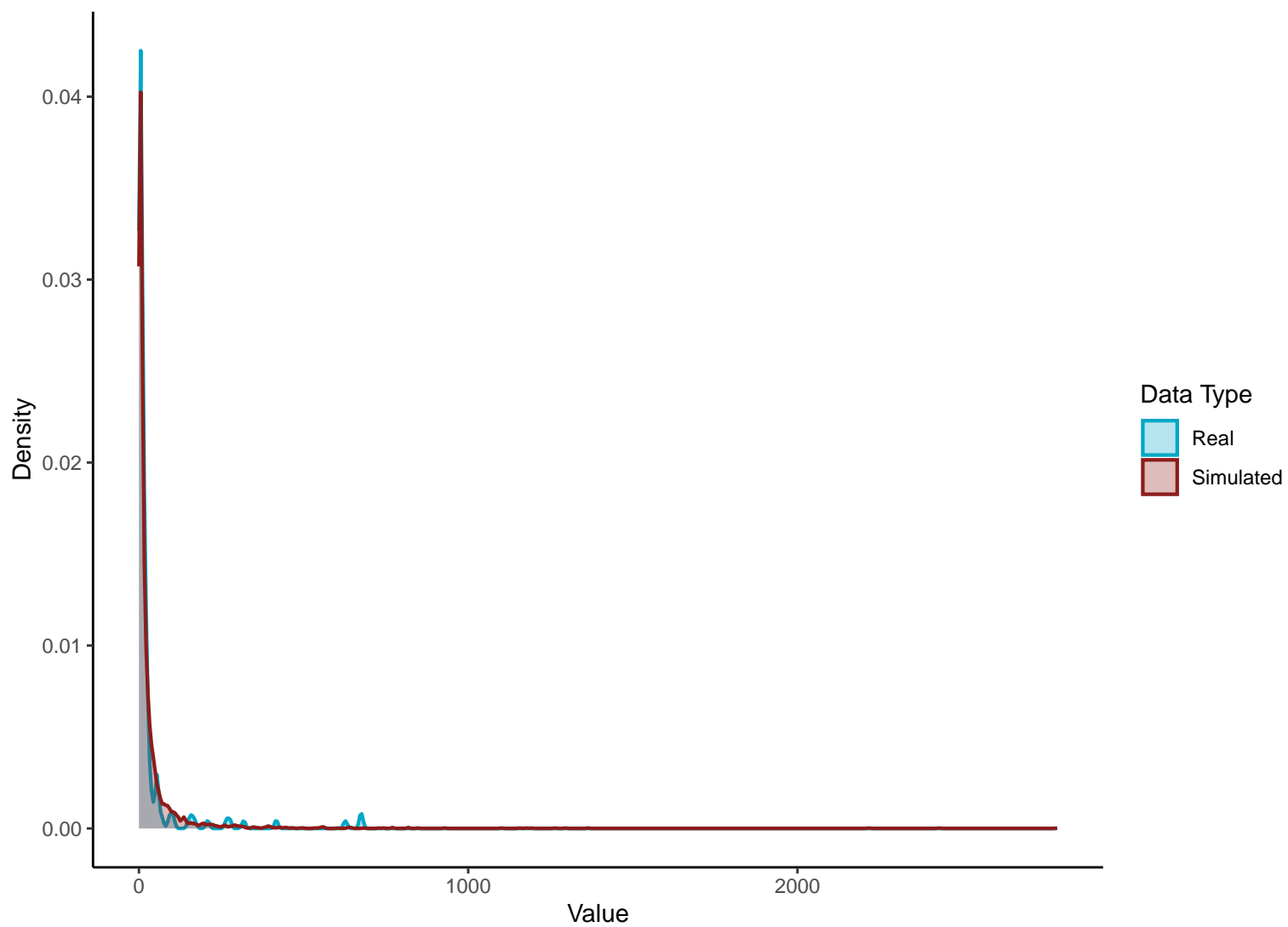
Colidextribacter



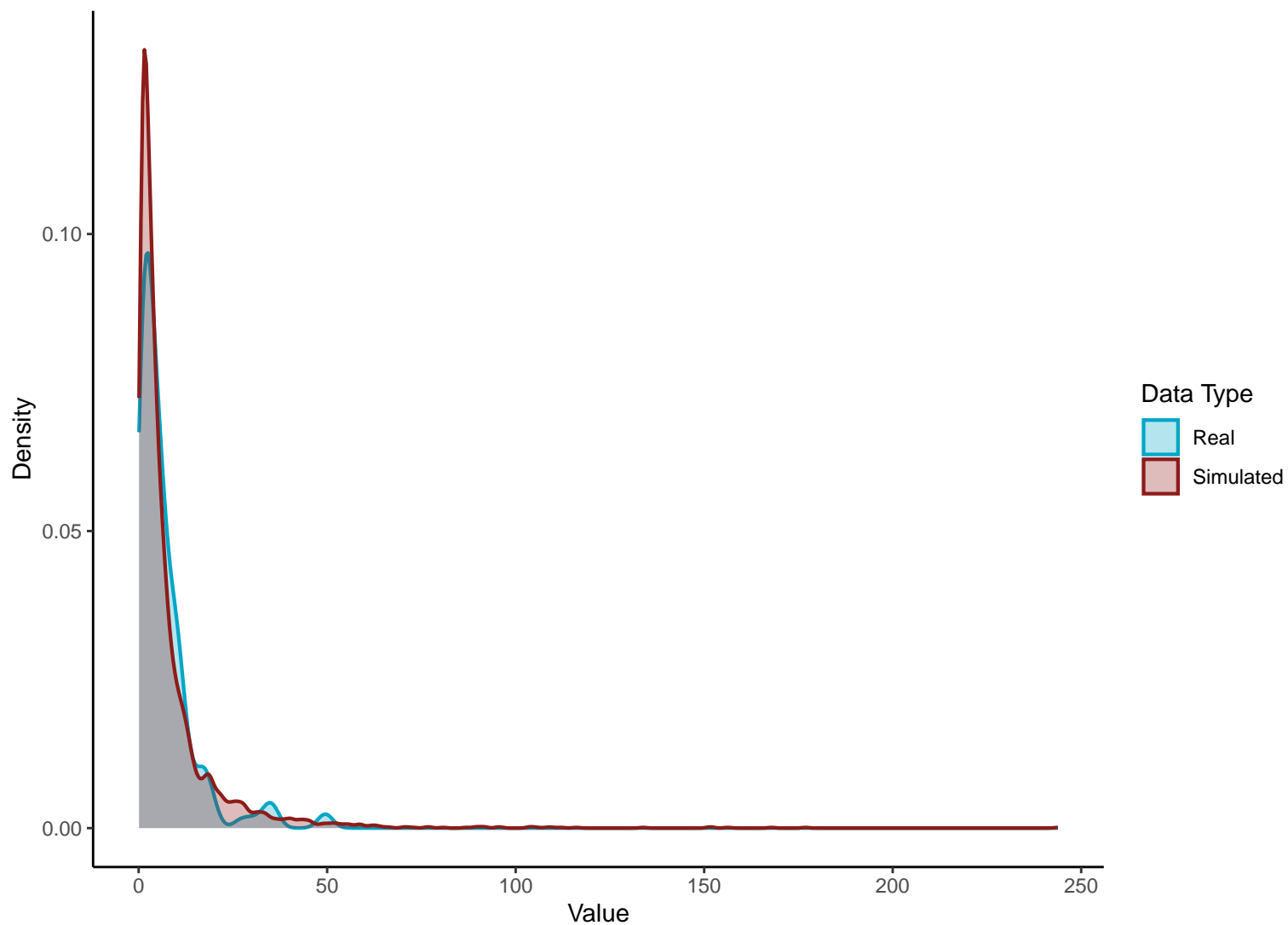
Acidaminococcus



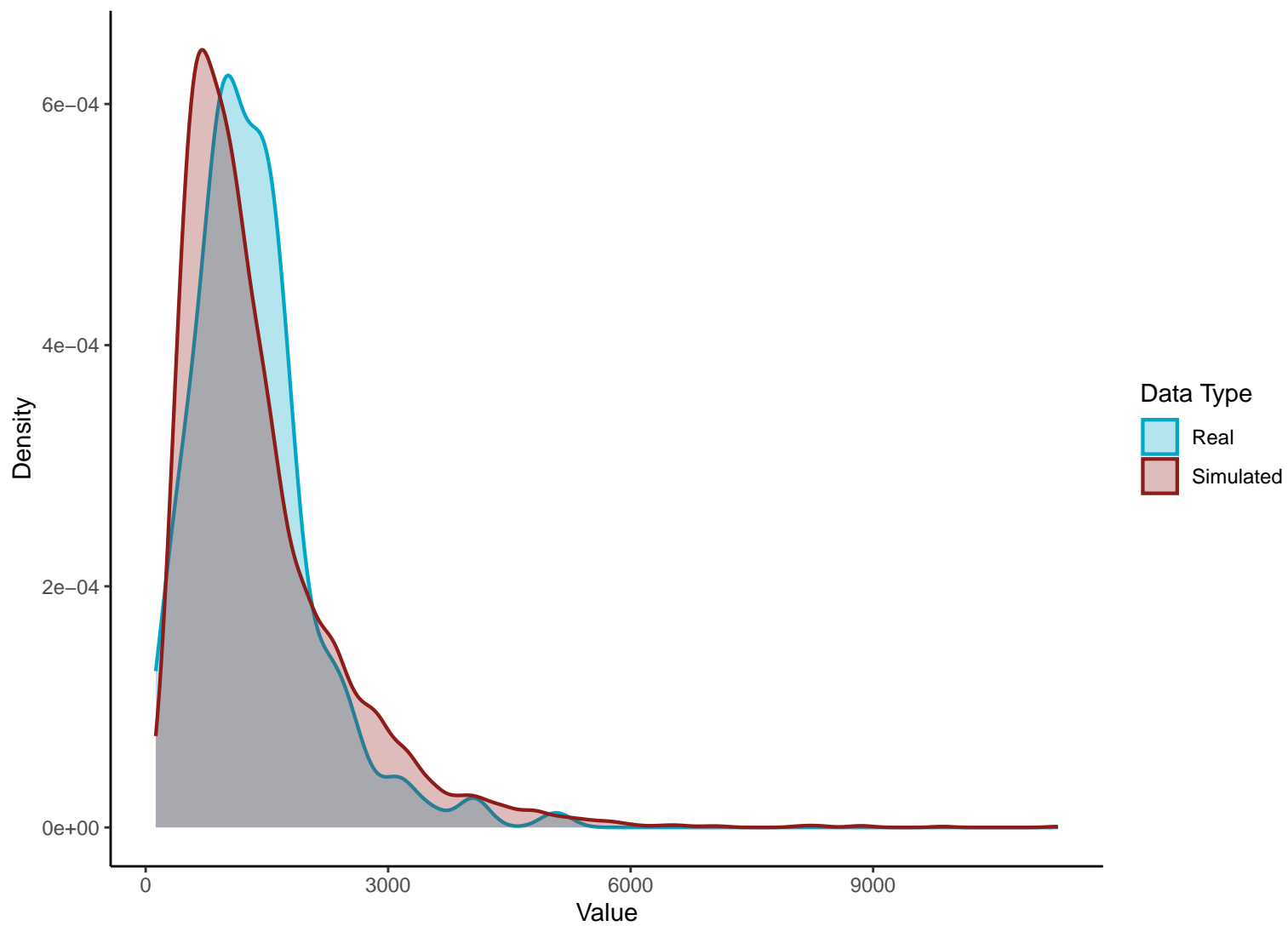
Parabacteroides



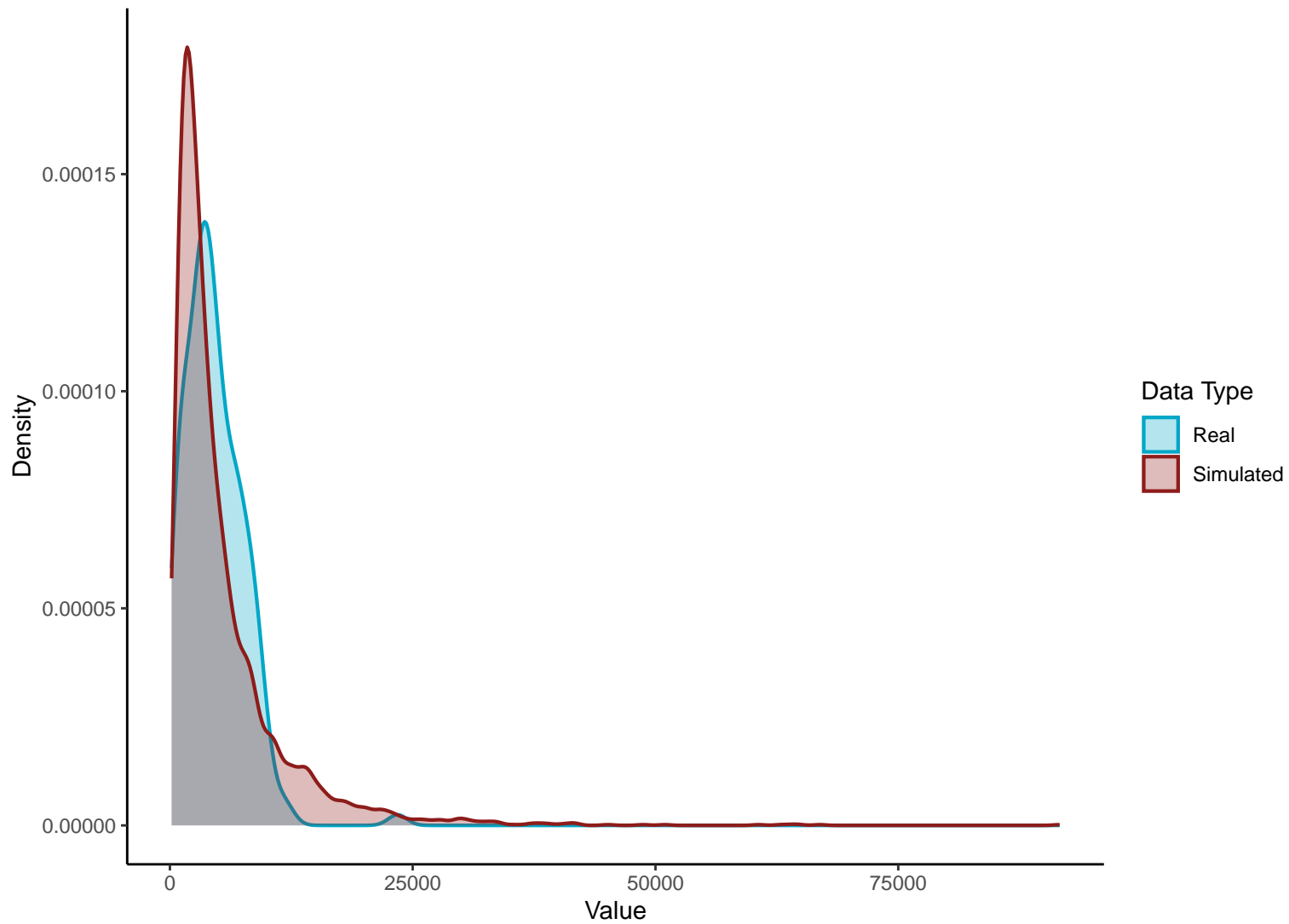
Allisonella



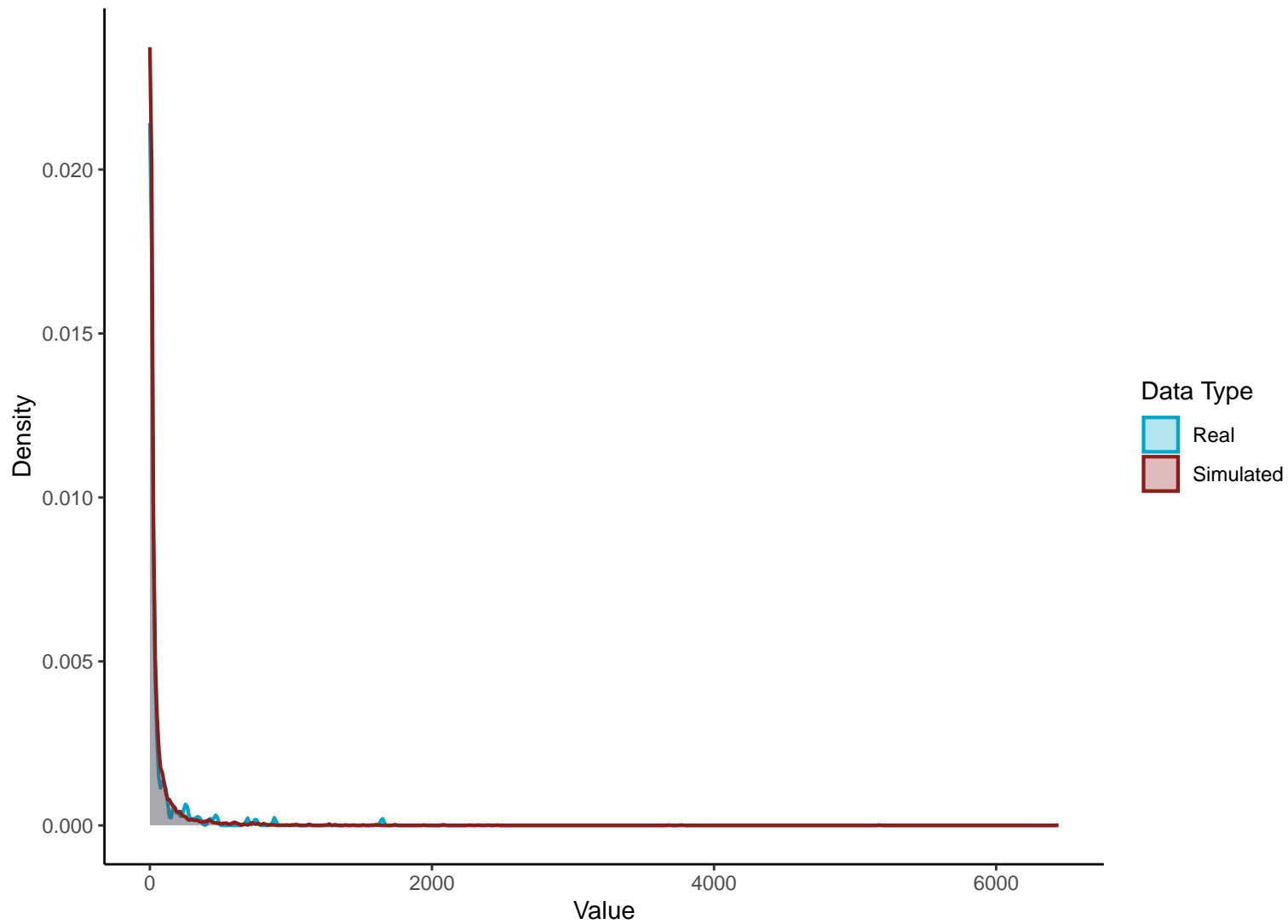
Blautia



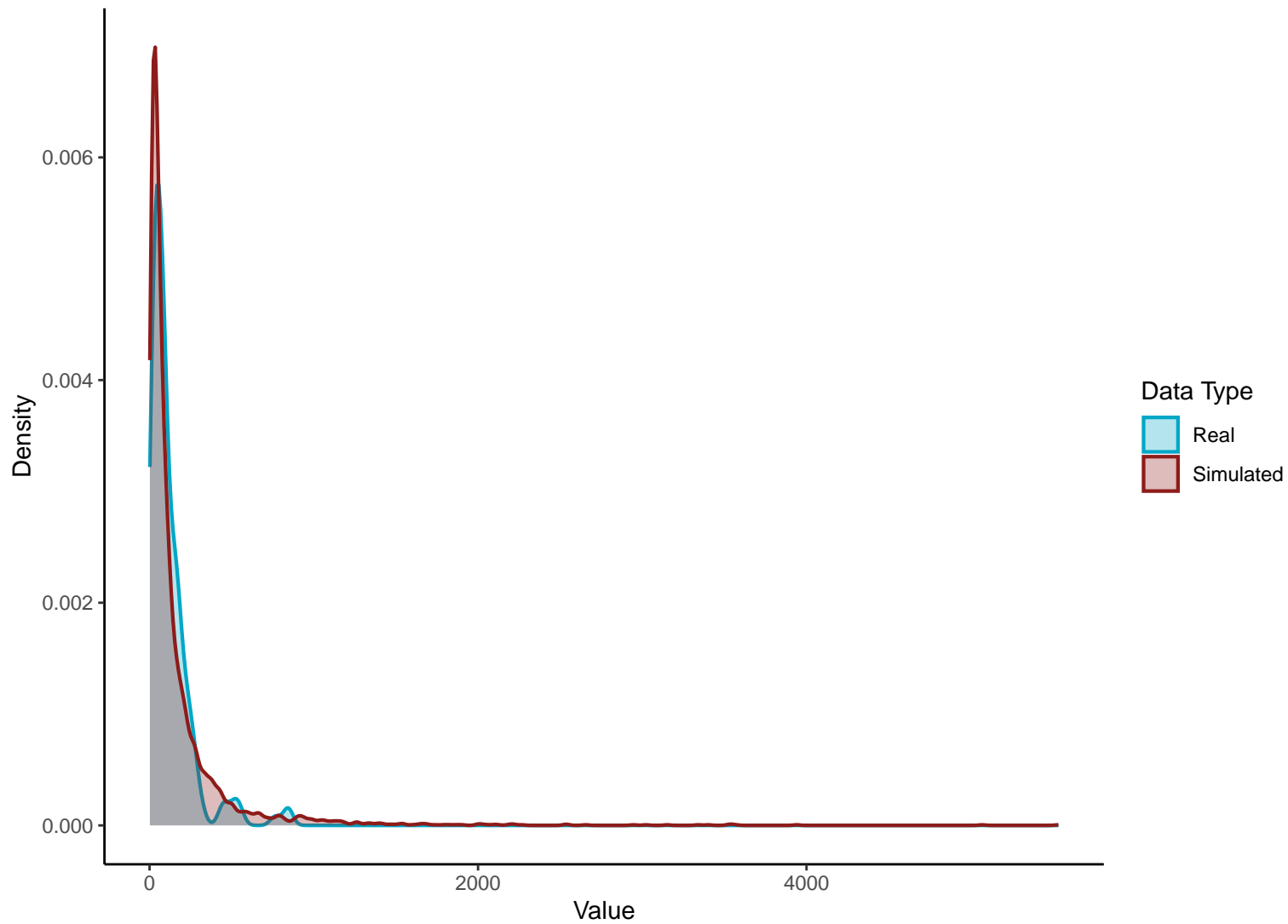
HT002



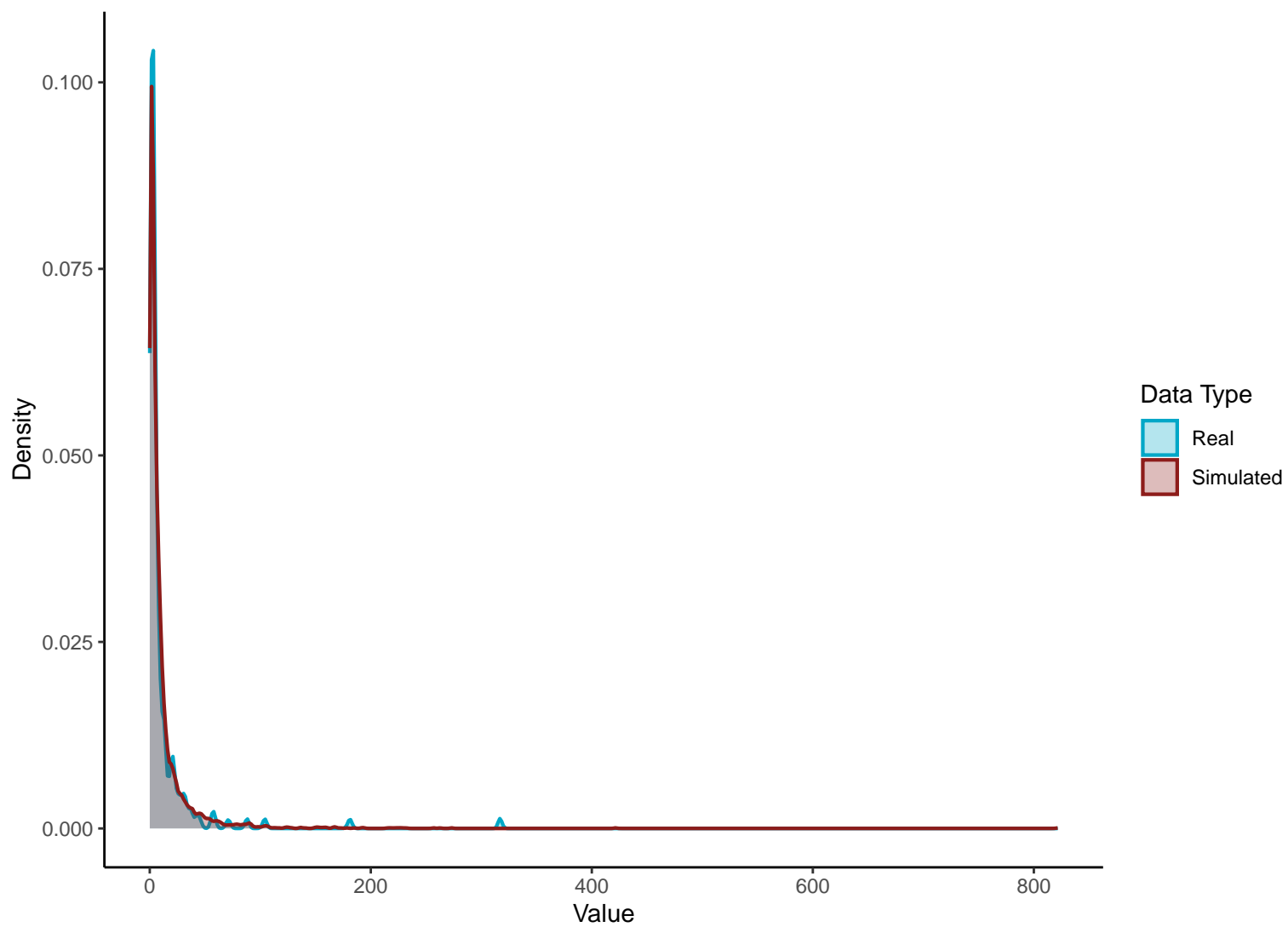
Frisingicoccus



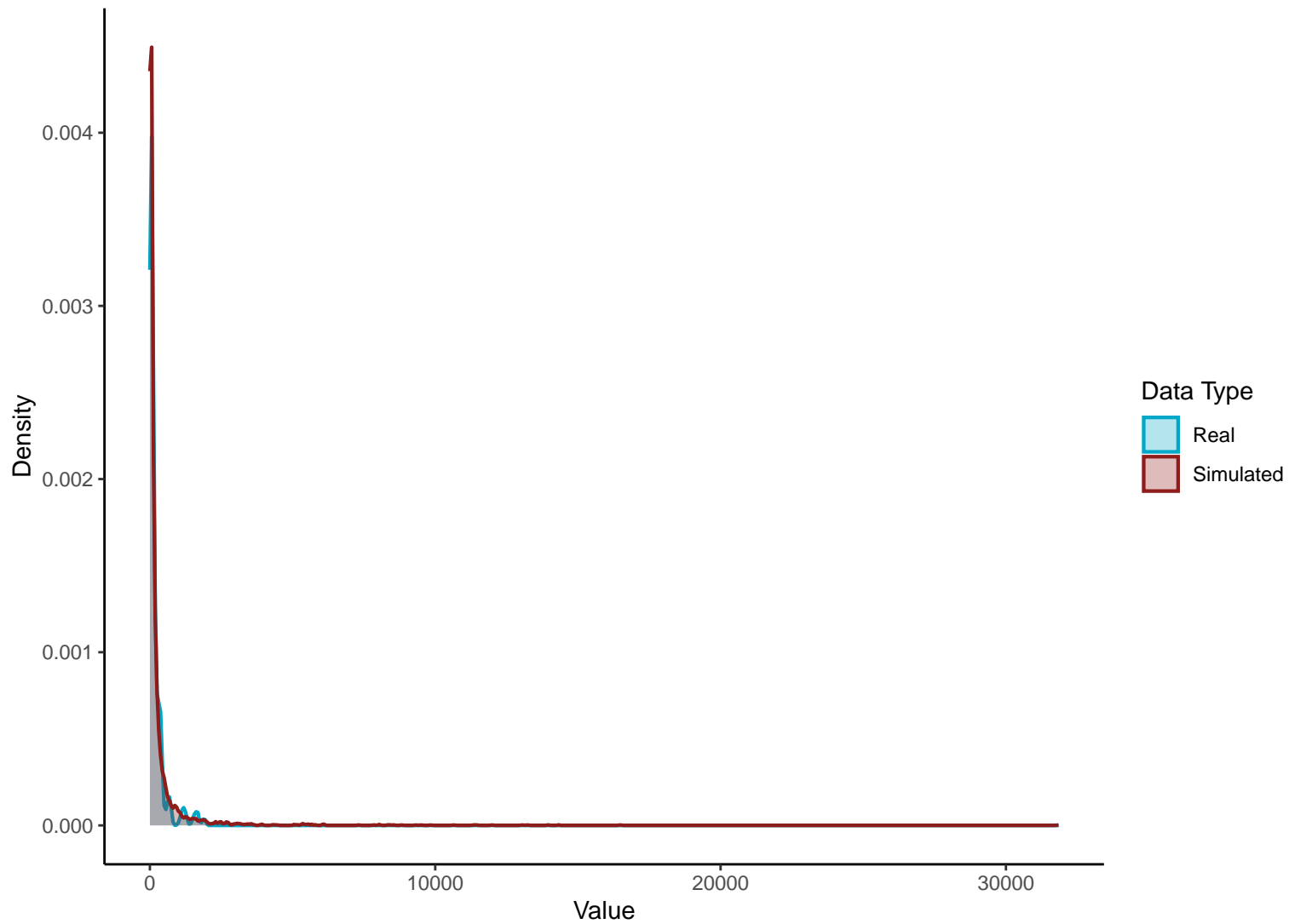
Ligilactobacillus



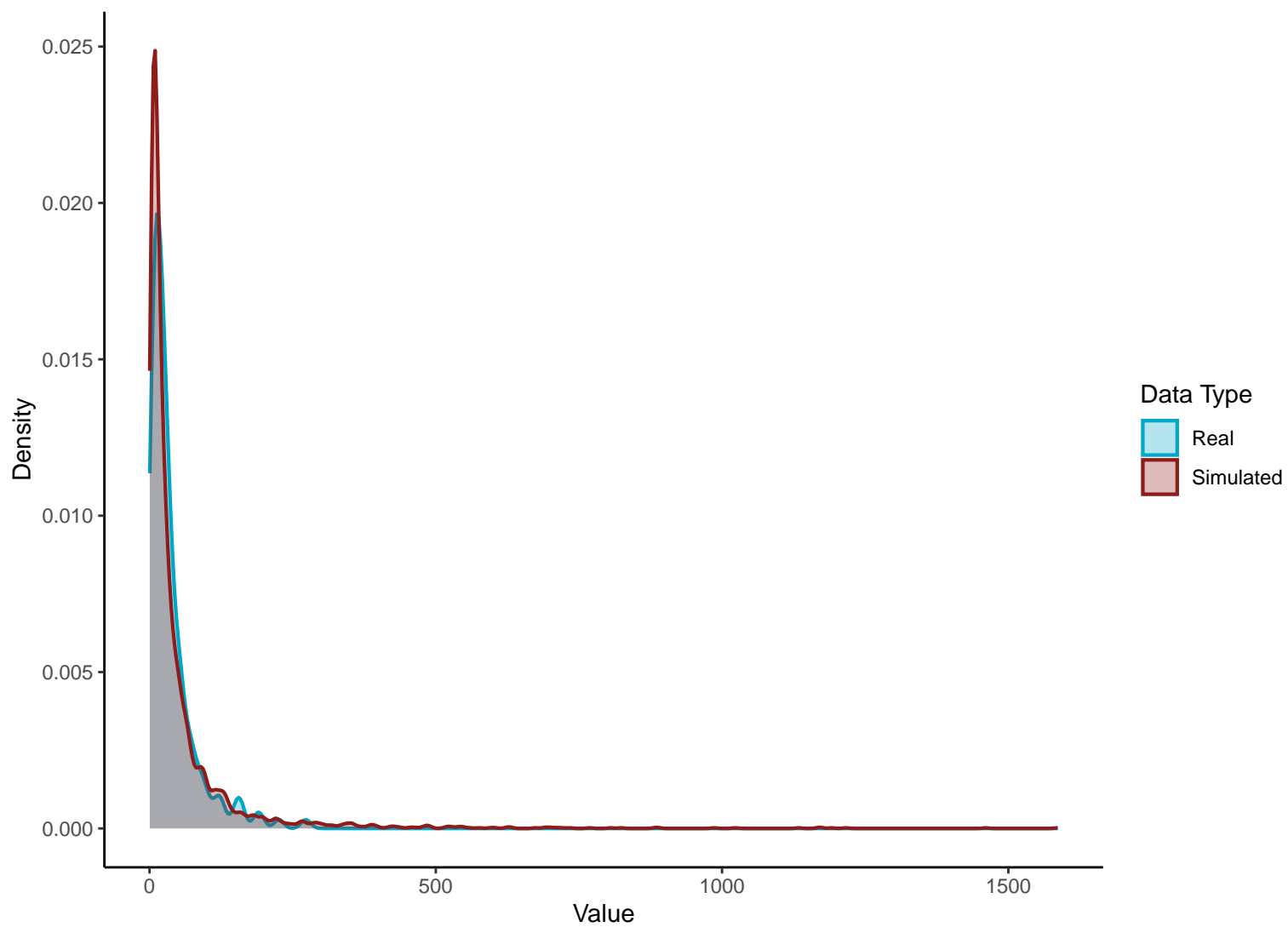
Sphaerochaeta



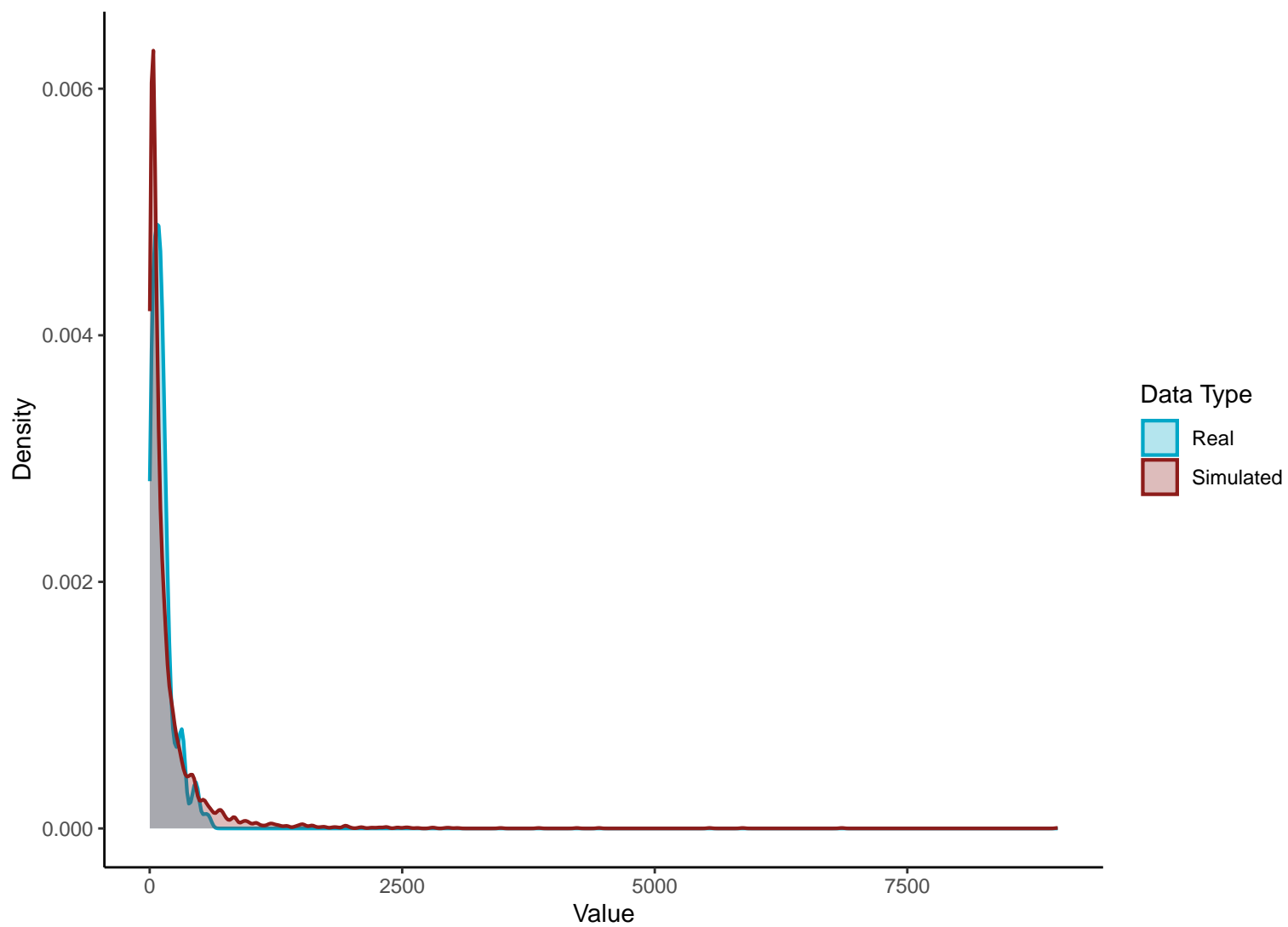
Romboutsia



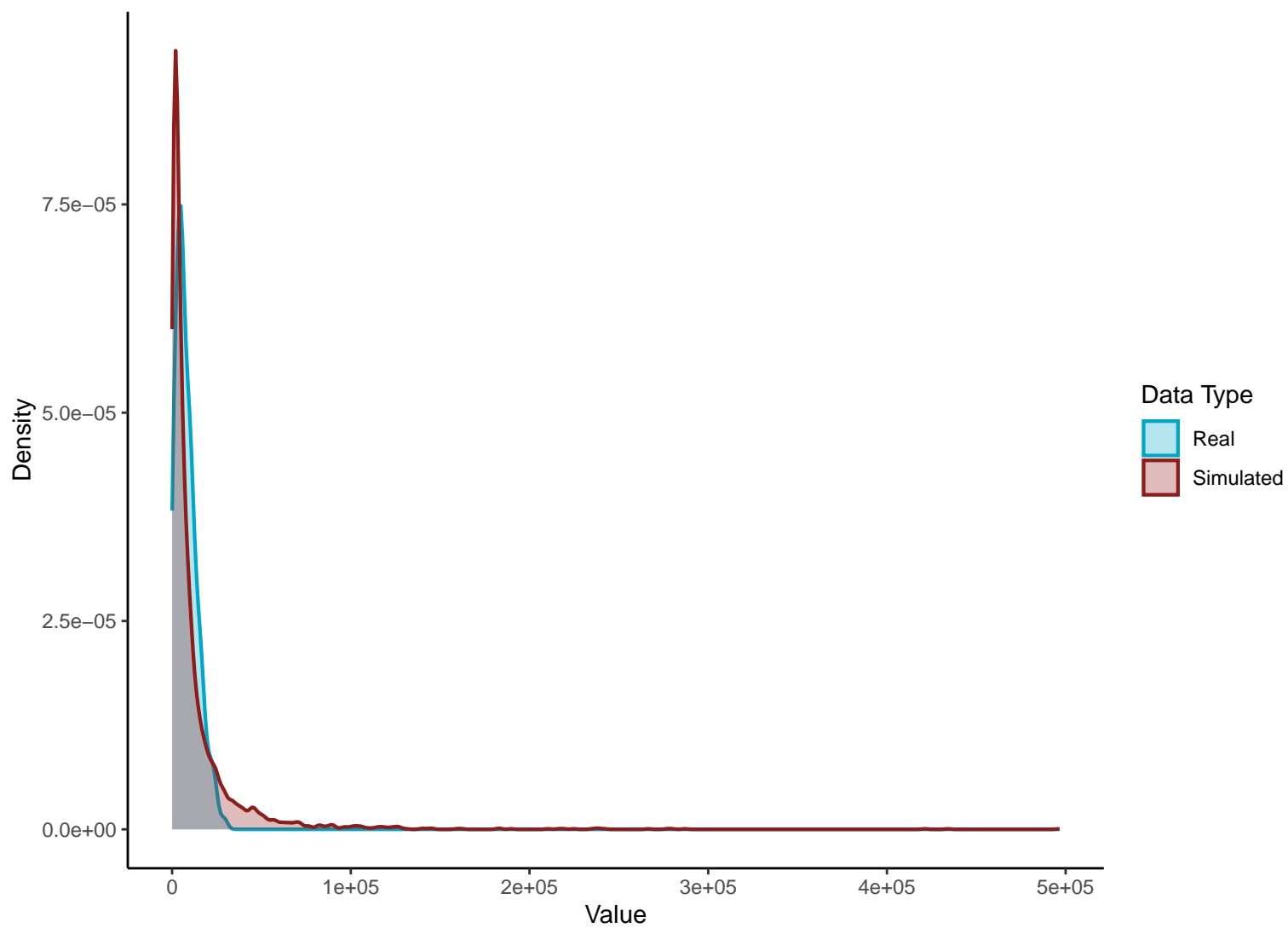
Lachnospiraceae.UCG.001



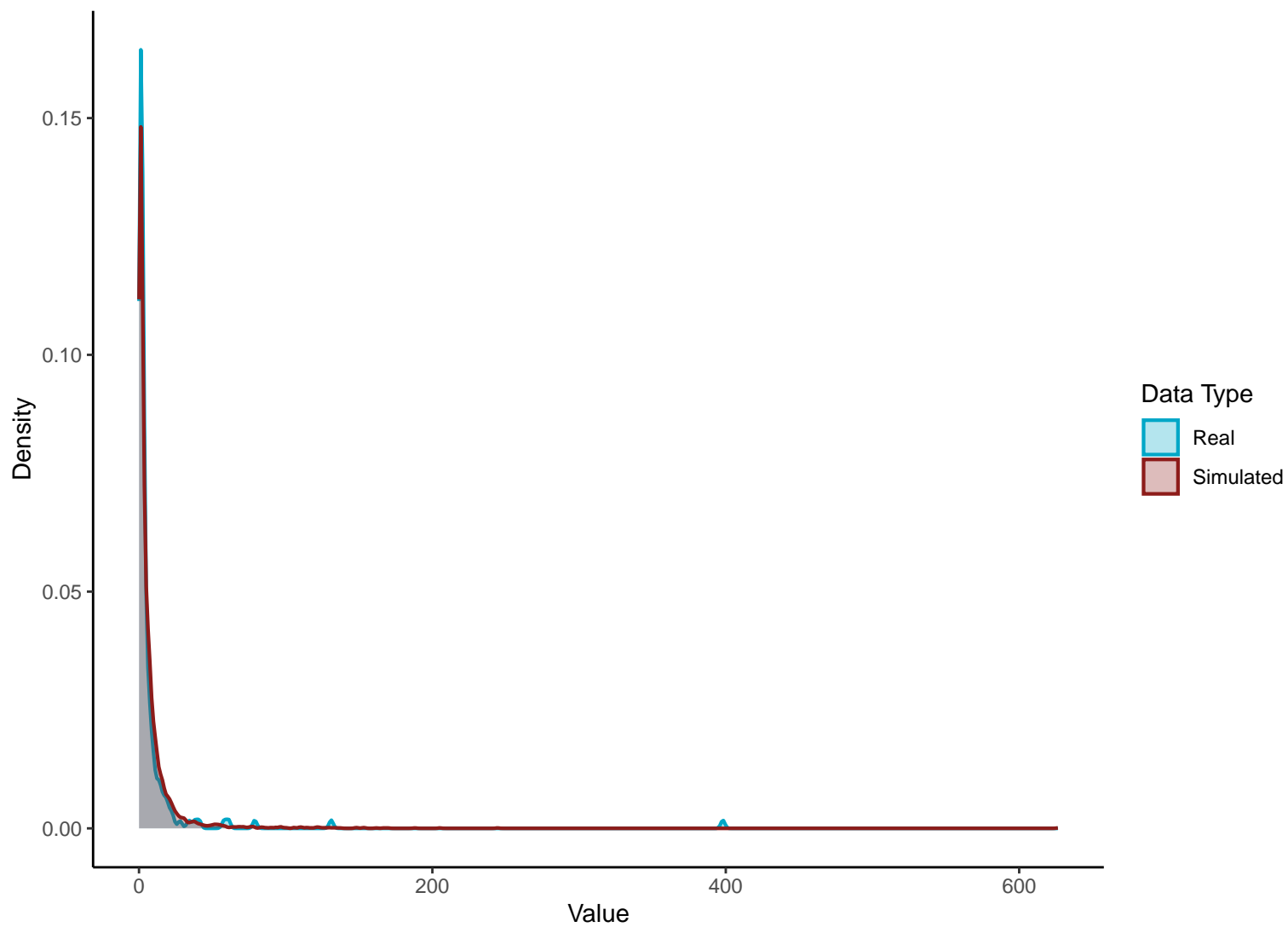
Oscillibacter



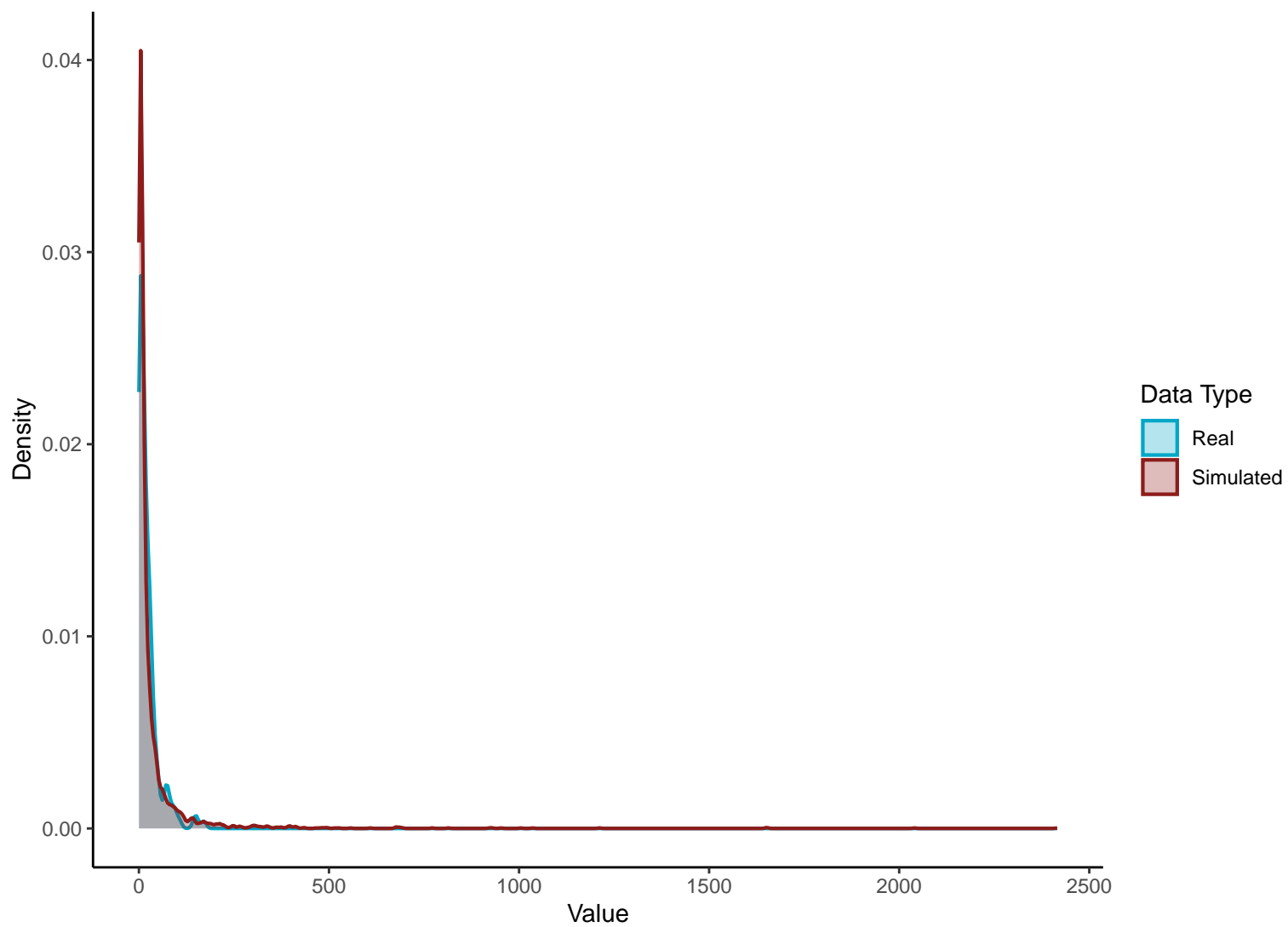
Streptococcus



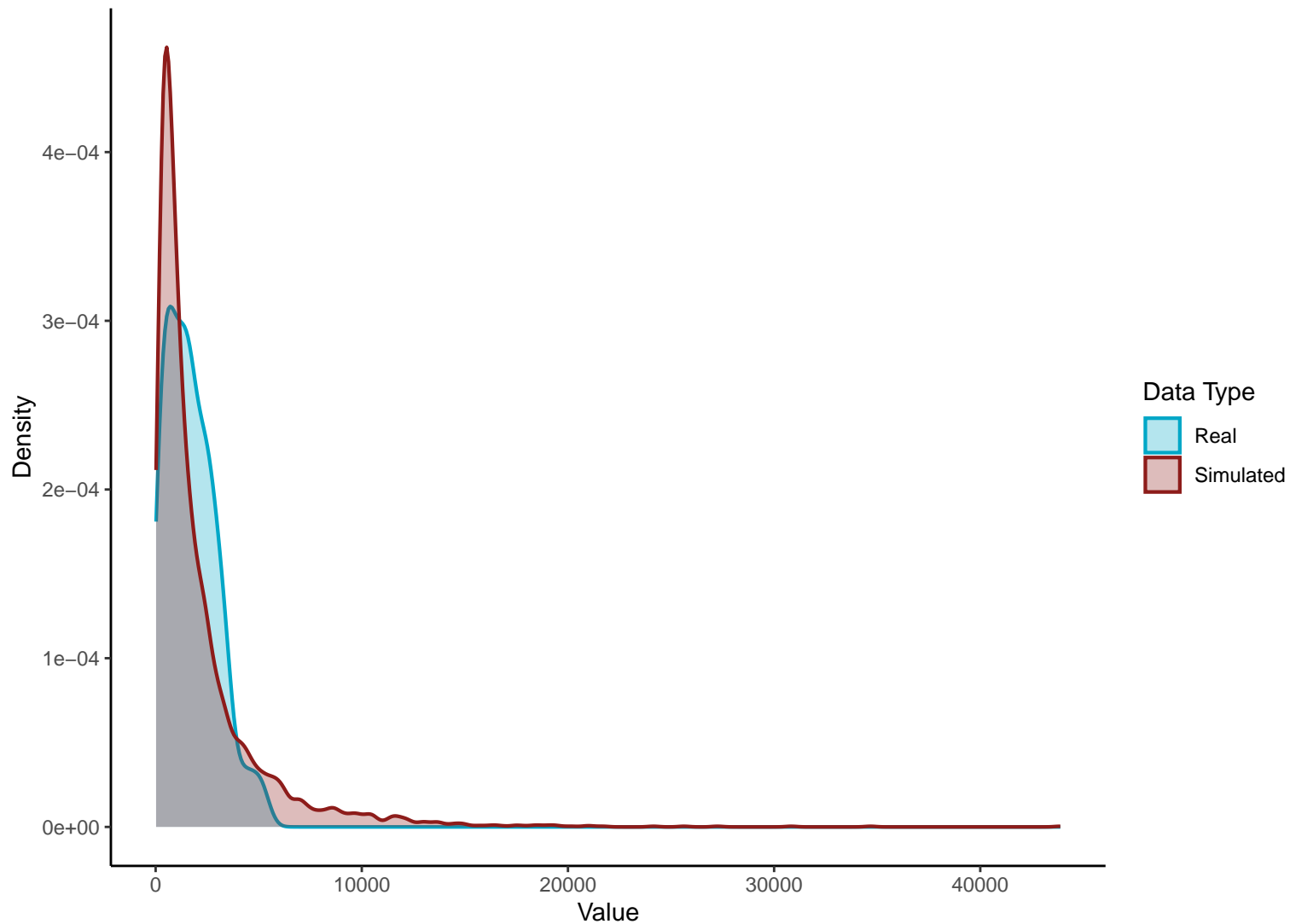
Cellulosilyticum



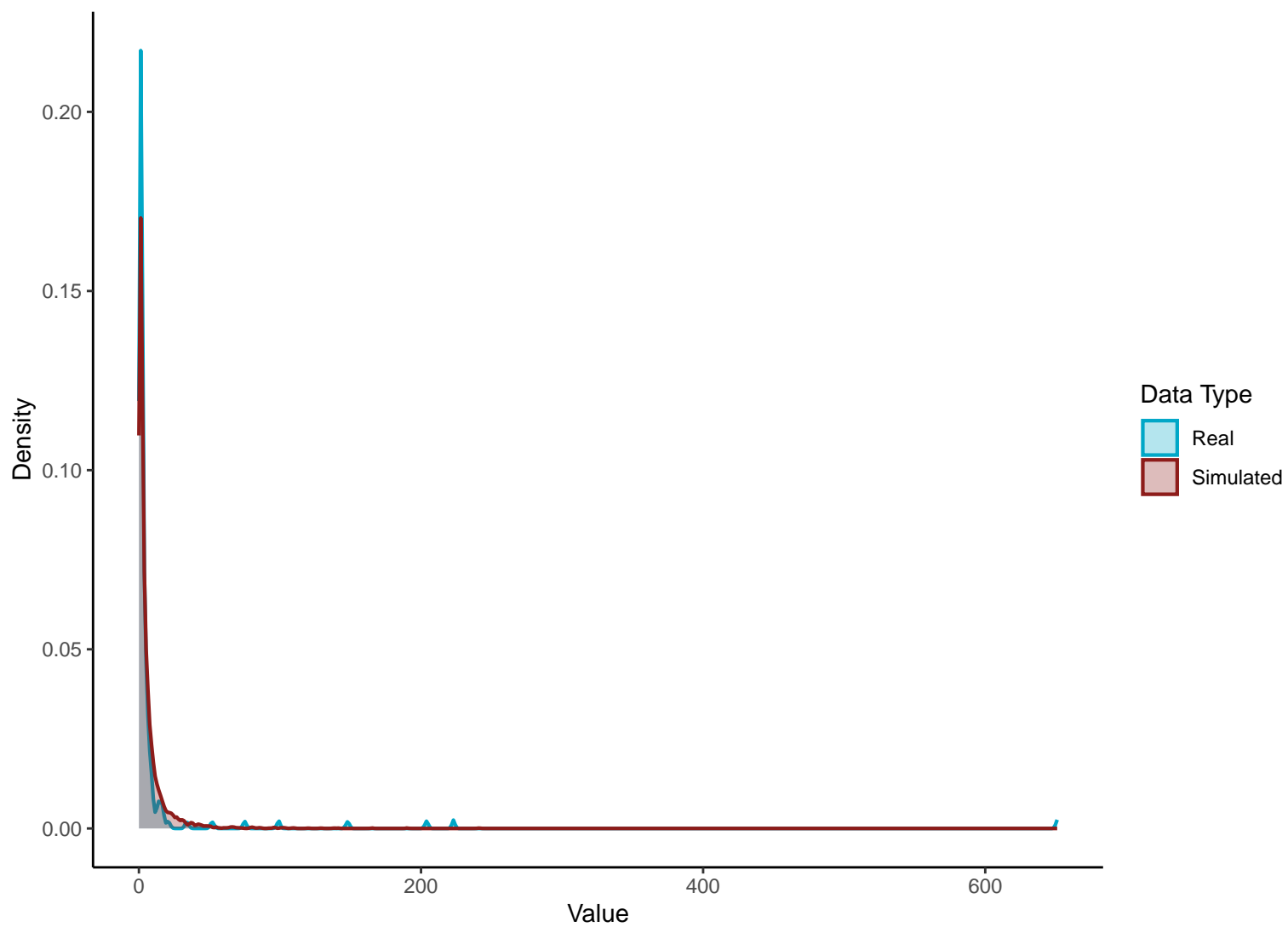
Mitsuokella



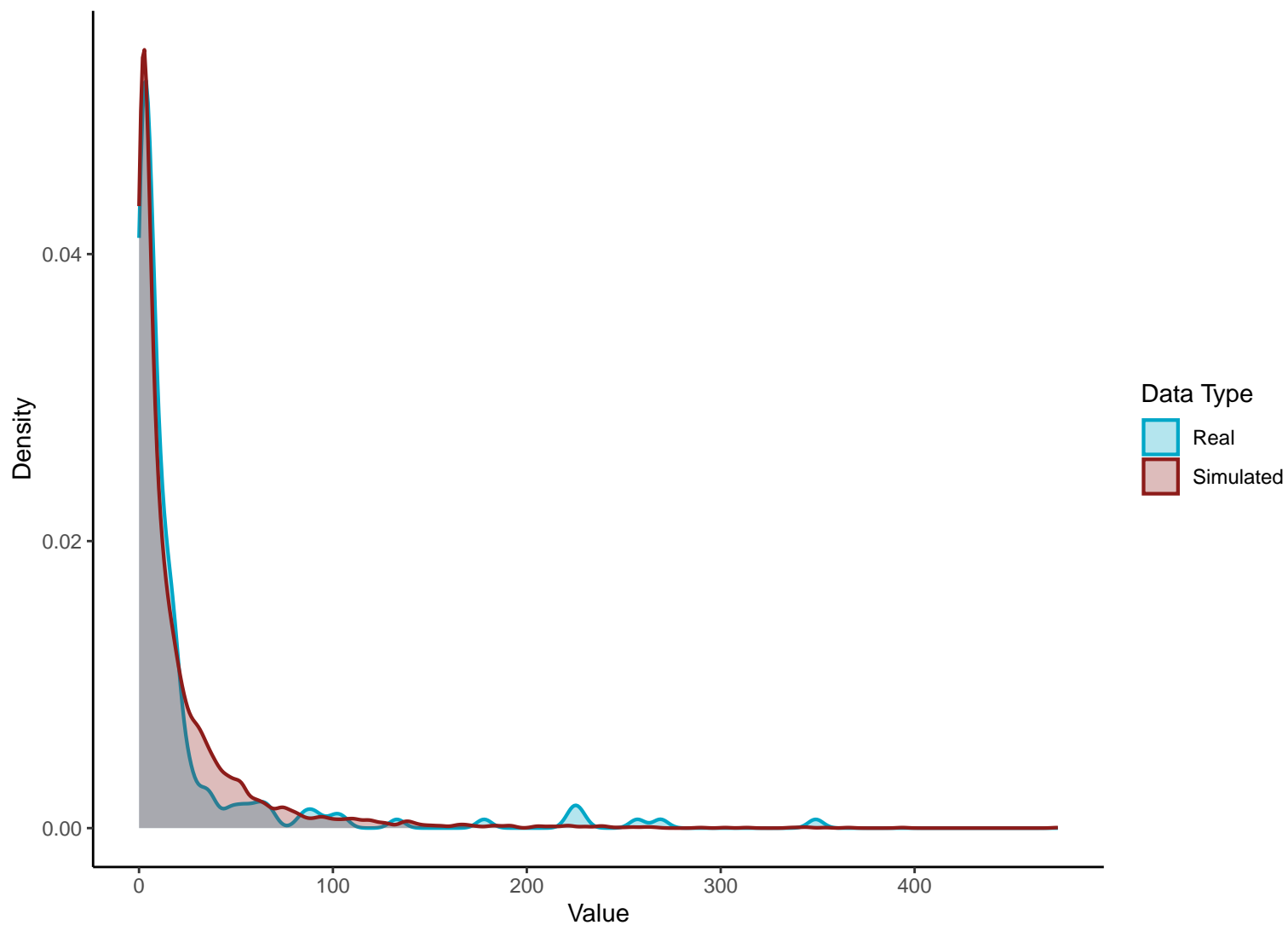
Agathobacter



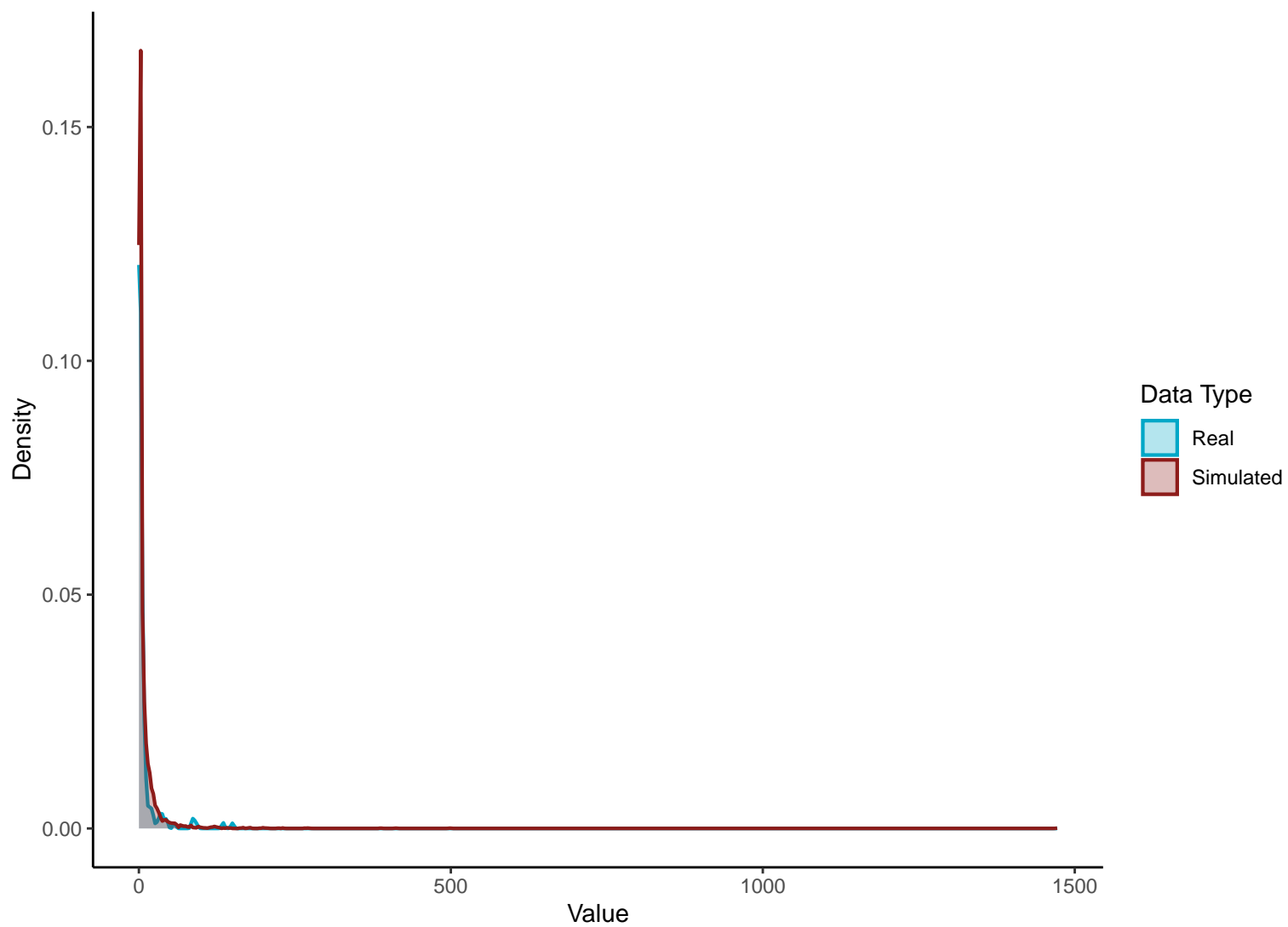
Bacteroides



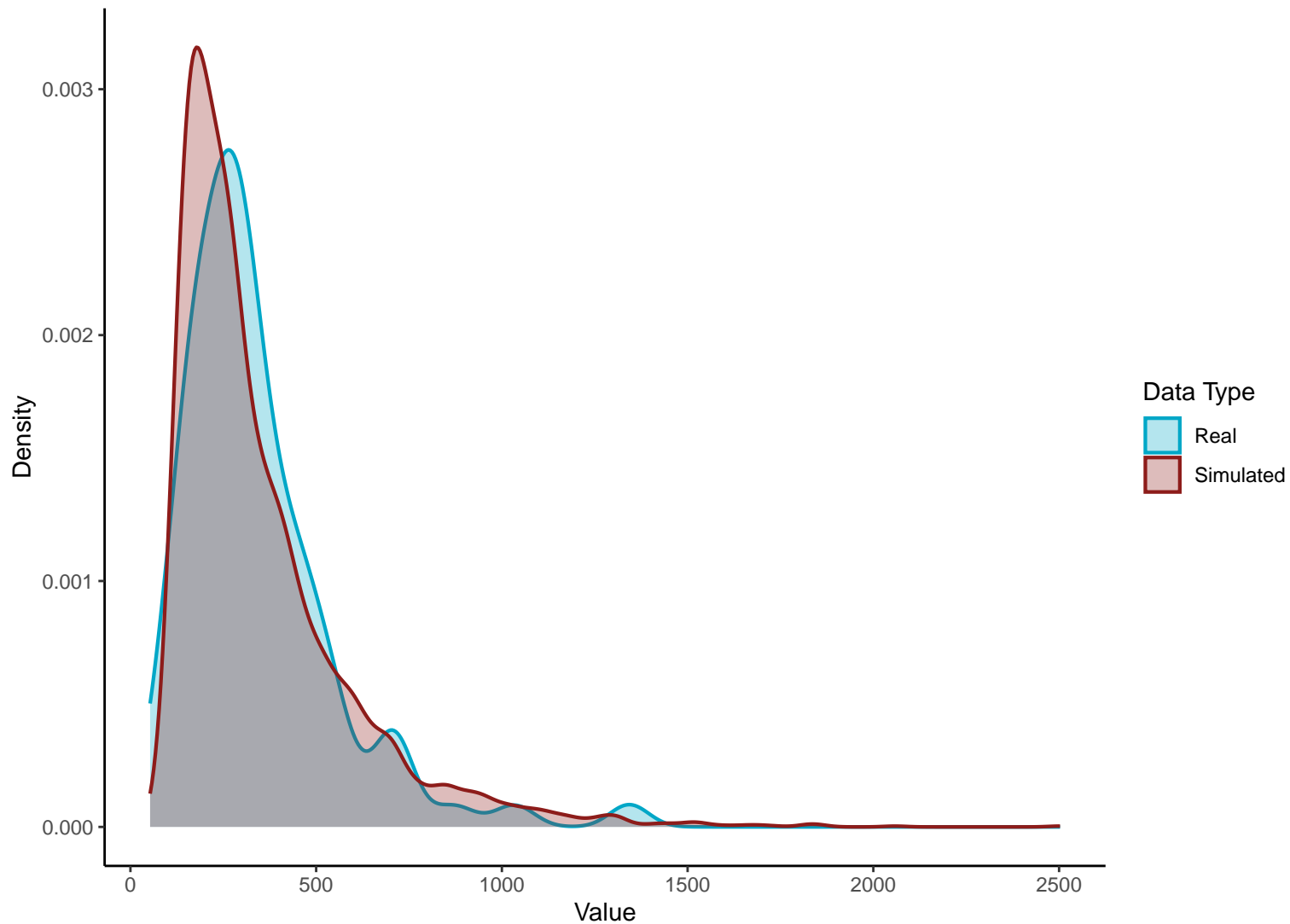
p.1088.a5.gut.group



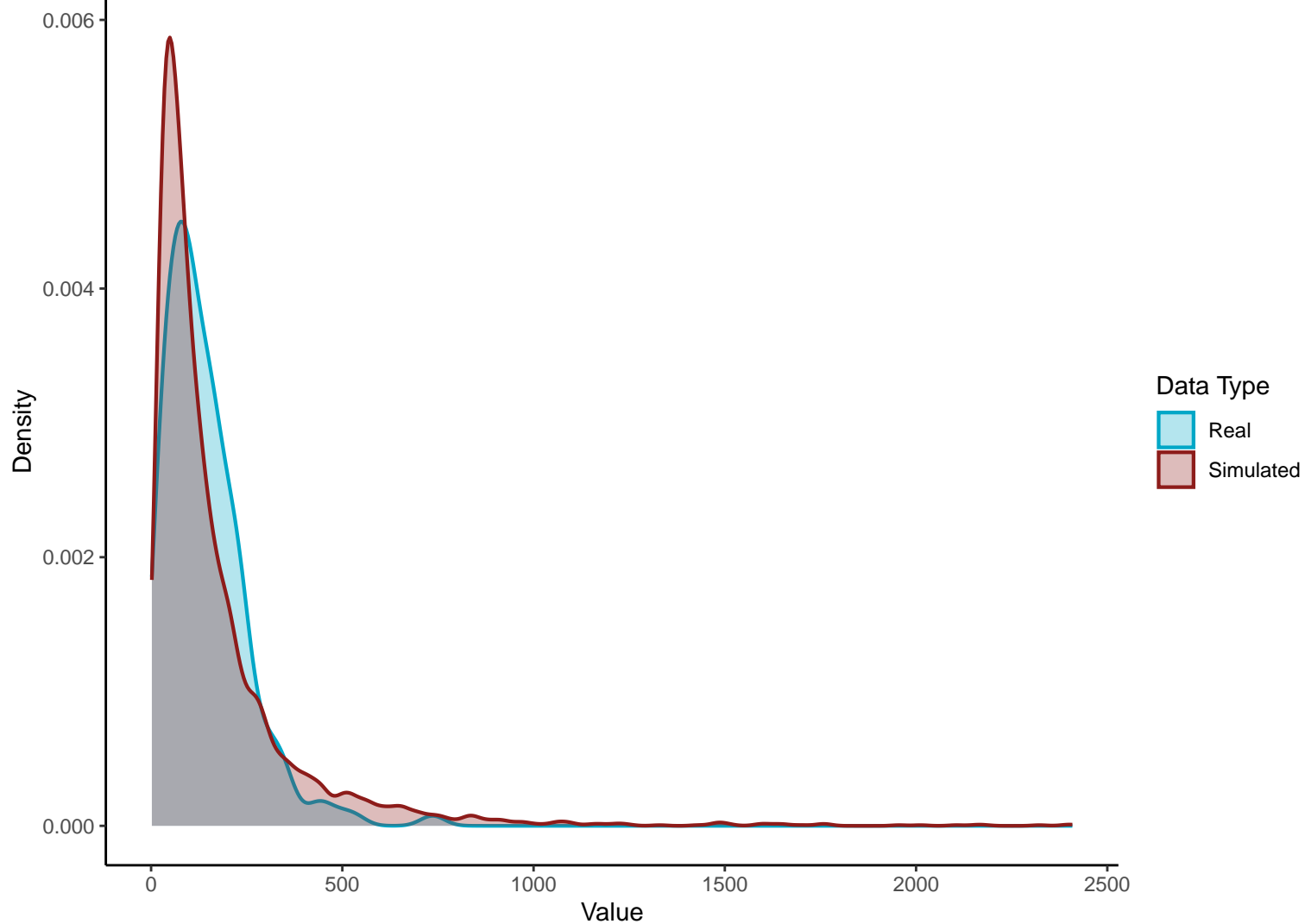
Anaeroplasma



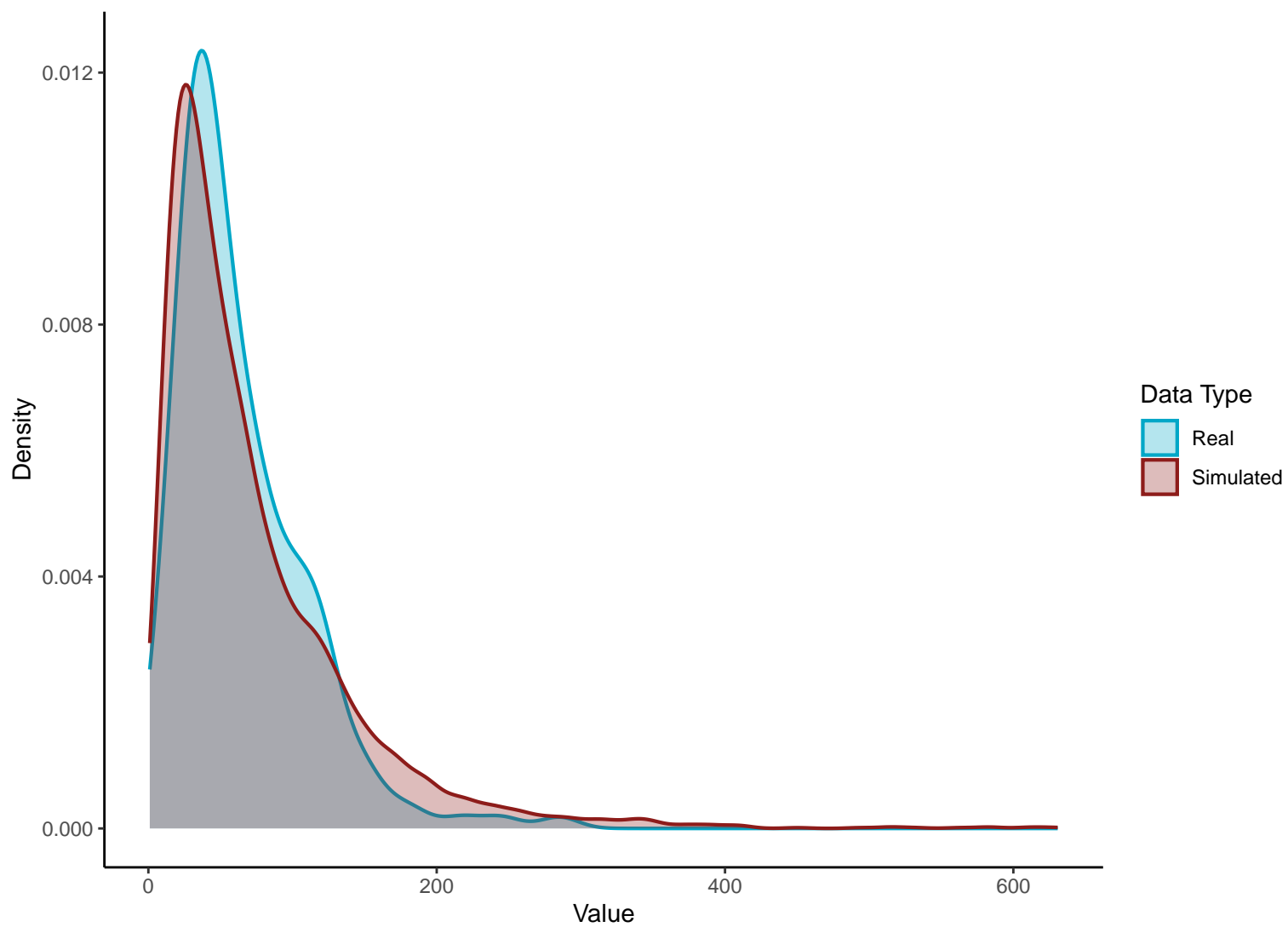
Marvinbryantia



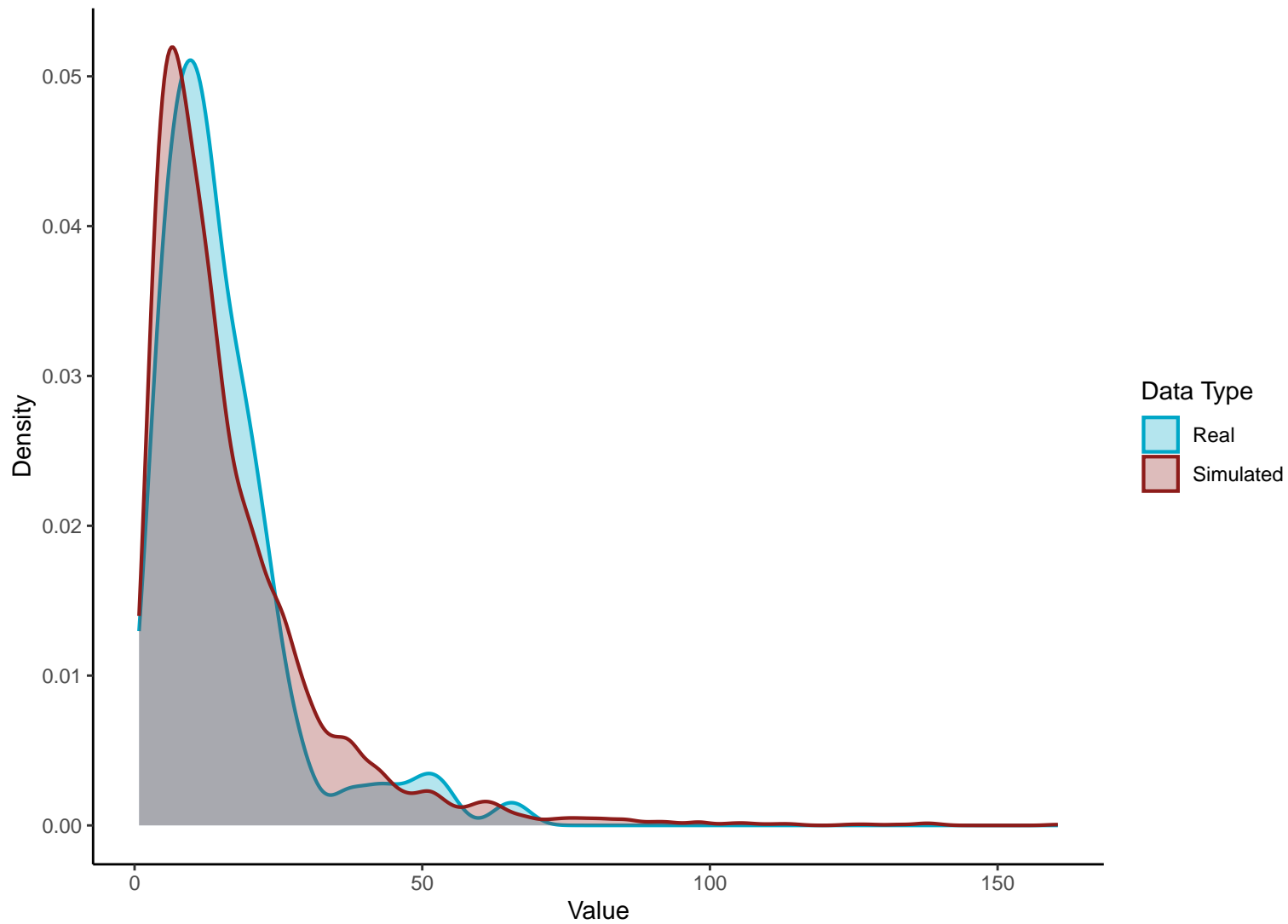
Mogibacterium



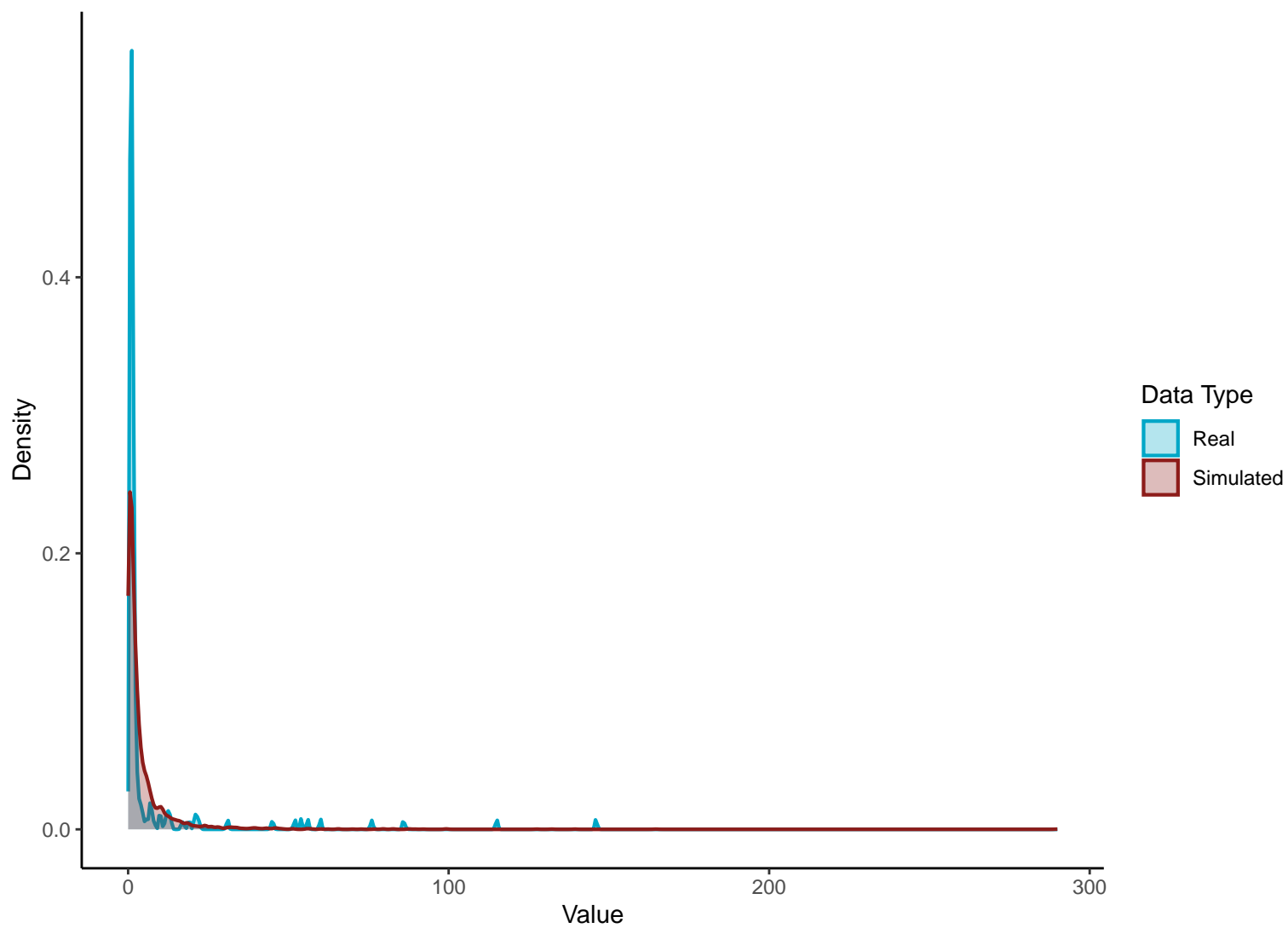
Family.XIII.UCG.001



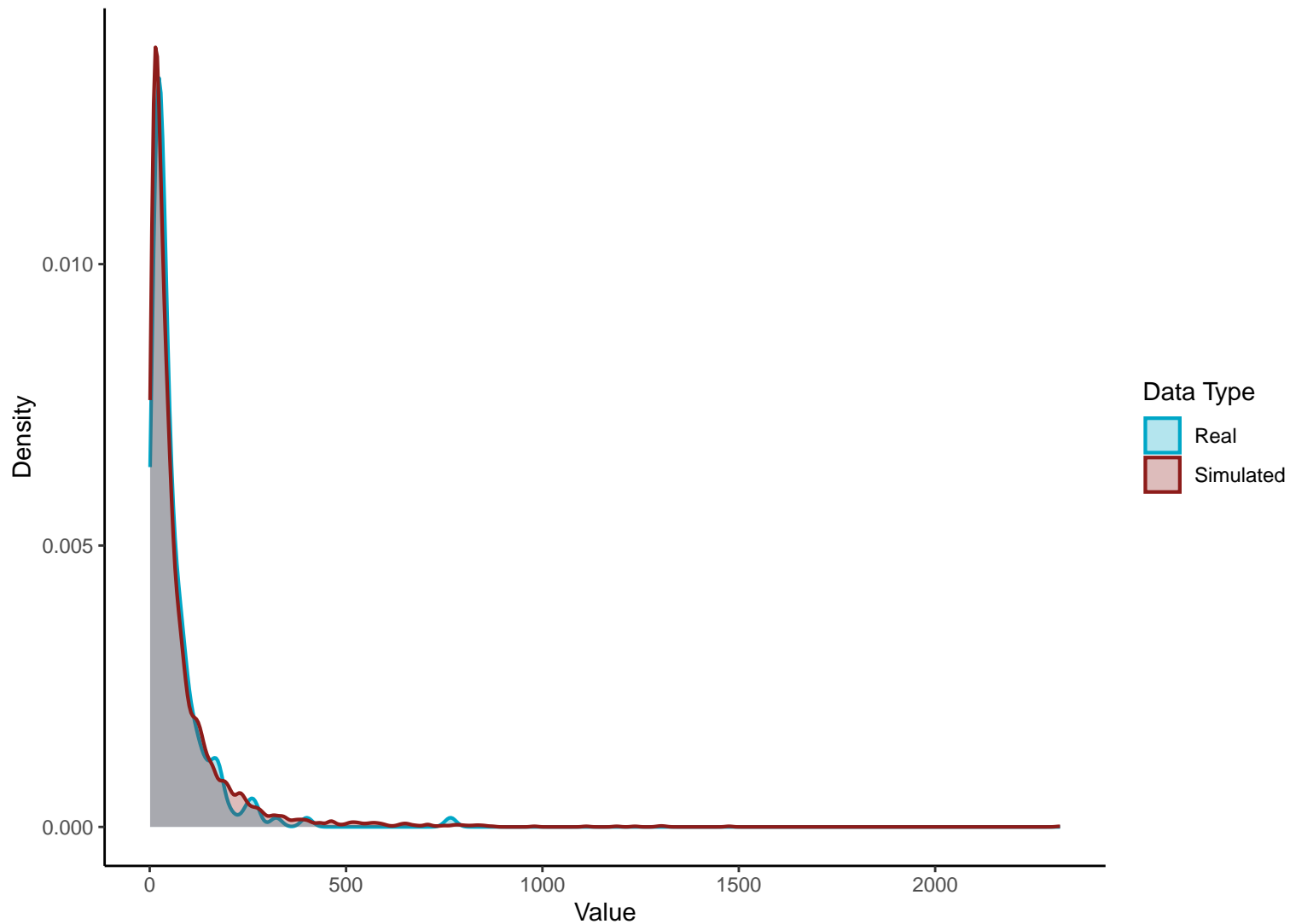
Lachnospiraceae.UCG.010



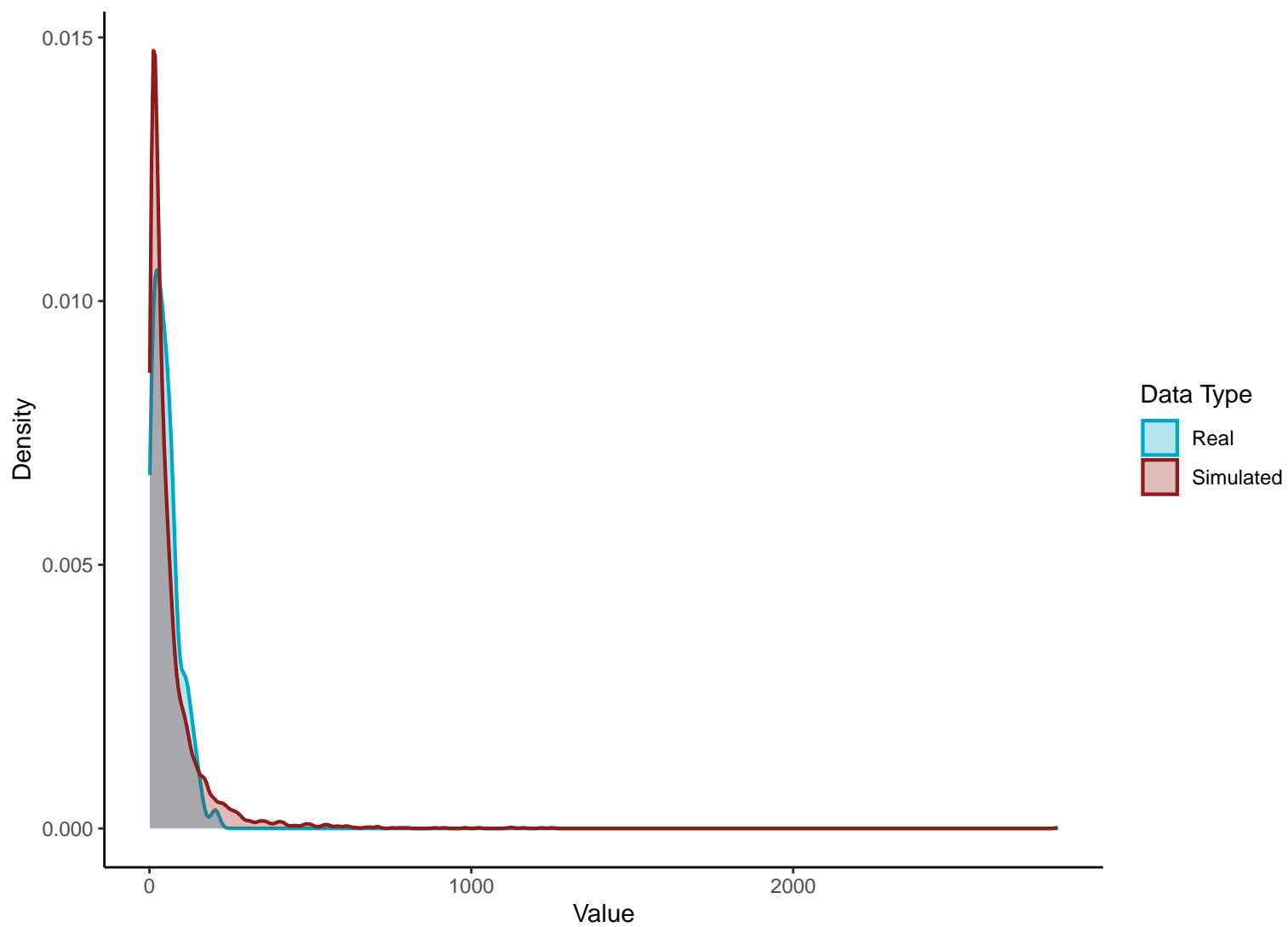
Megamonas



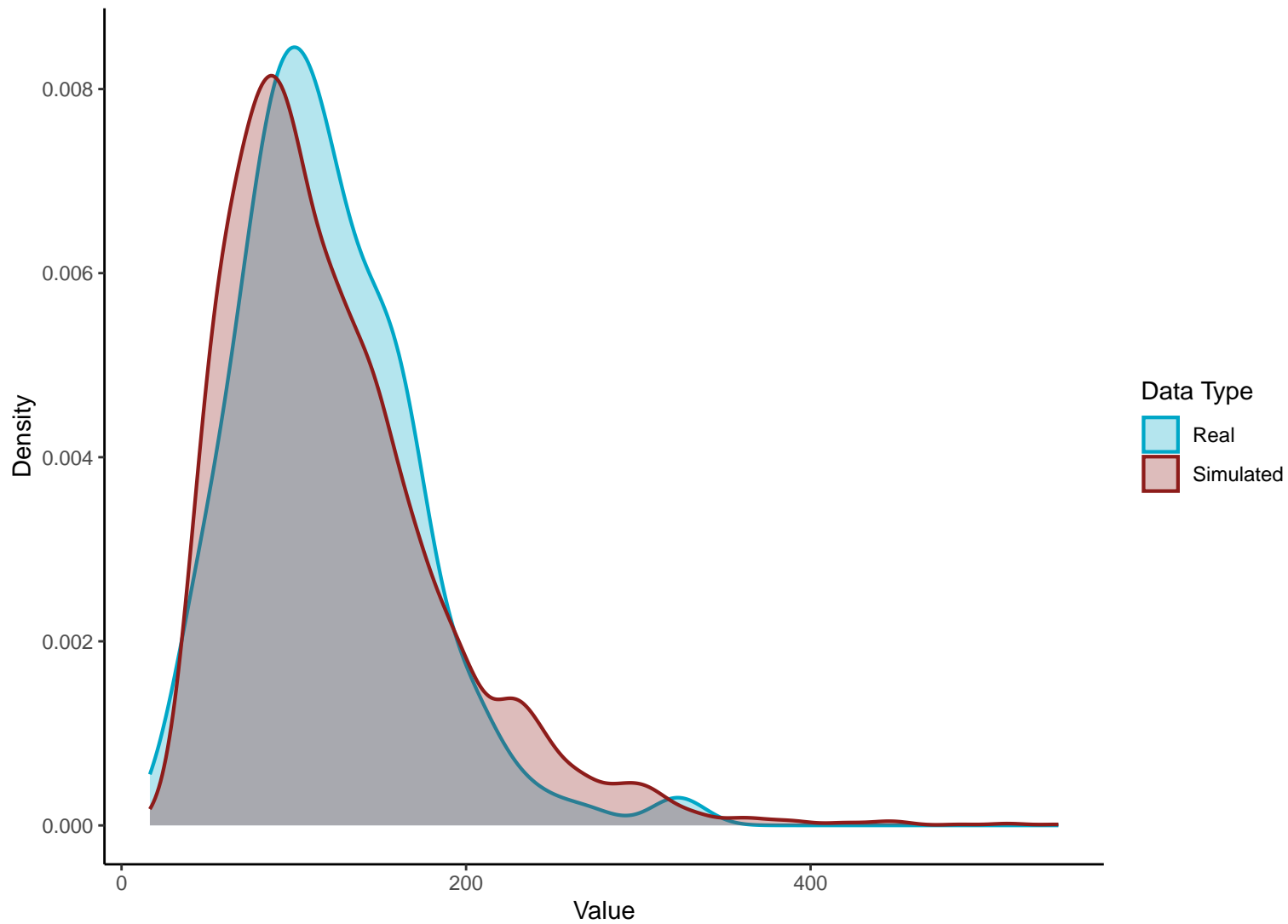
X.Eubacterium..nodatum.group



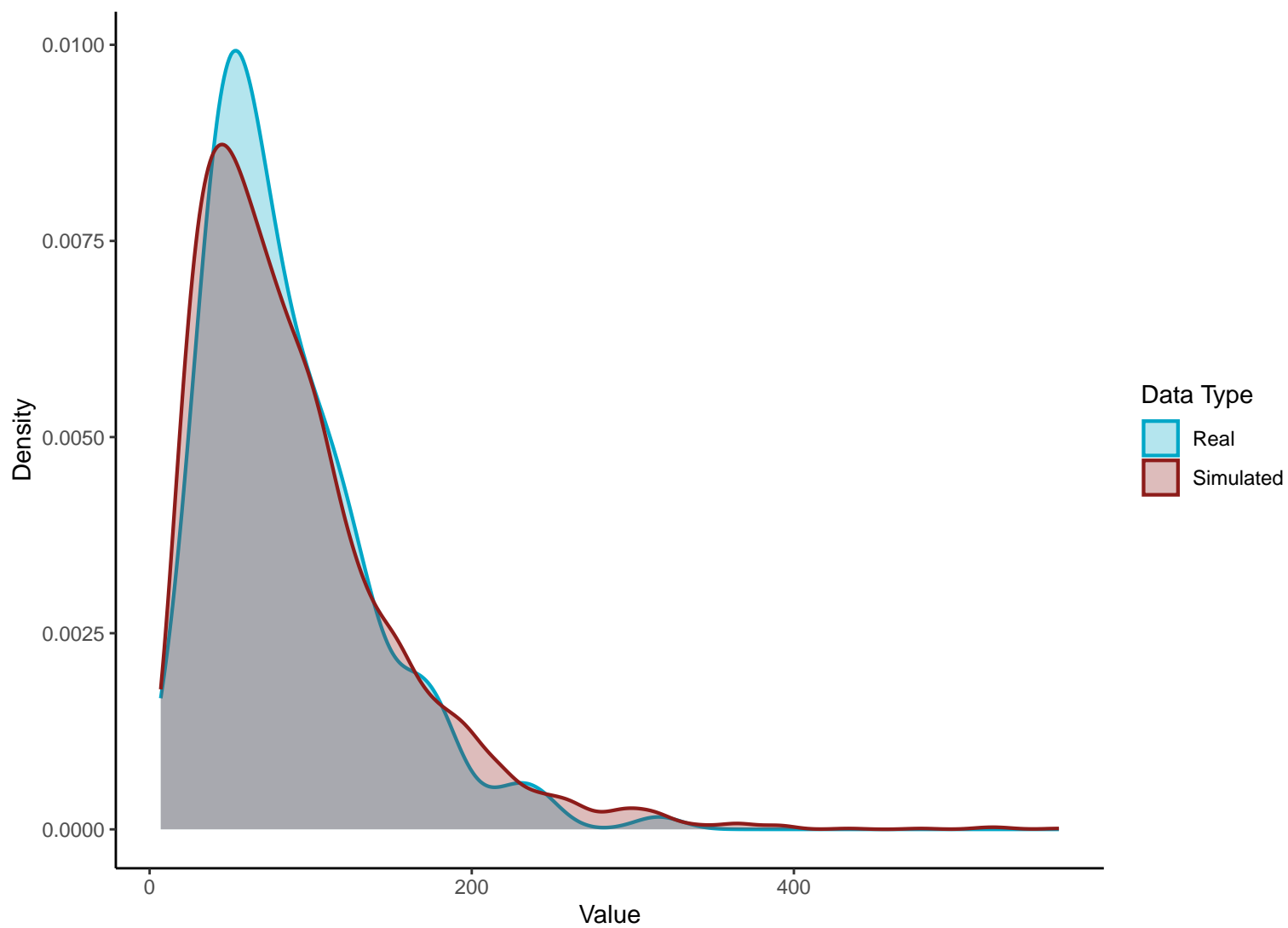
Lachnospiraceae.NK3A20.group



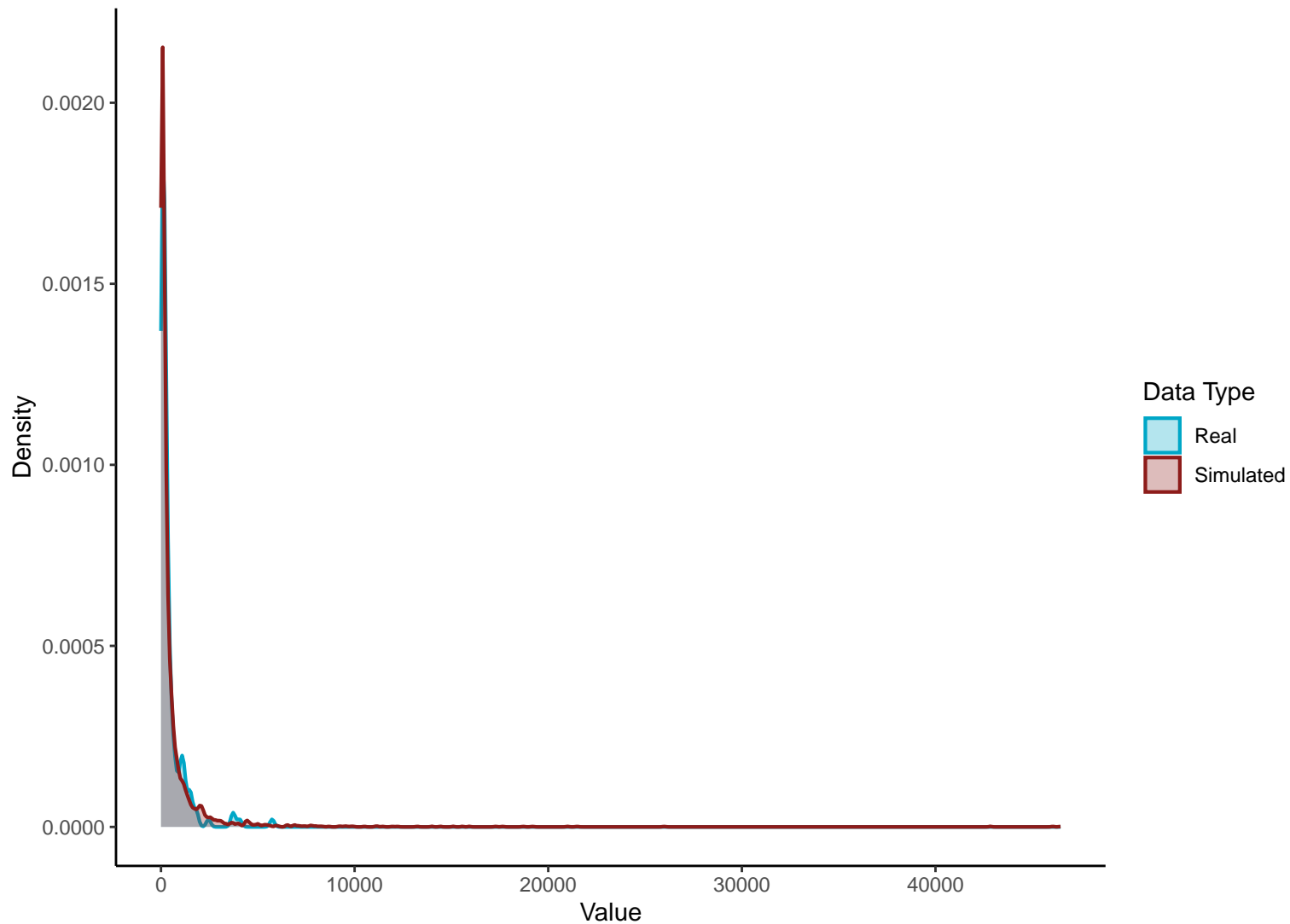
Lachnospiraceae.FCS020.group



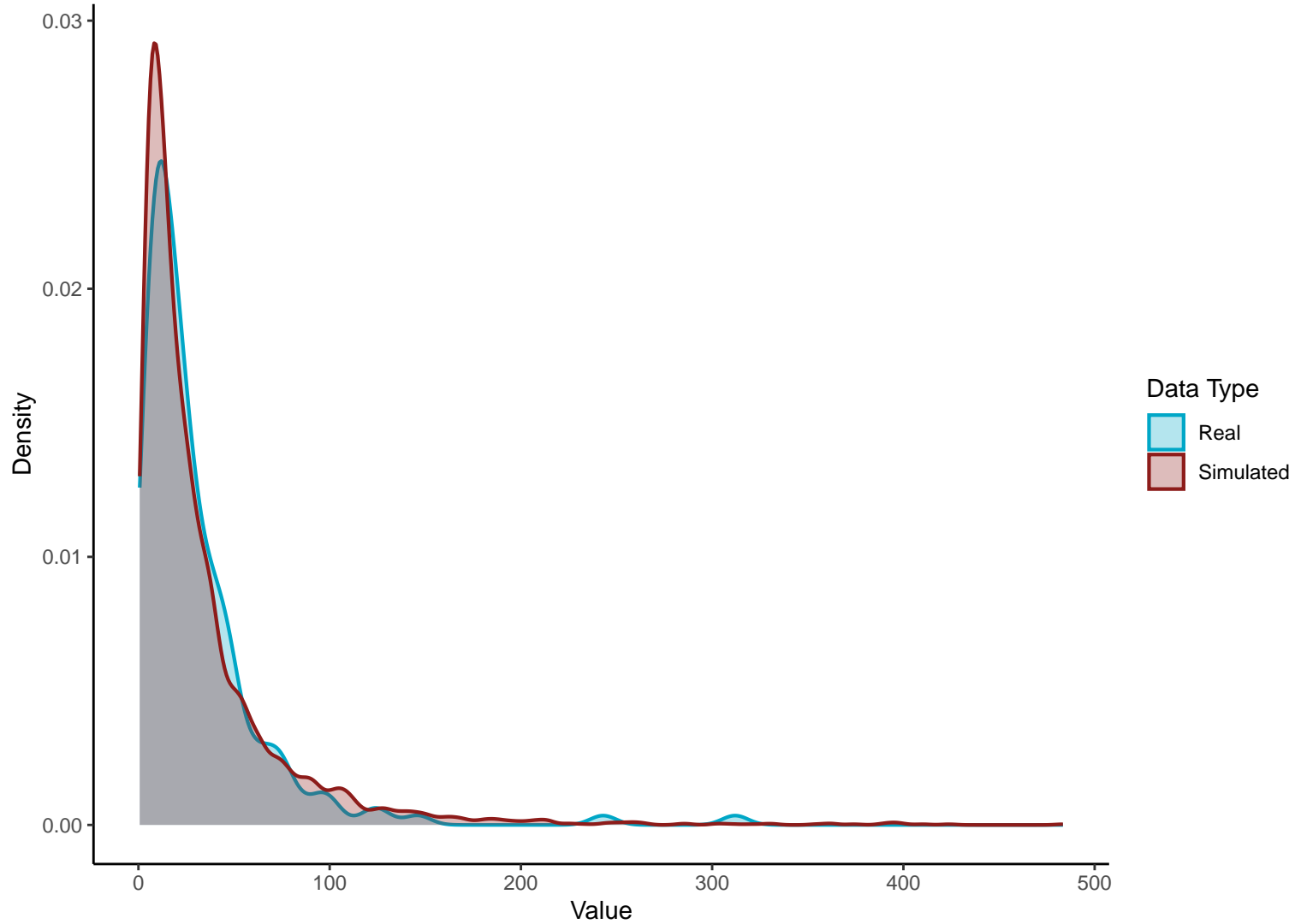
Incertae.Sedis



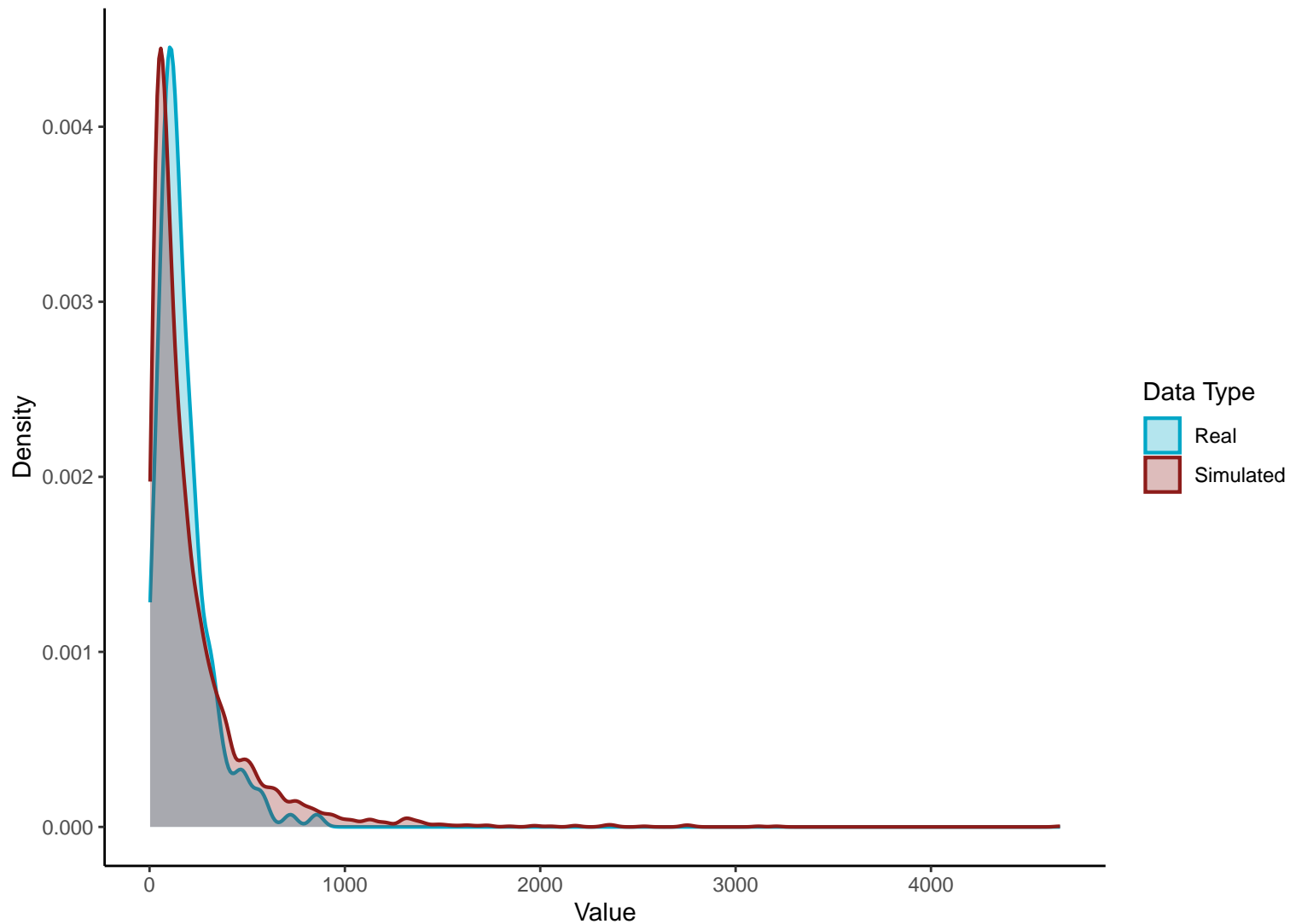
Limosilactobacillus



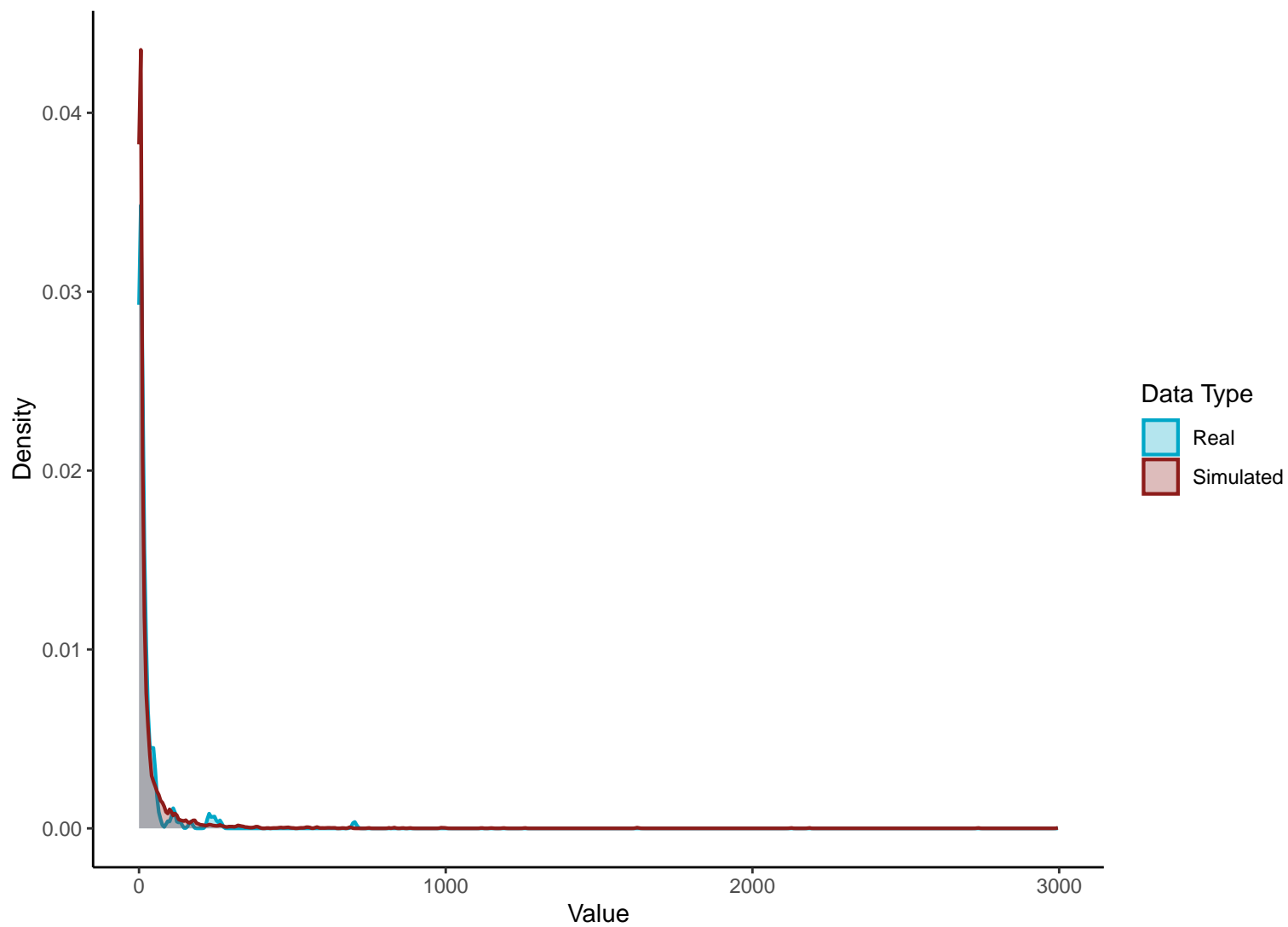
Desulfovibrio



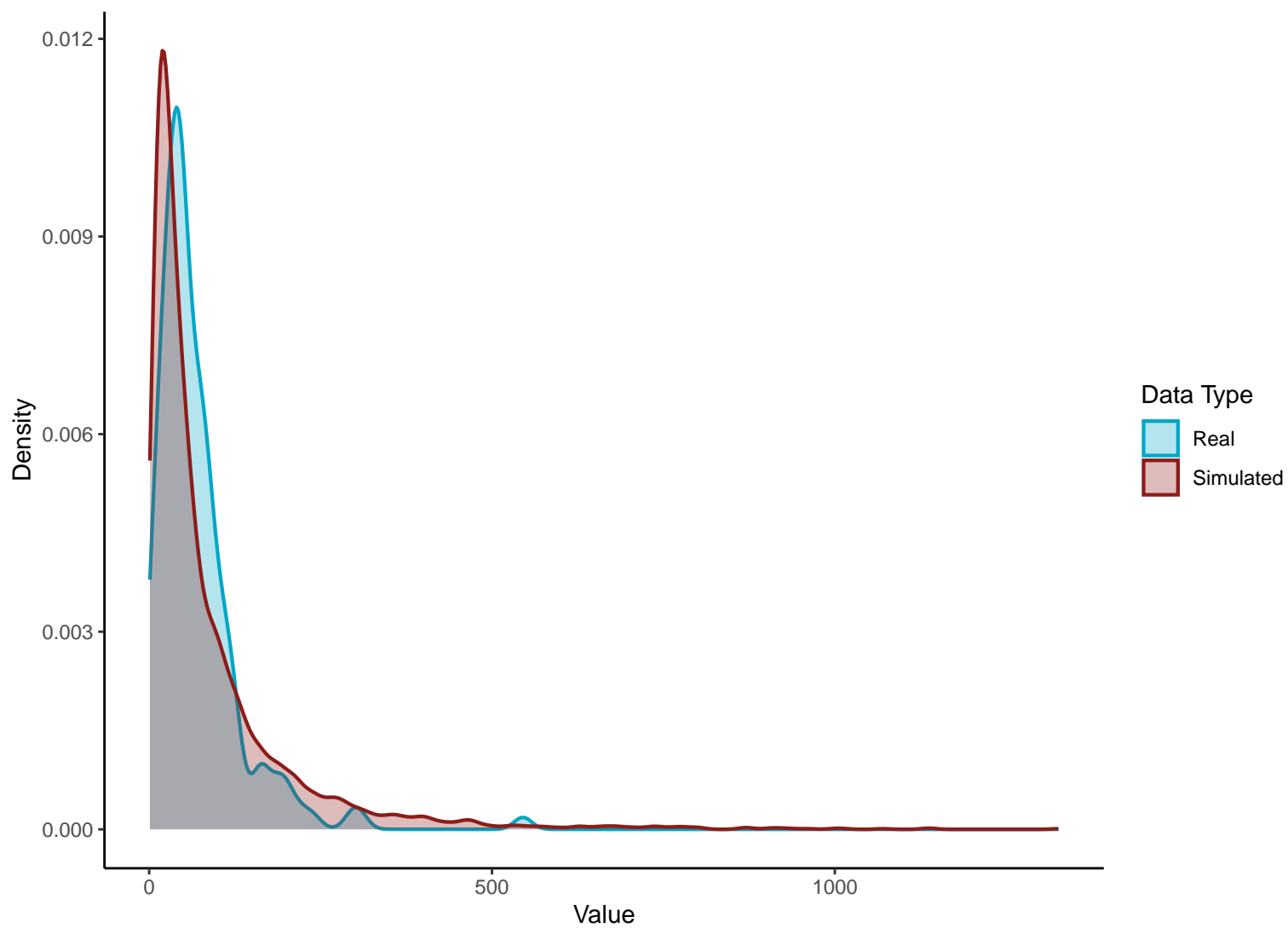
X.Eubacterium..ruminantium.group



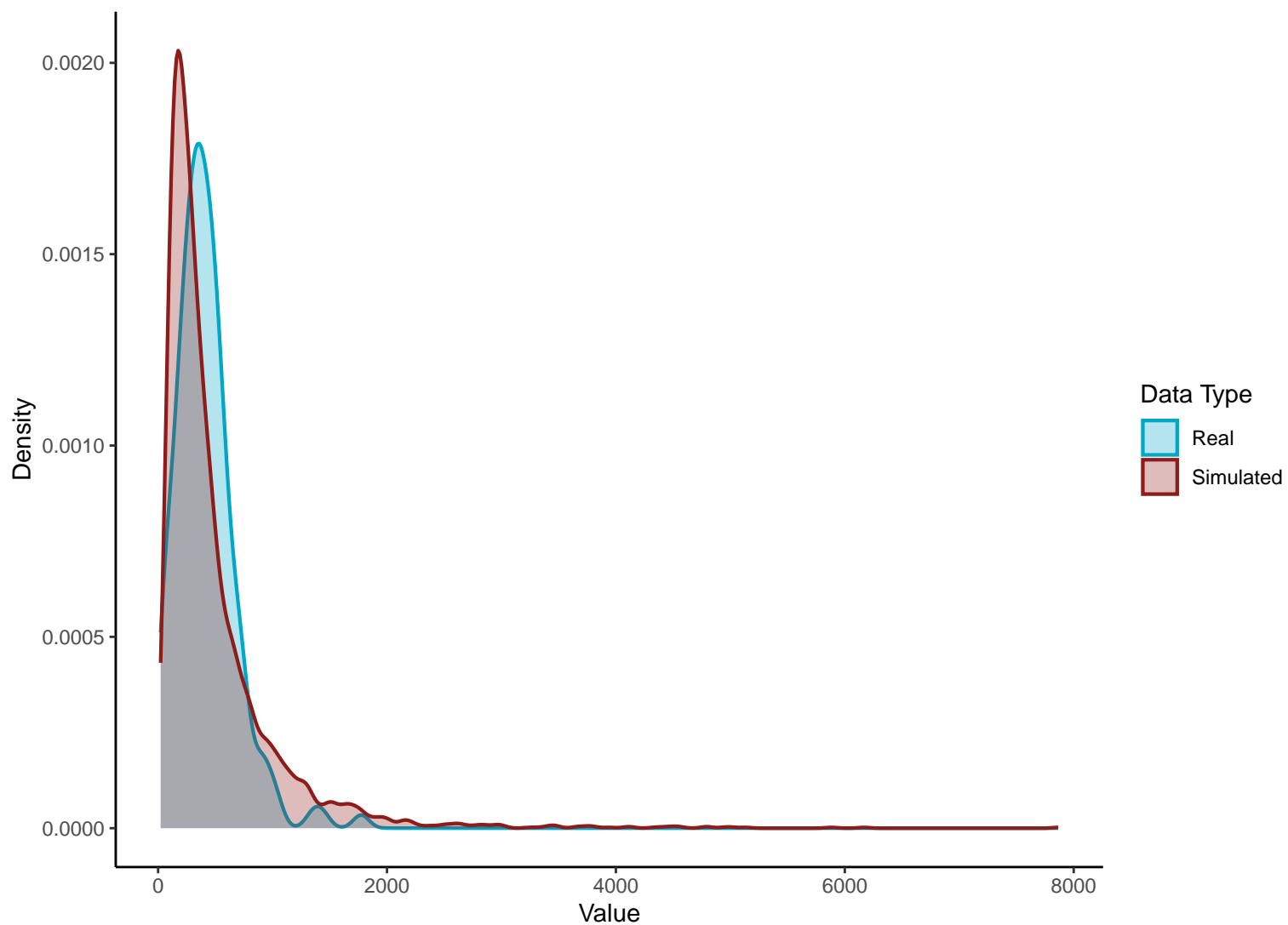
Prevotellaceae.UGC.001



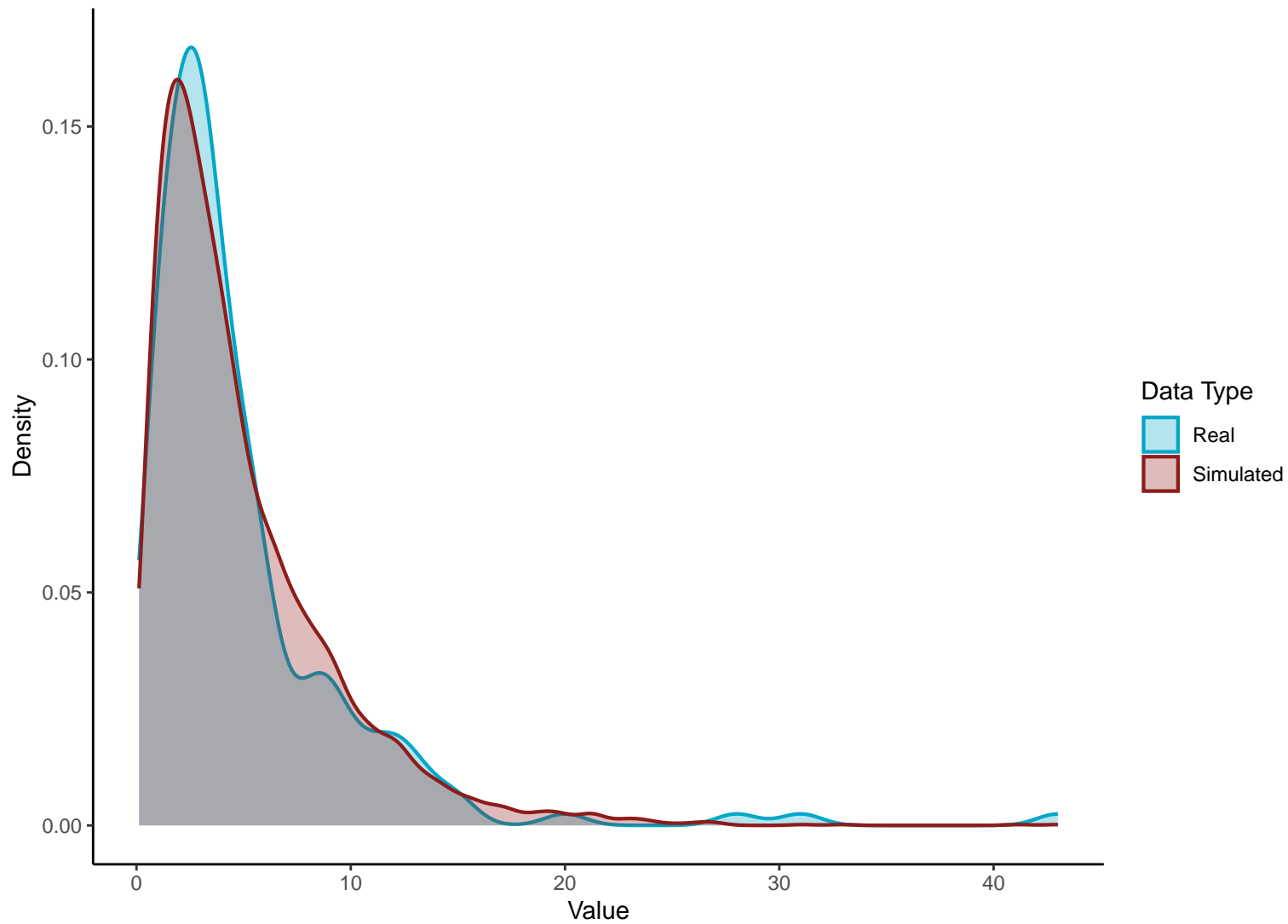
Lachnospiraceae.NK4B4.group



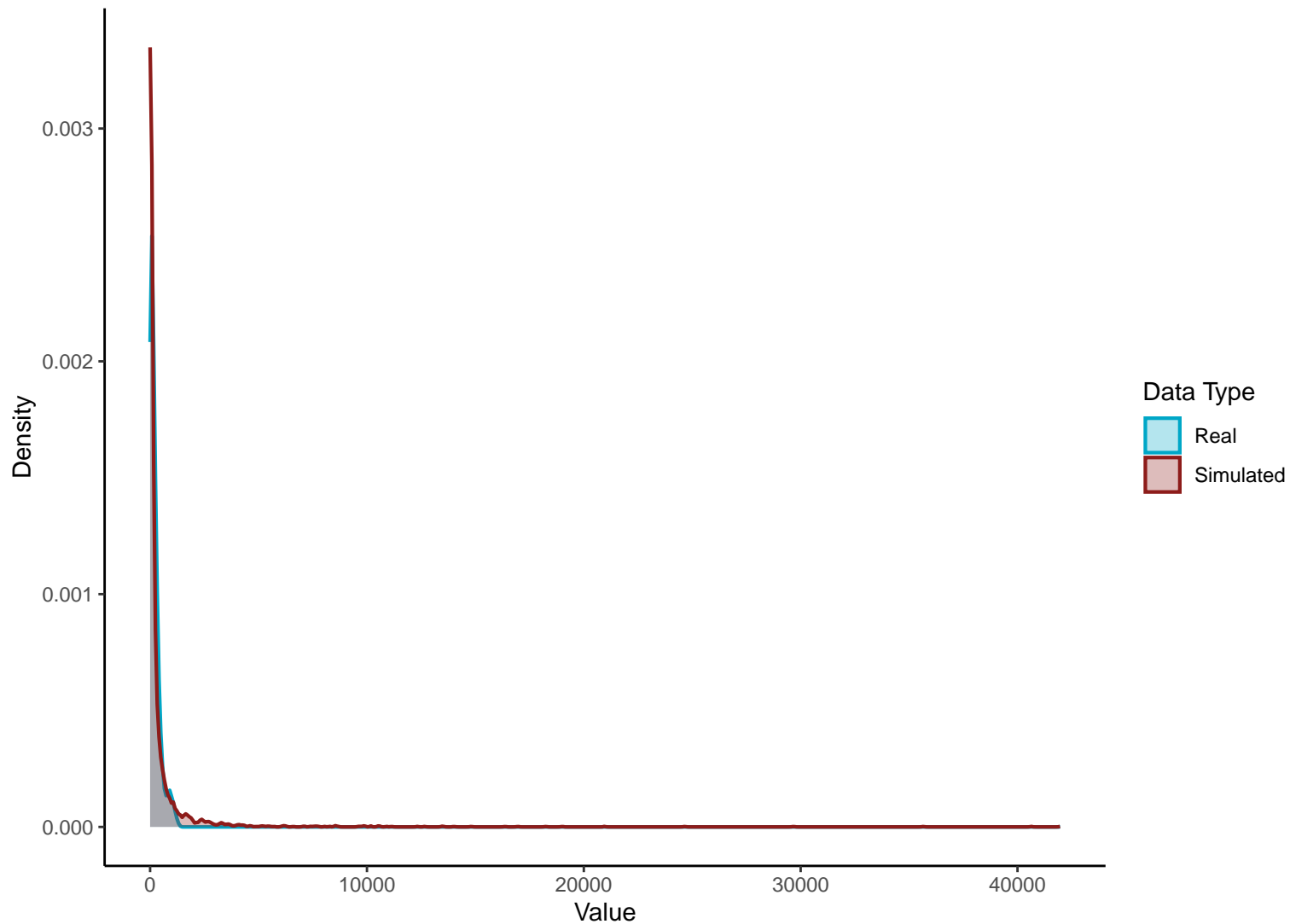
Holdemanella



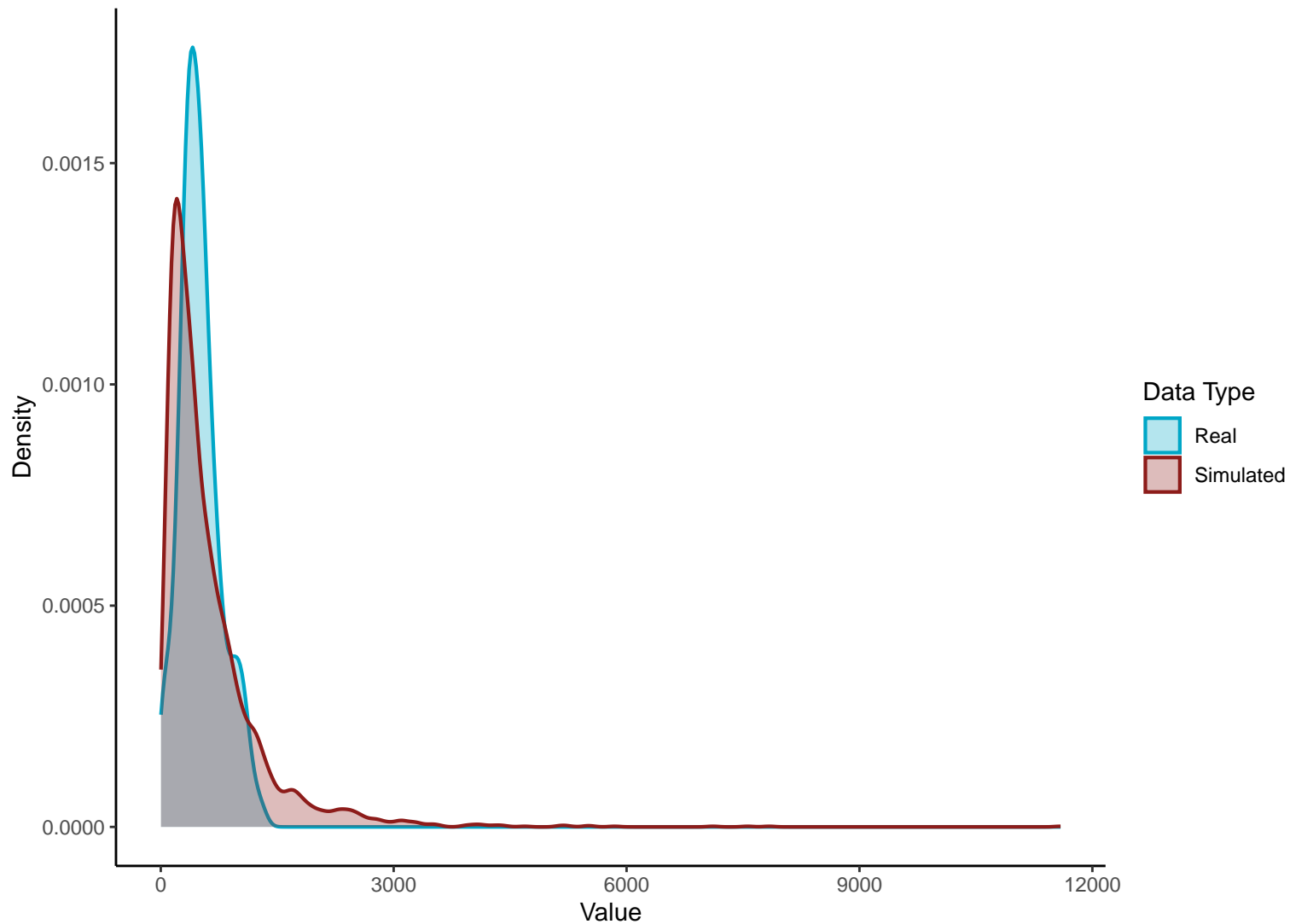
Papillibacter



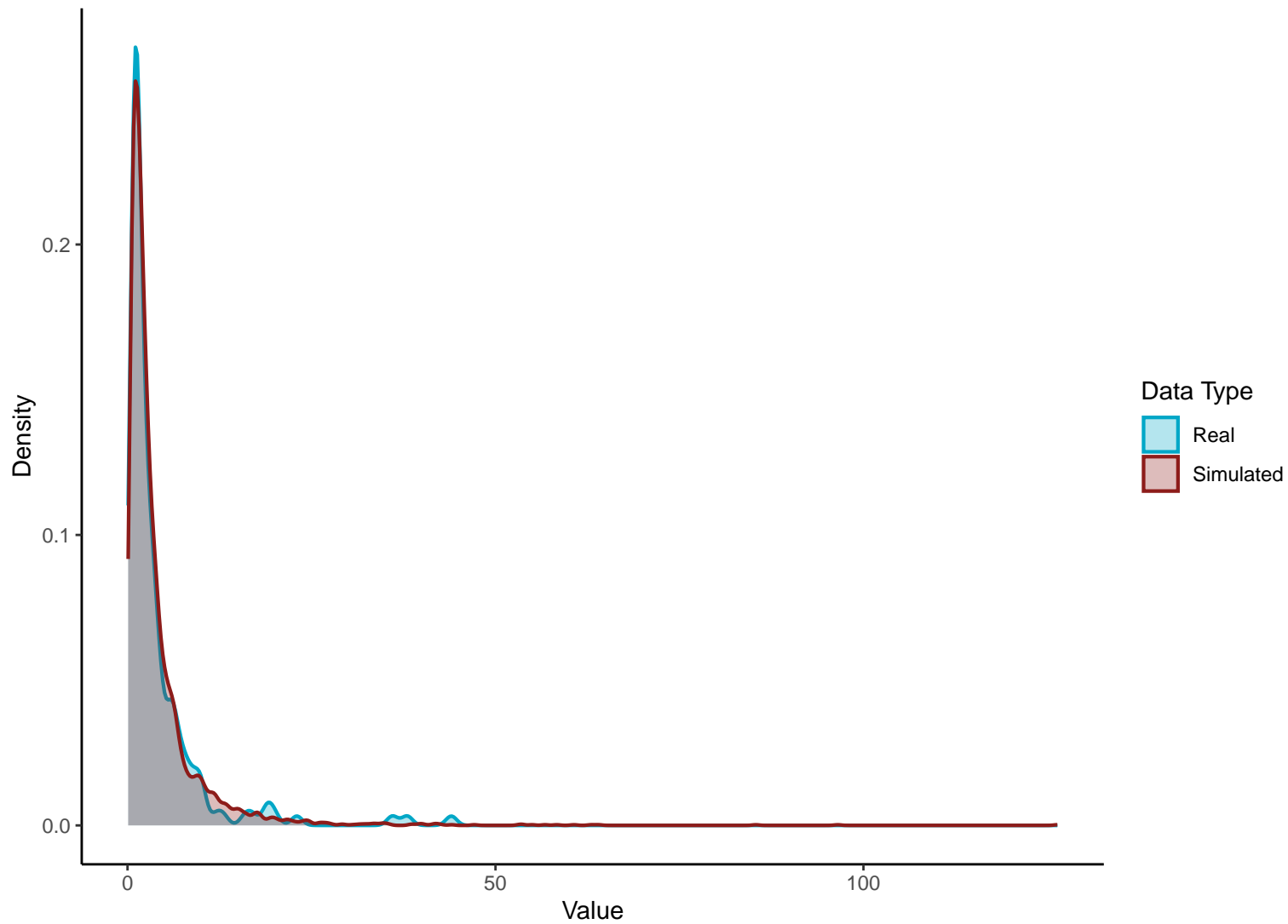
Lachnospiraceae.AC2044.group



Phascolarctobacterium



Fibrobacter



Akkermansia

Density

1.00

0.75

0.50

0.25

0.00

0

20

40

60

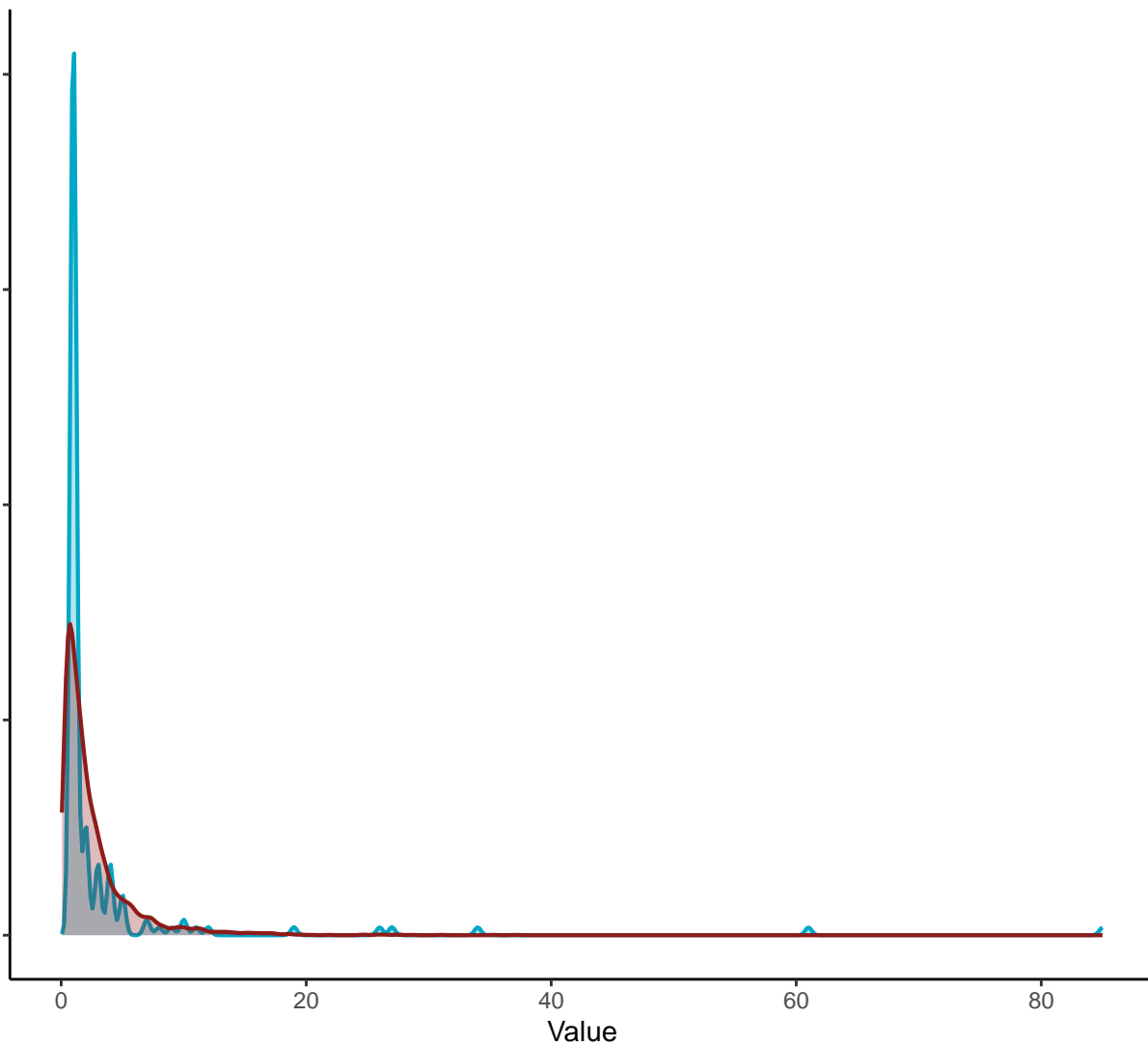
80

Value

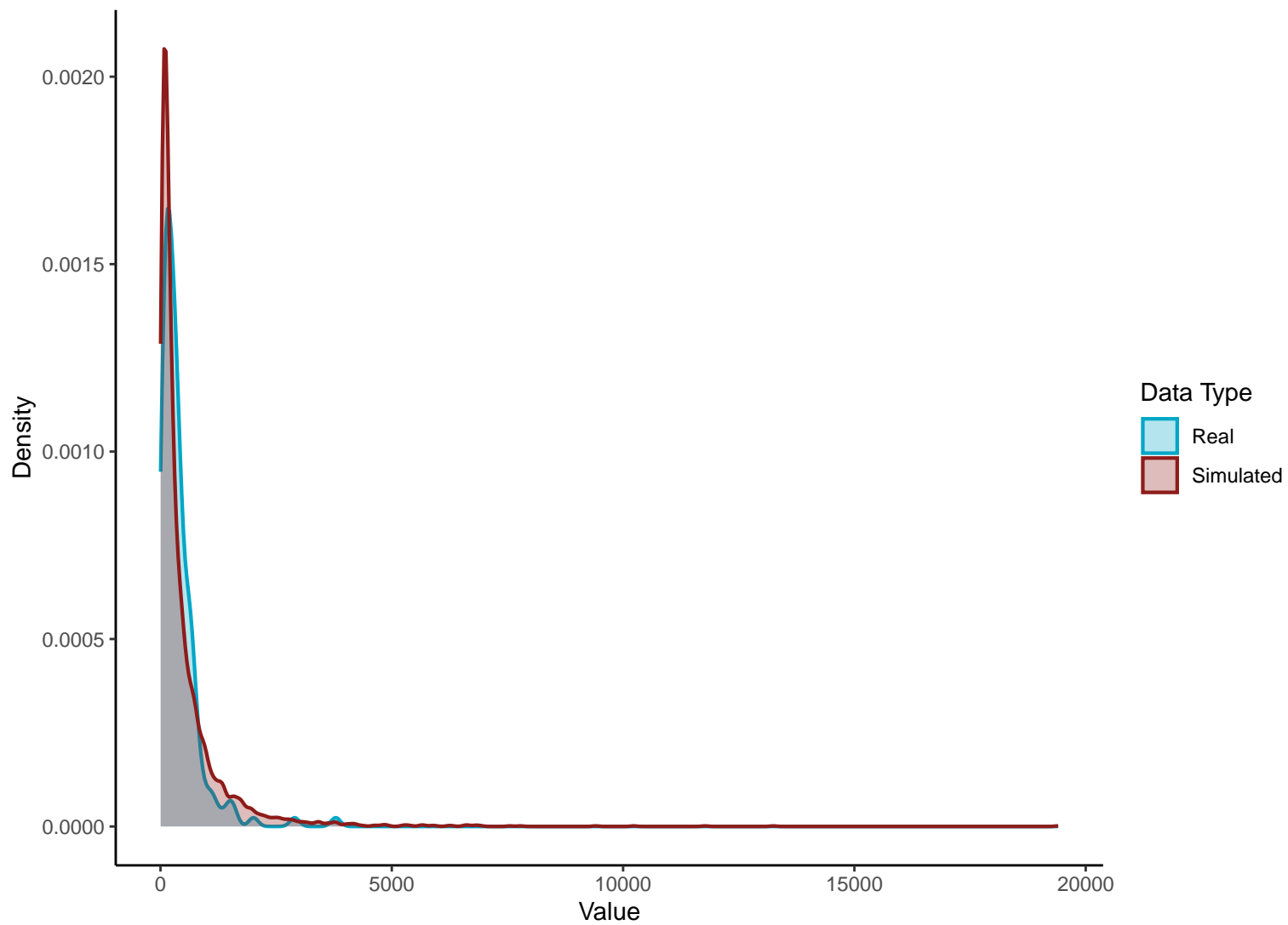
Data Type

Real

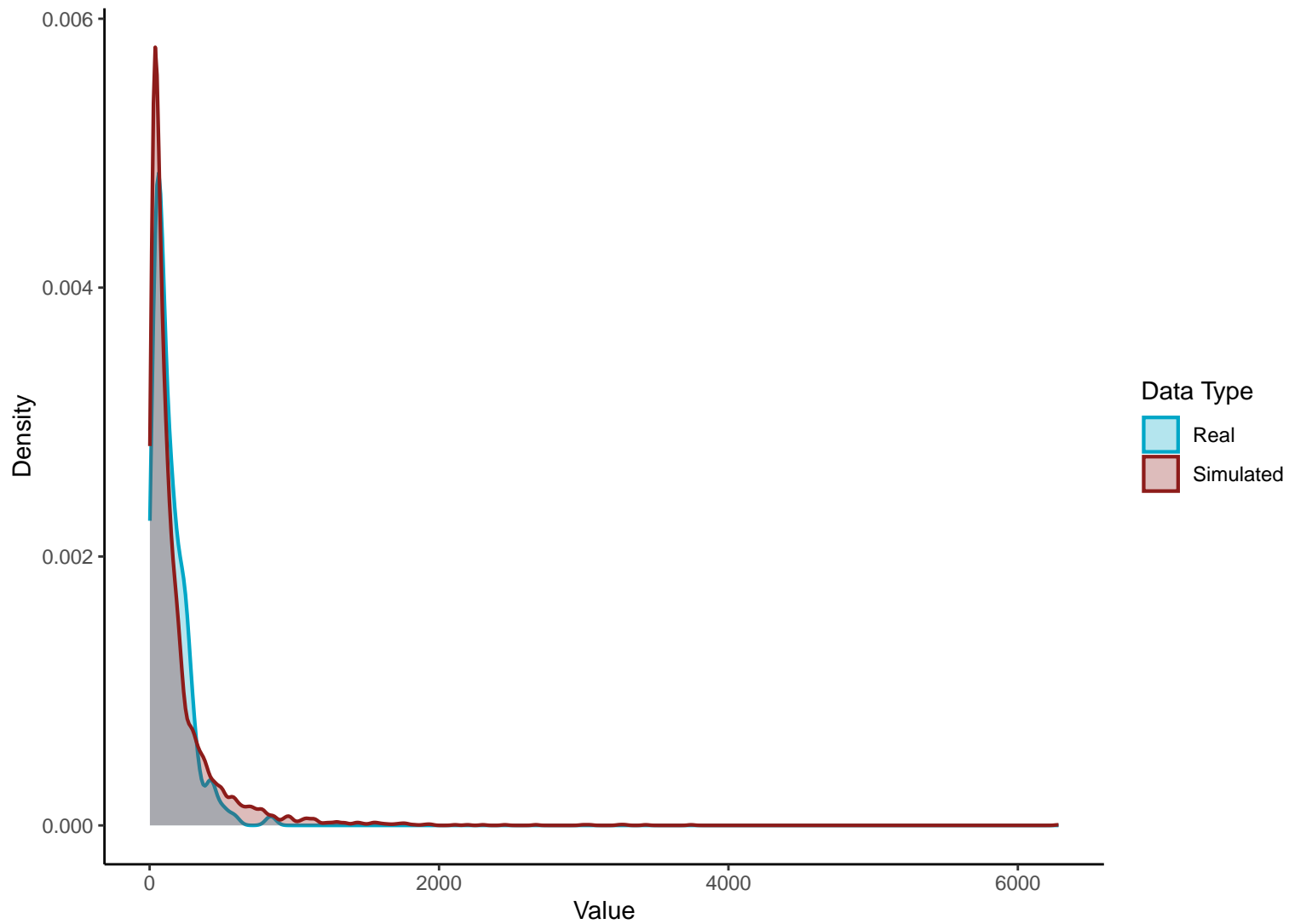
Simulated



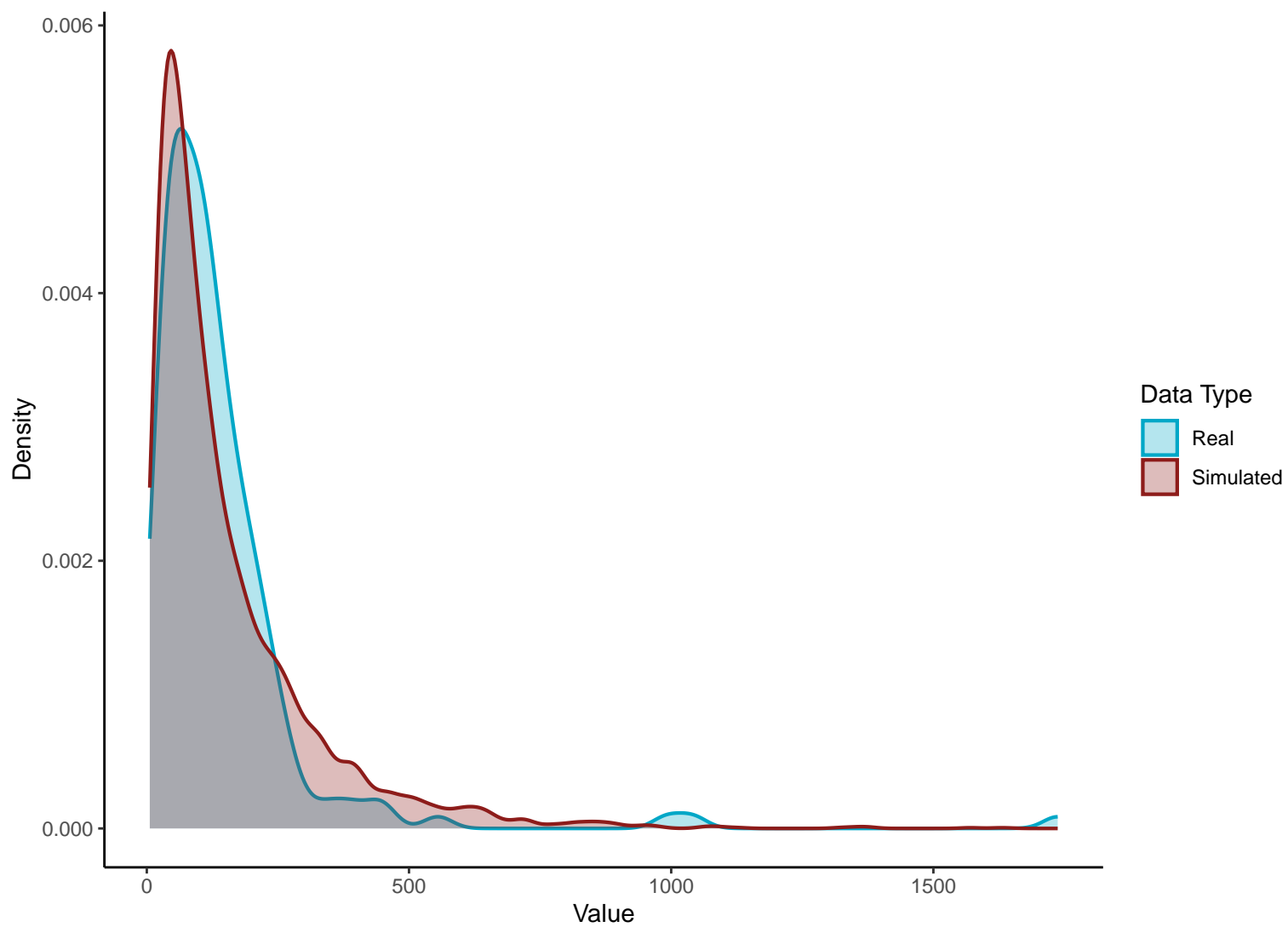
UCG.002



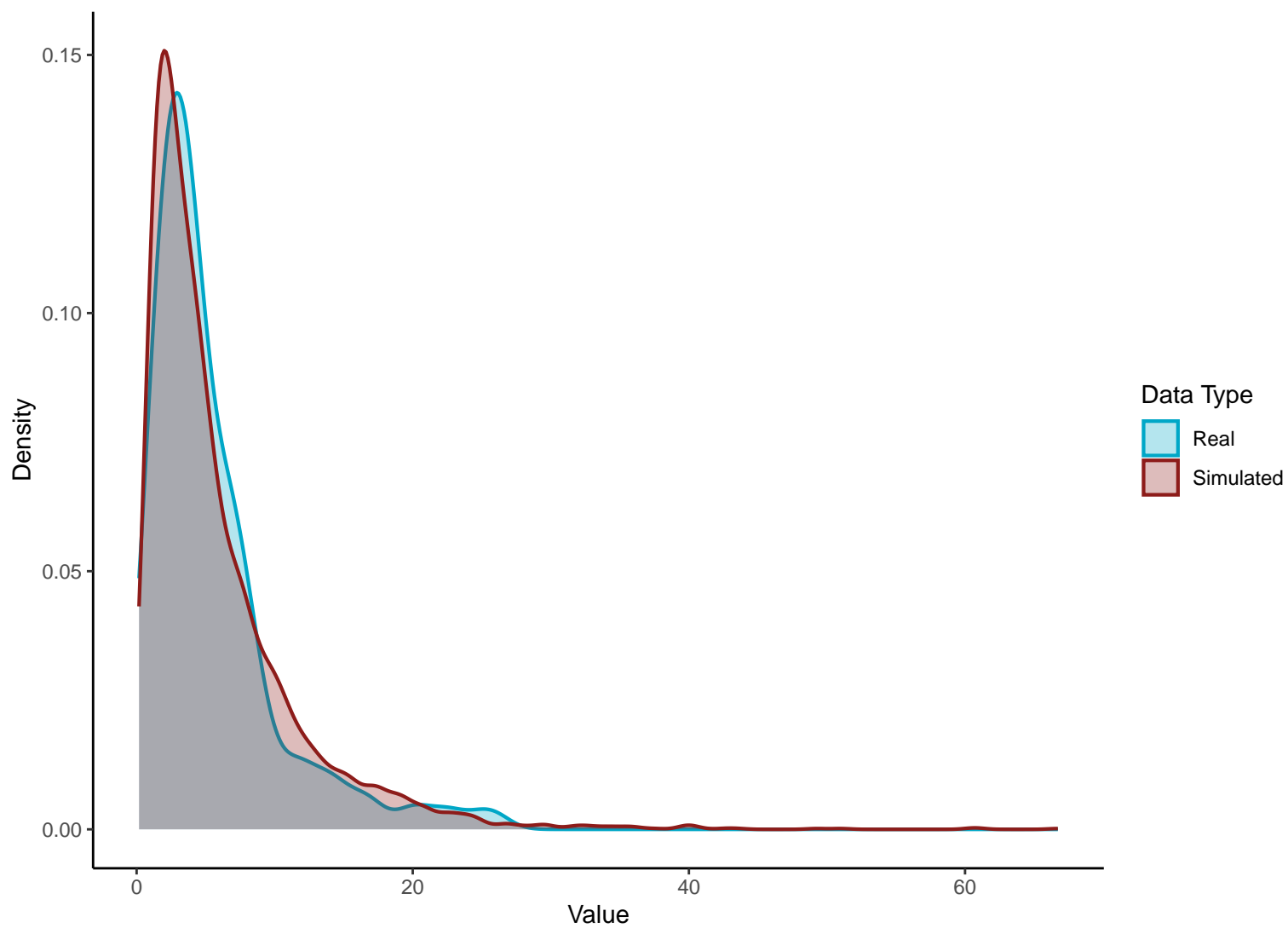
Olsenella



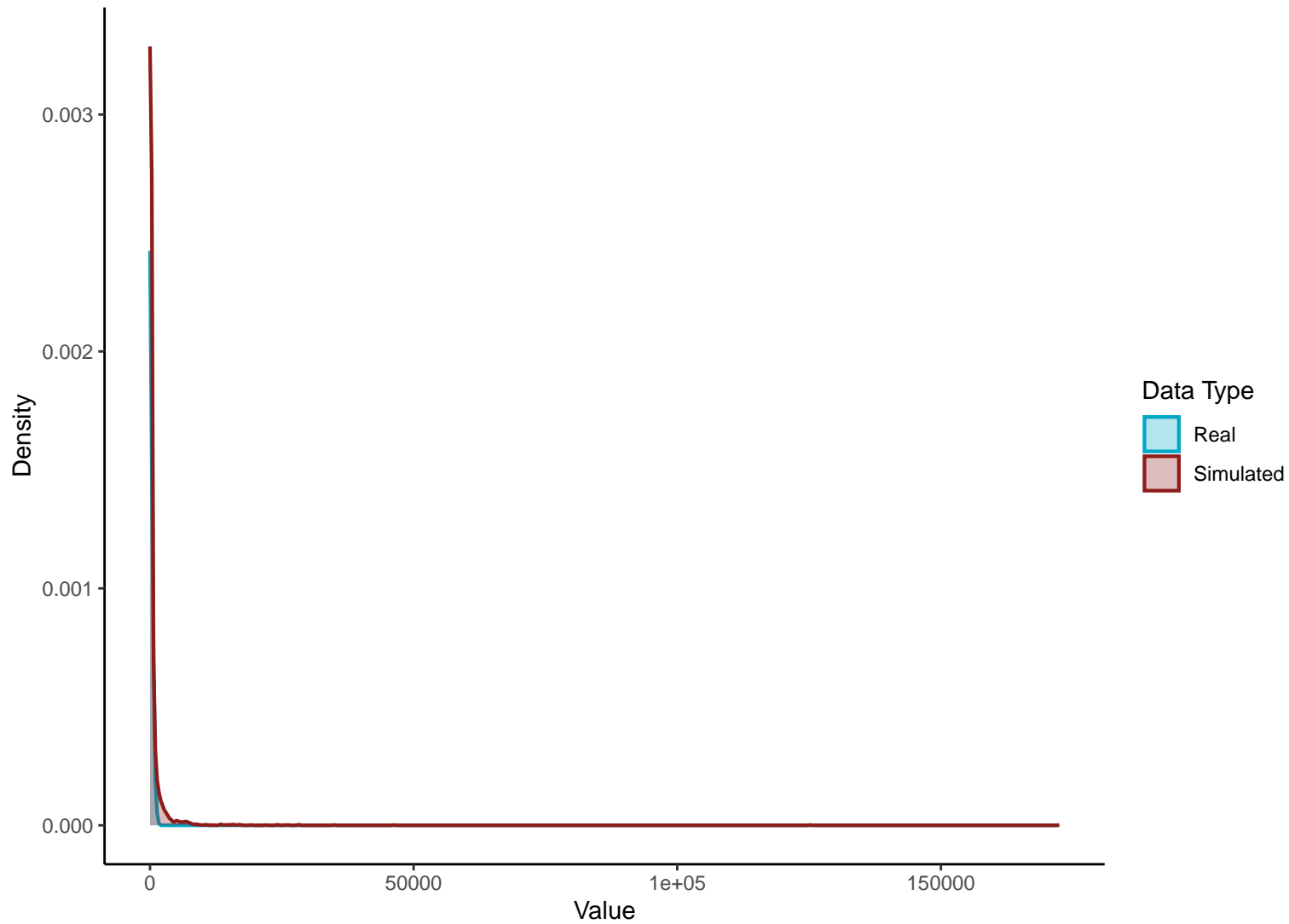
Shuttleworthia



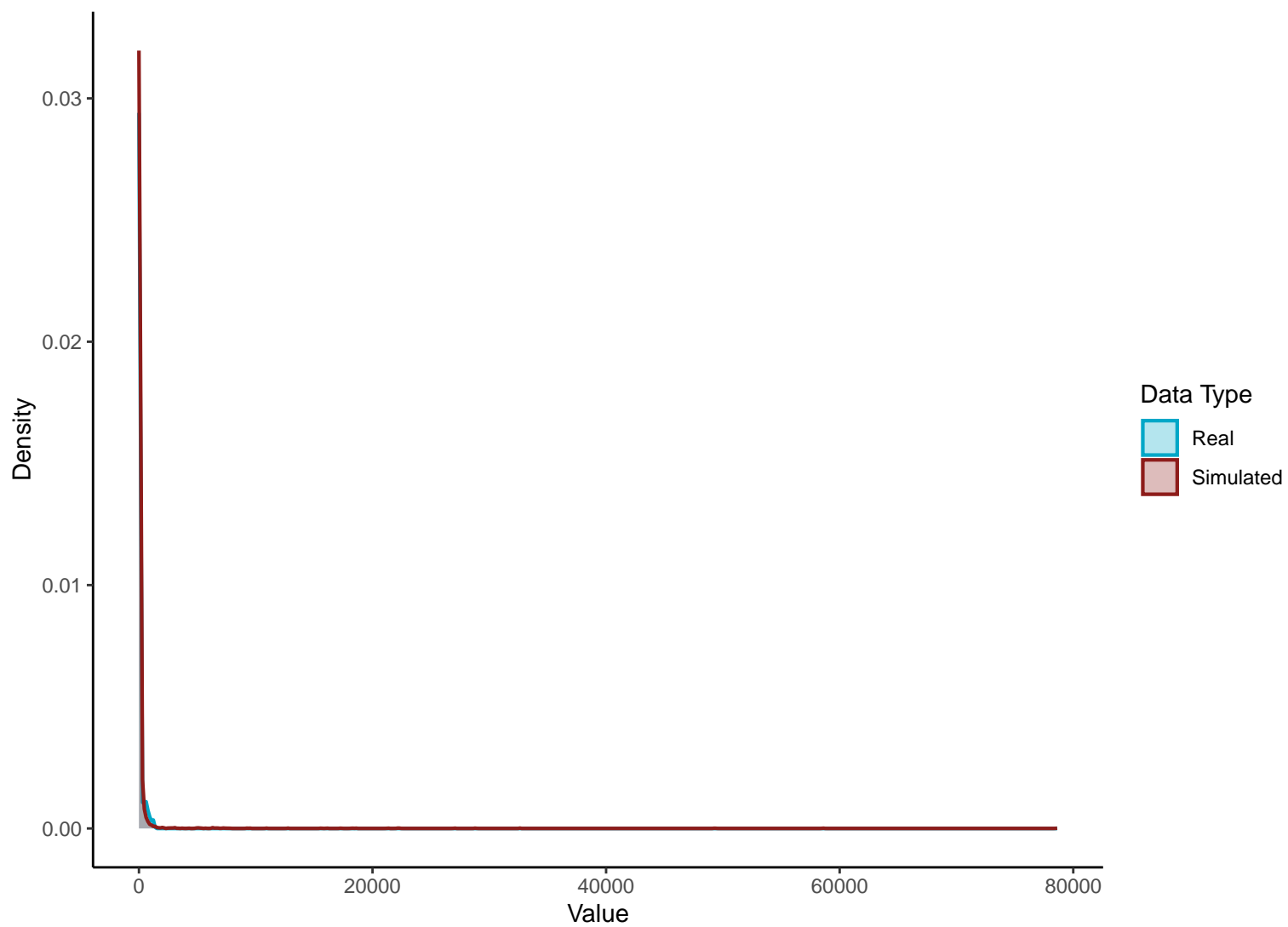
Pygmaibacter



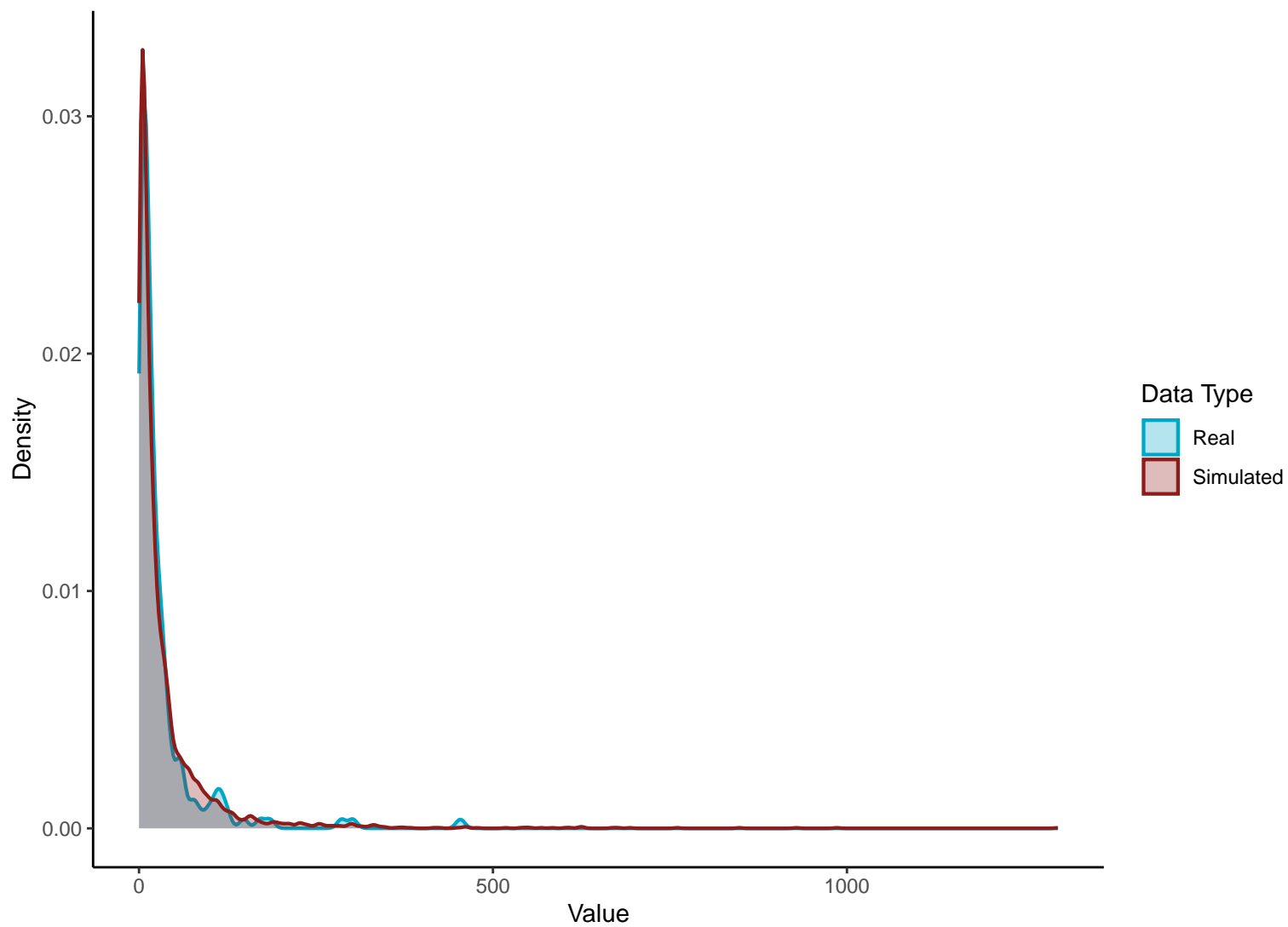
Dialister



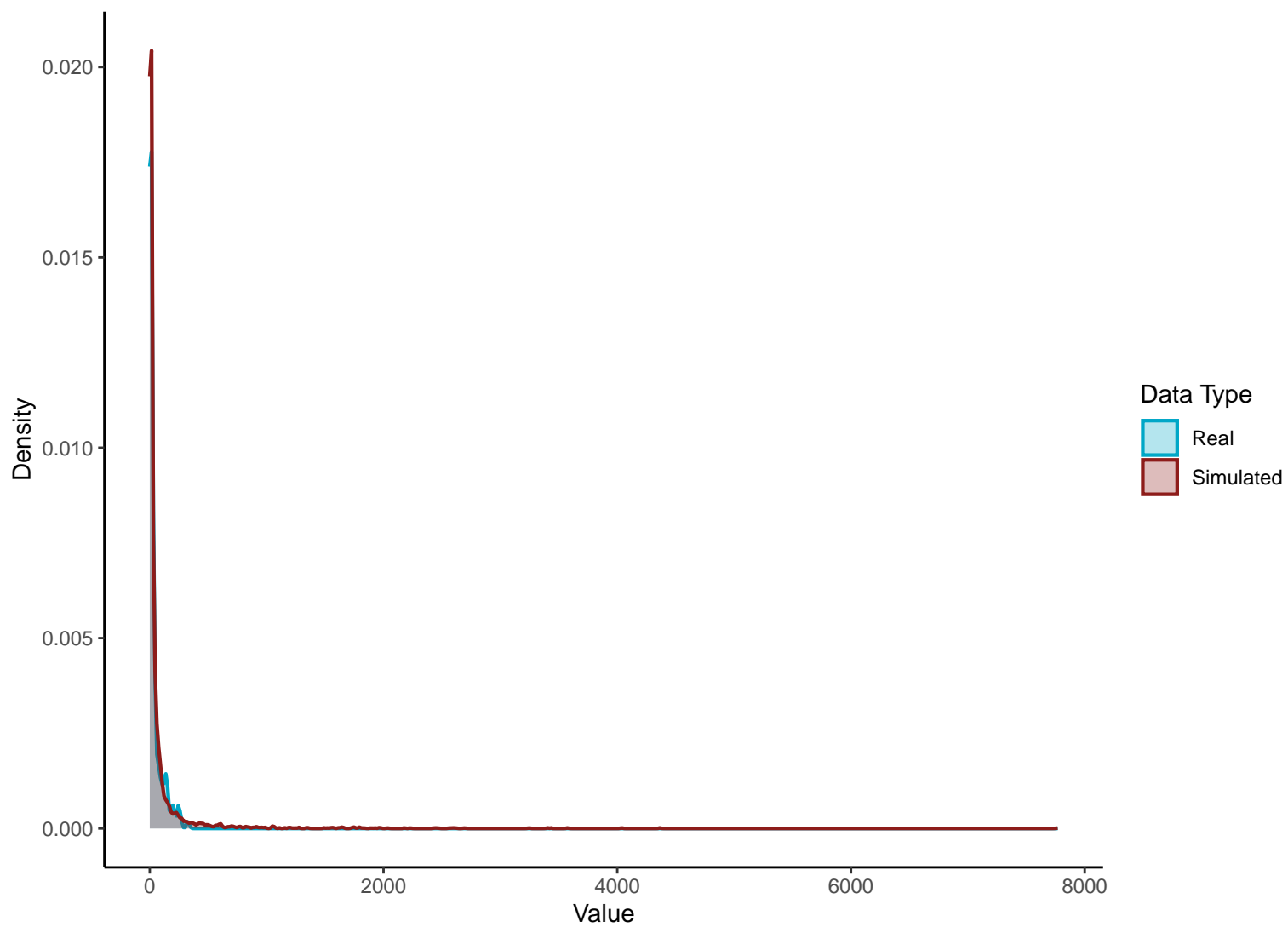
Acetitomaculum



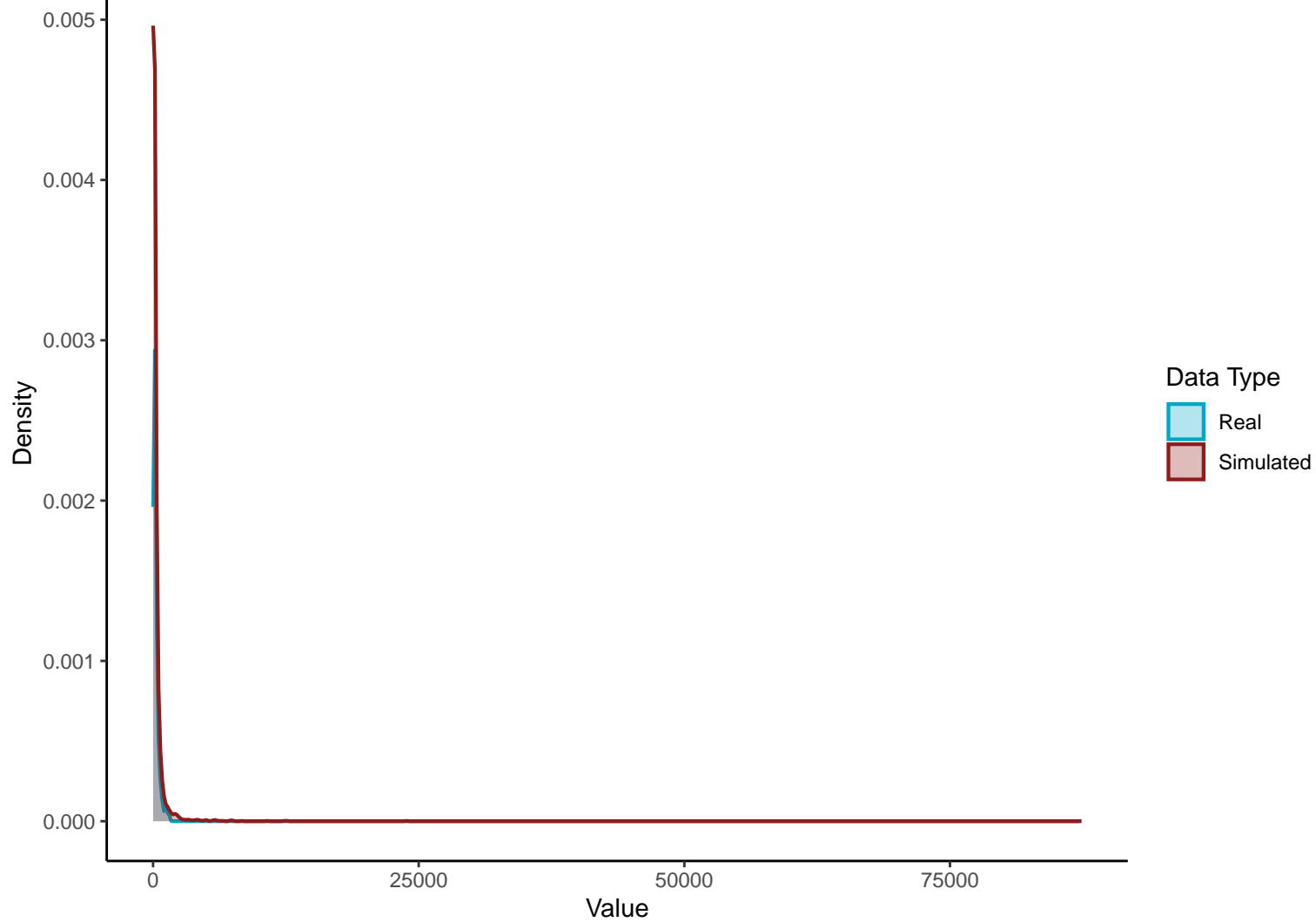
Campylobacter



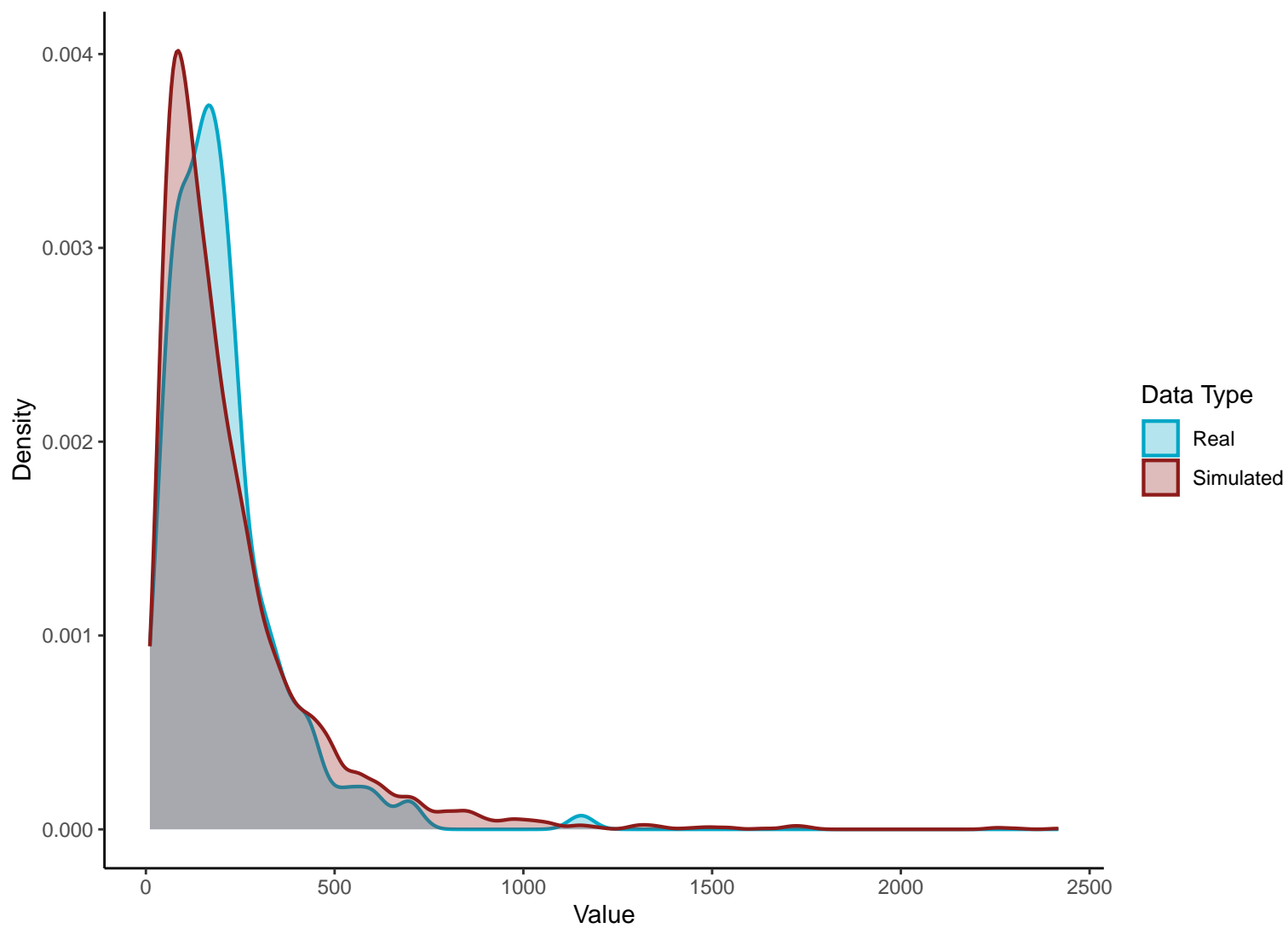
Anaerosporobacter



Anaerostipes



Collinsella



Sarcina

Density

0.04

0.03

0.02

0.01

0.00

0

1000

2000

3000

4000

Value

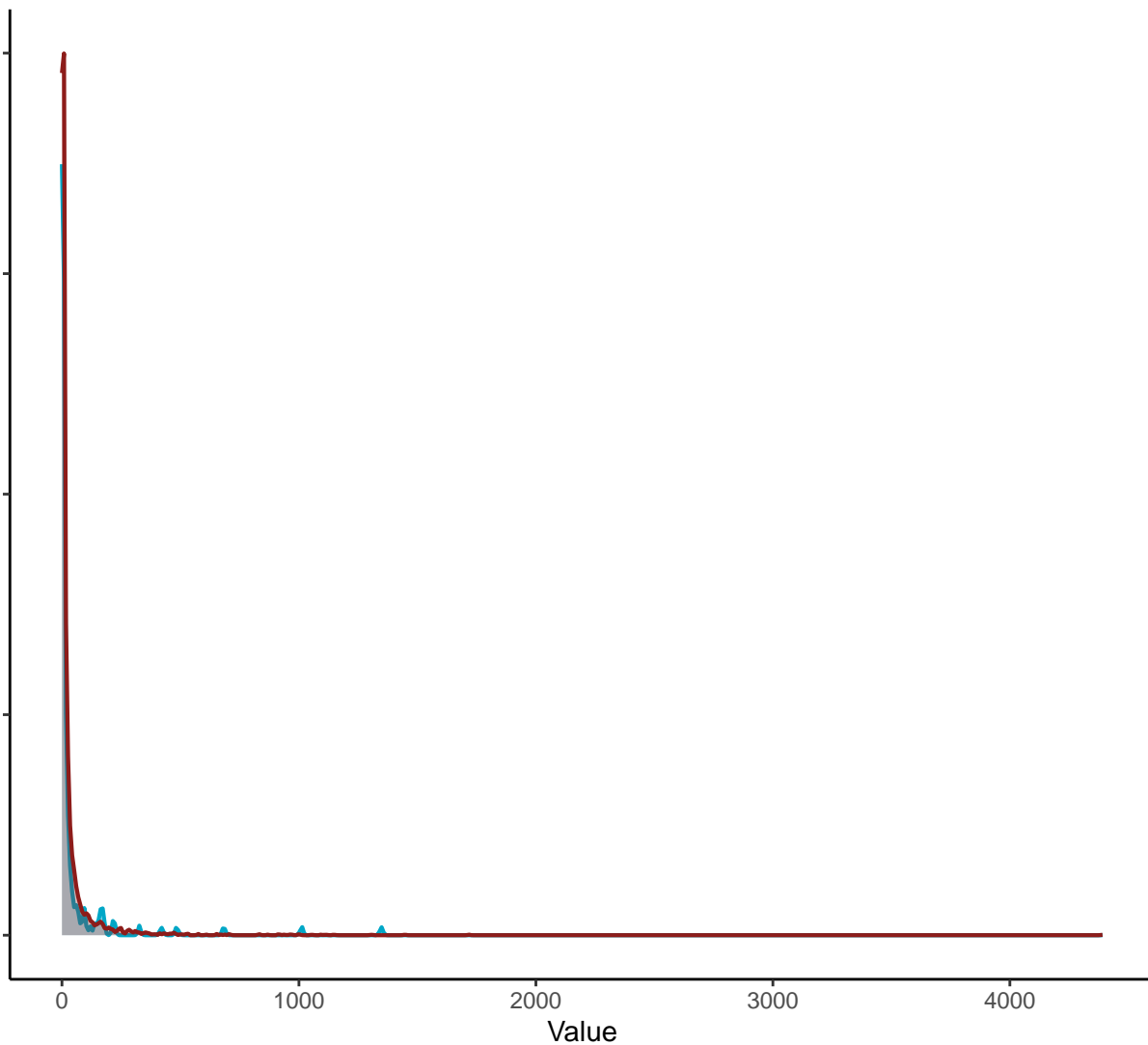
Data Type



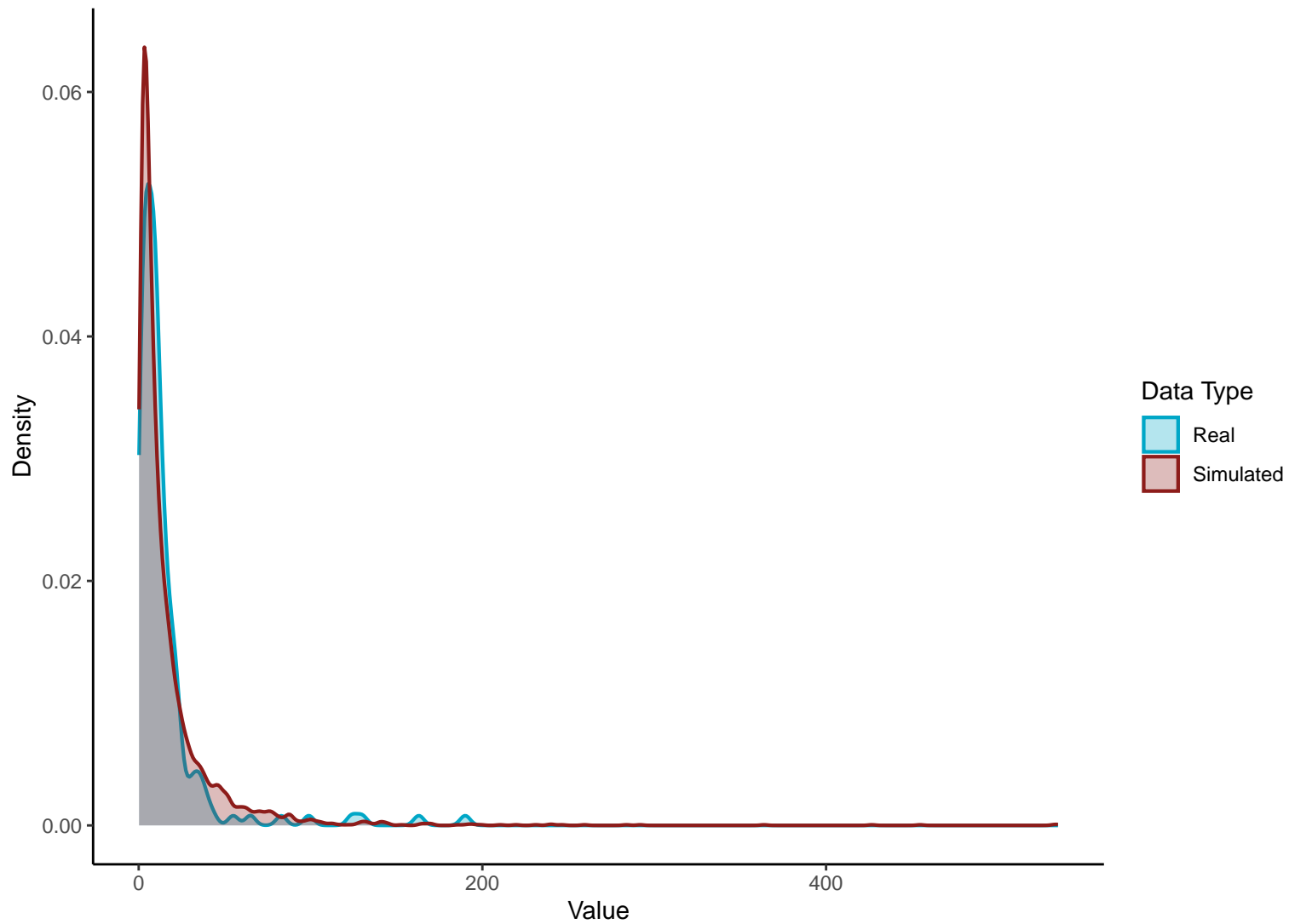
Real



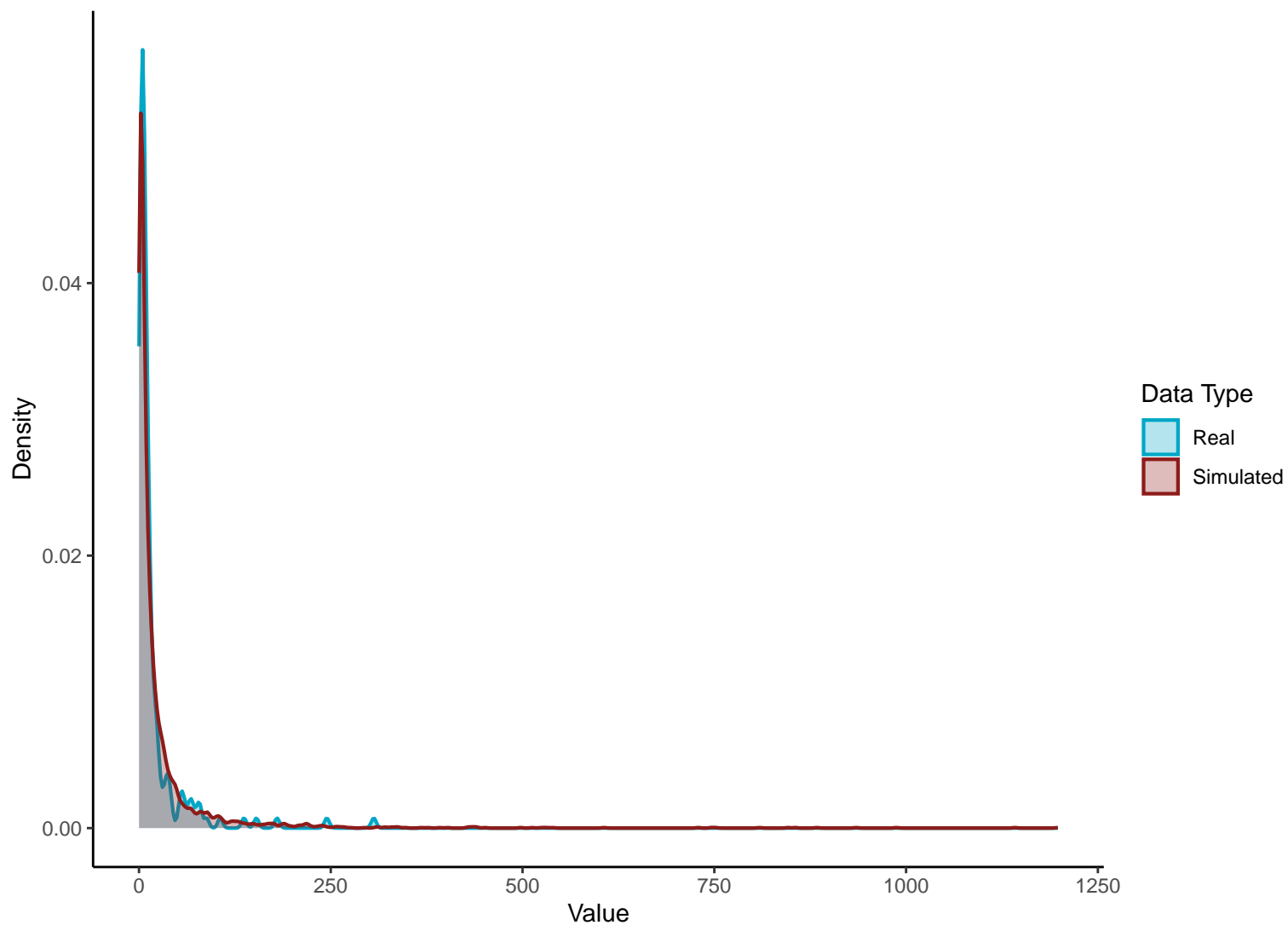
Simulated



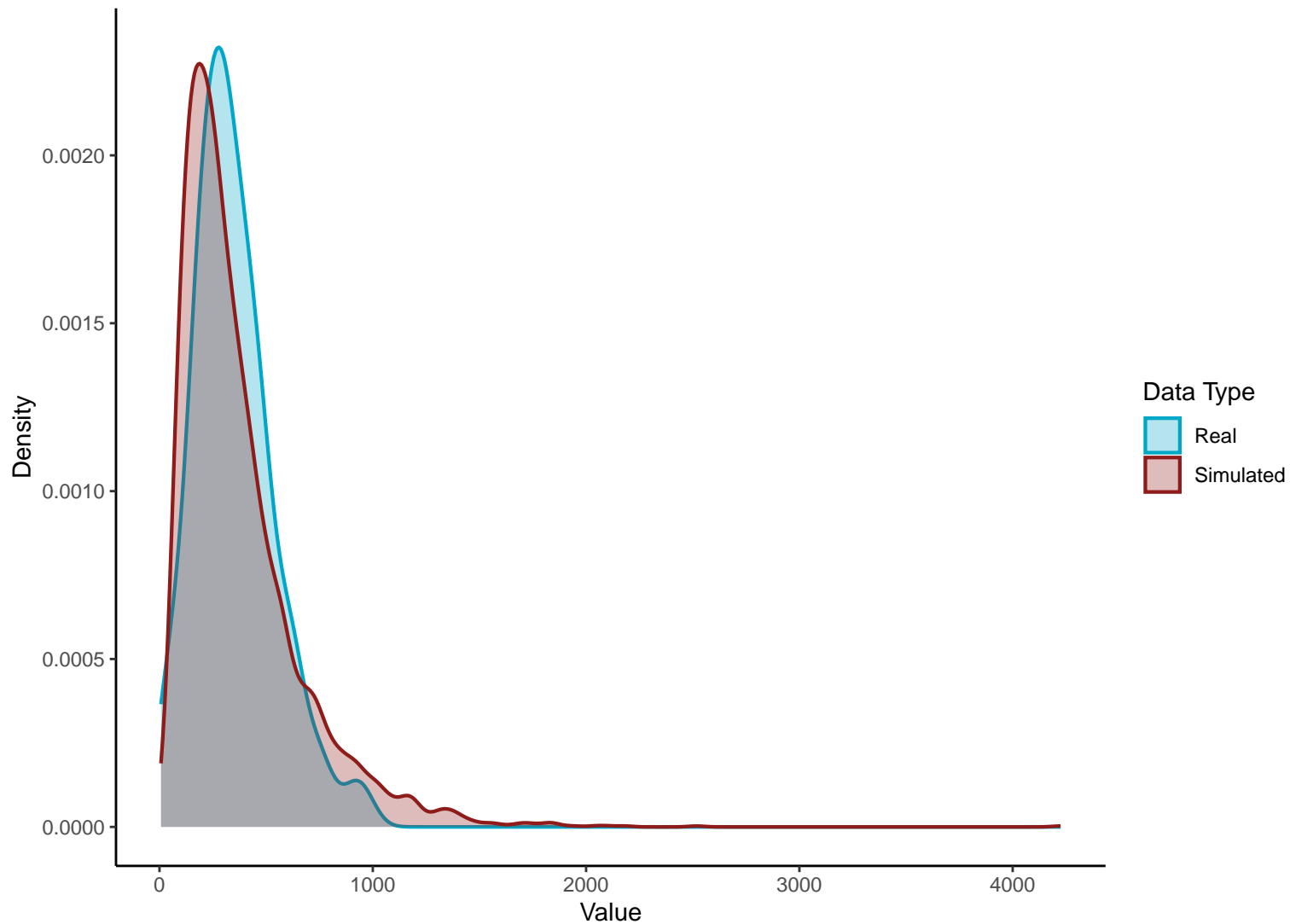
X.Eubacterium..eligens.group



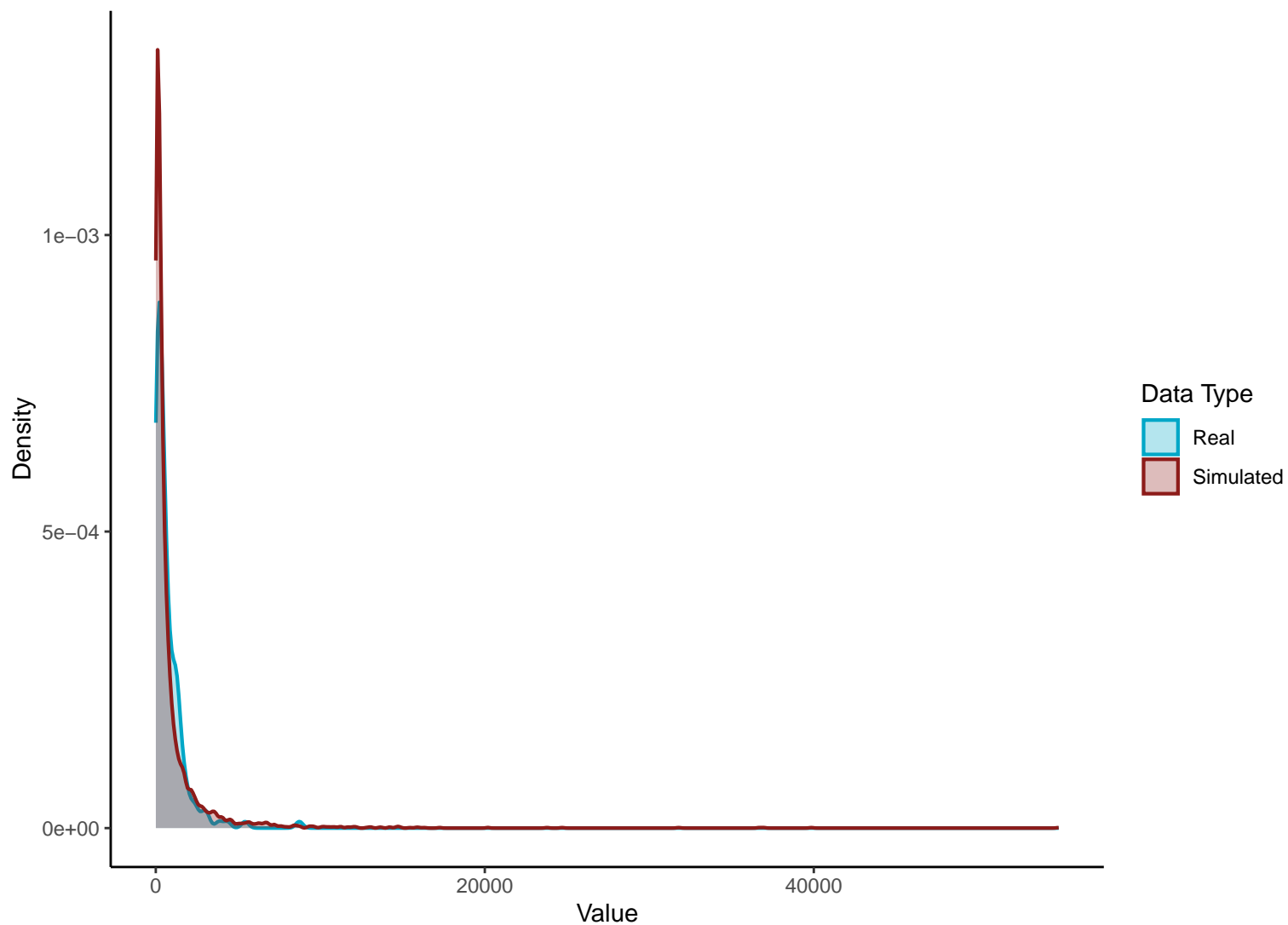
Corynebacterium



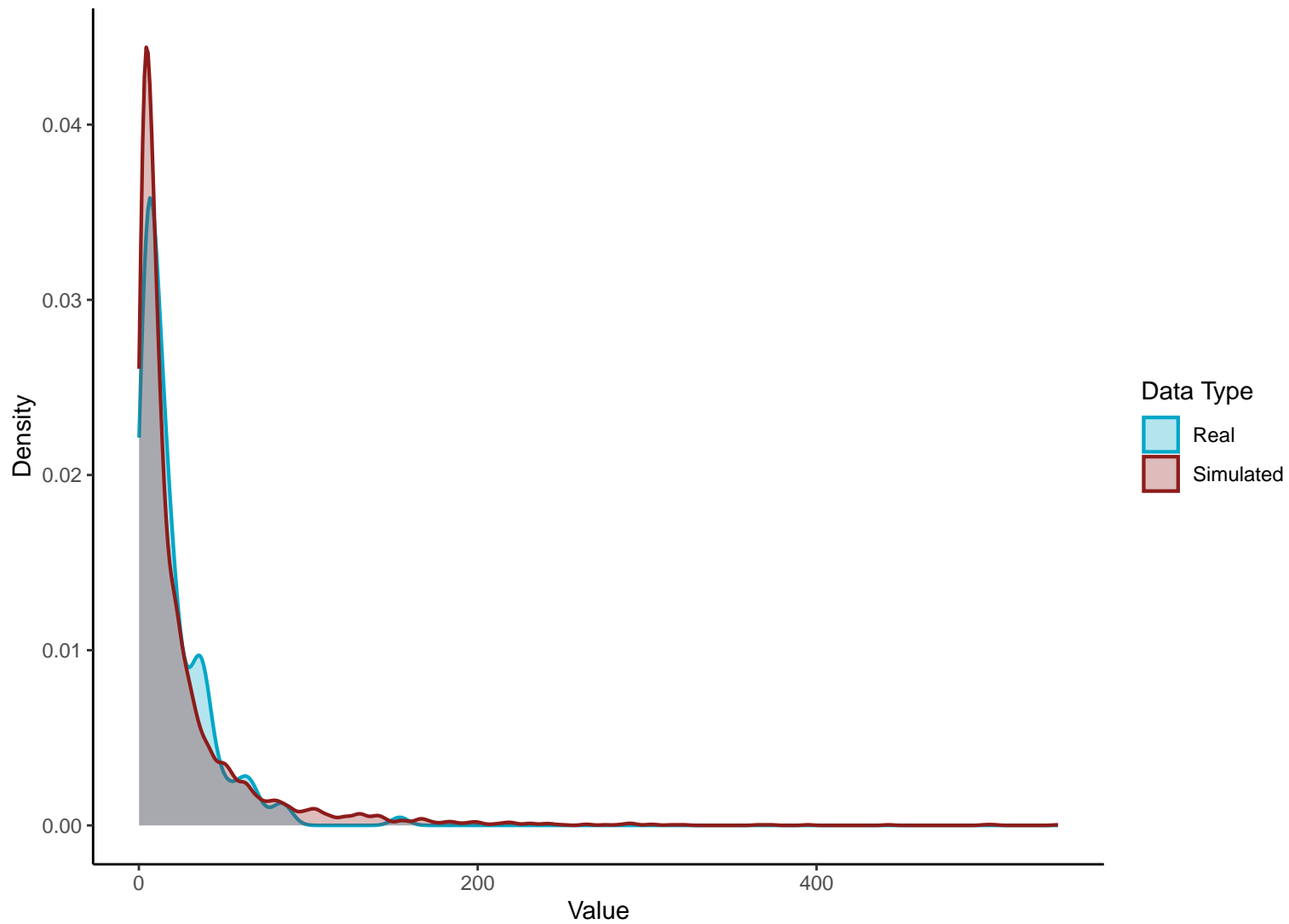
X.Ruminococcus..gauvreauii.group



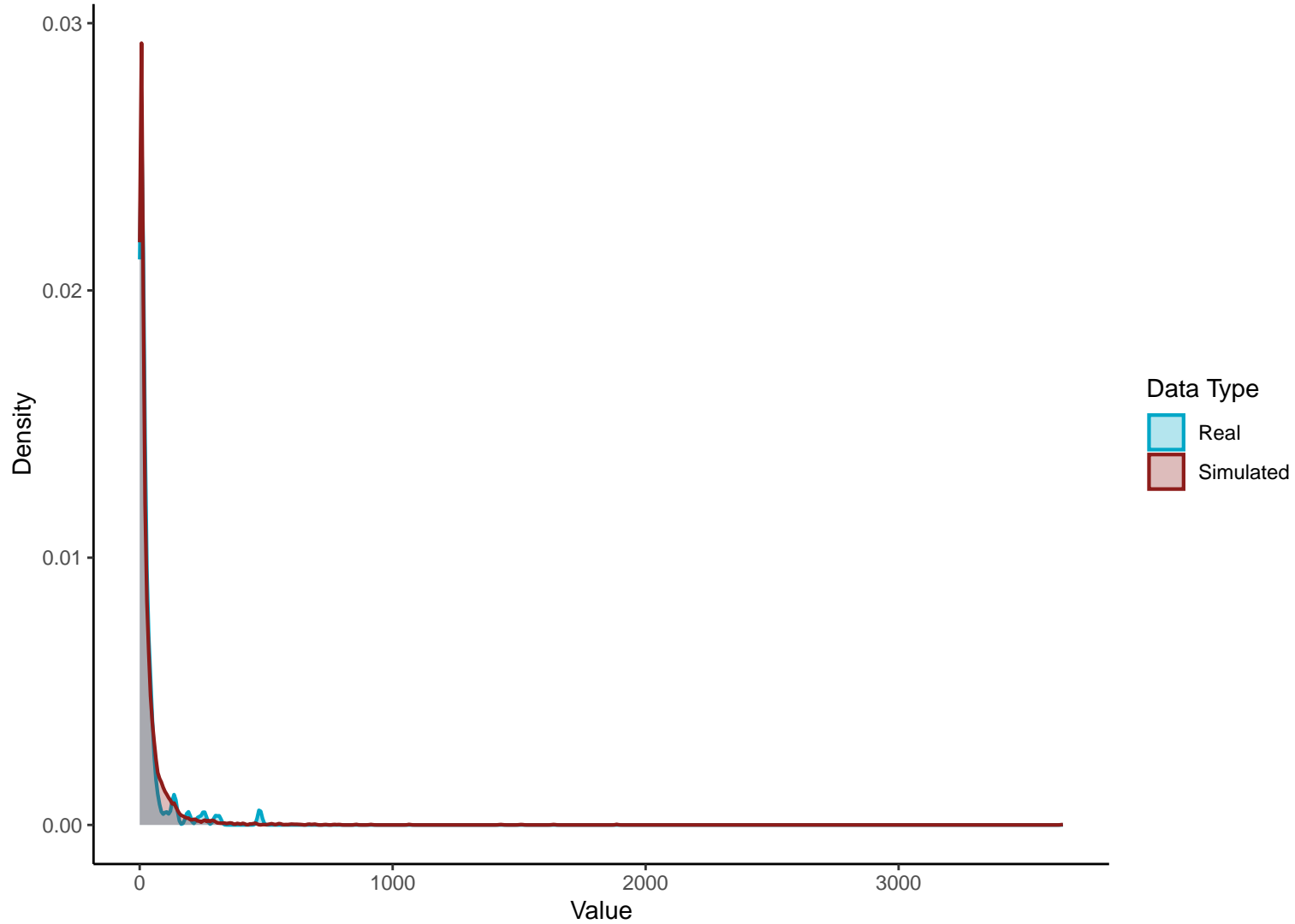
Megasphaera



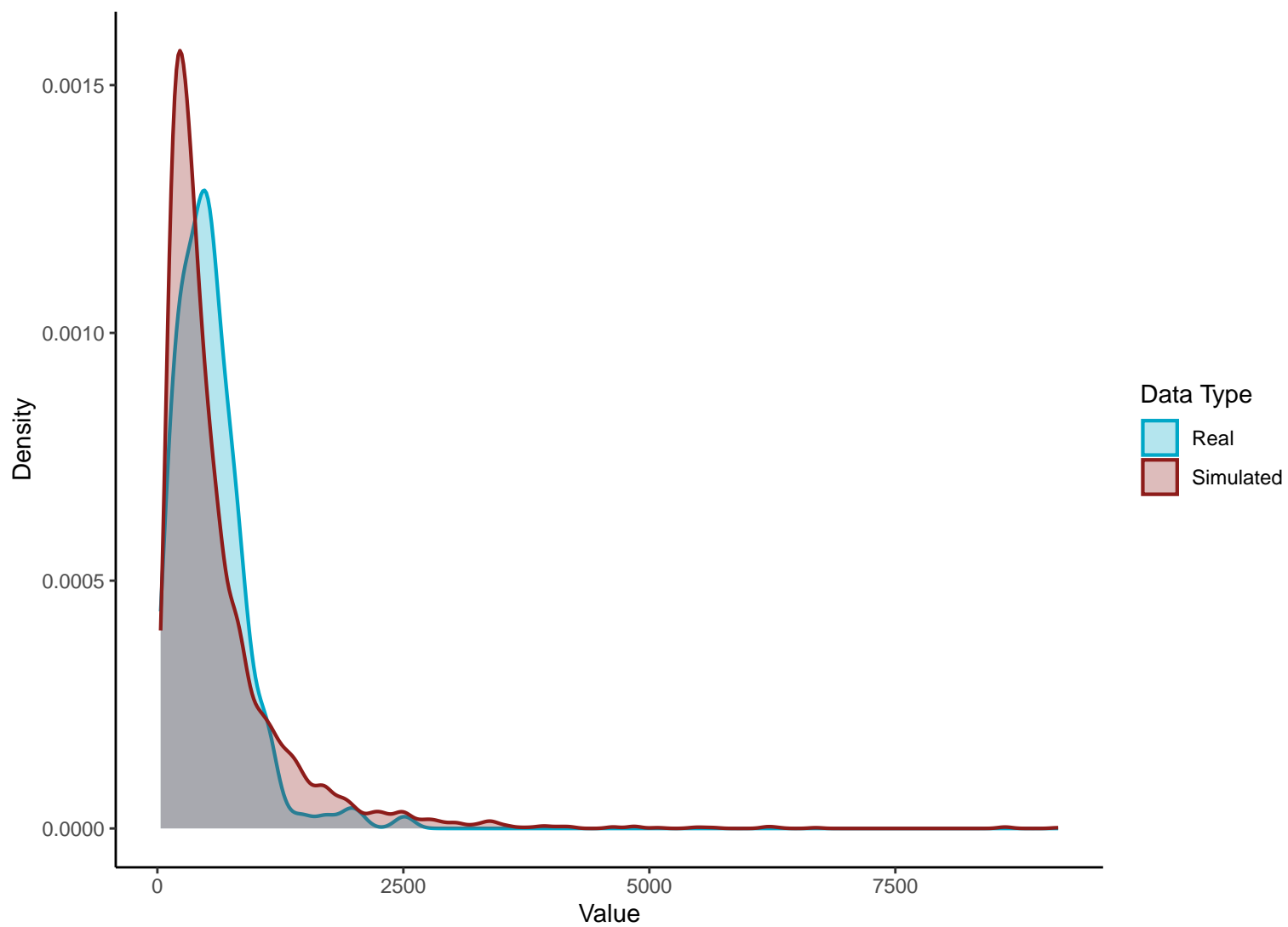
Candidatus.Saccharimonas



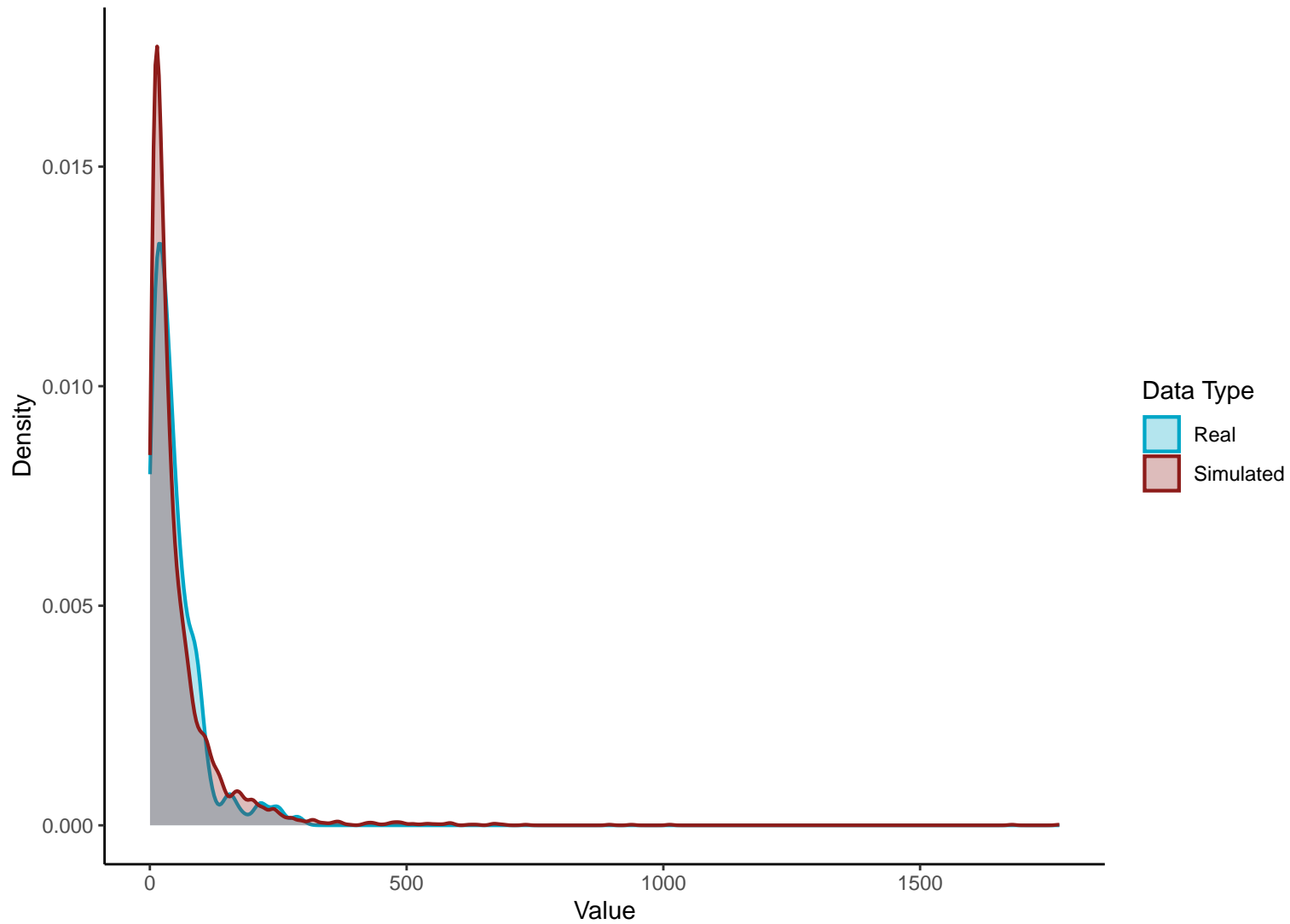
Lachnospira



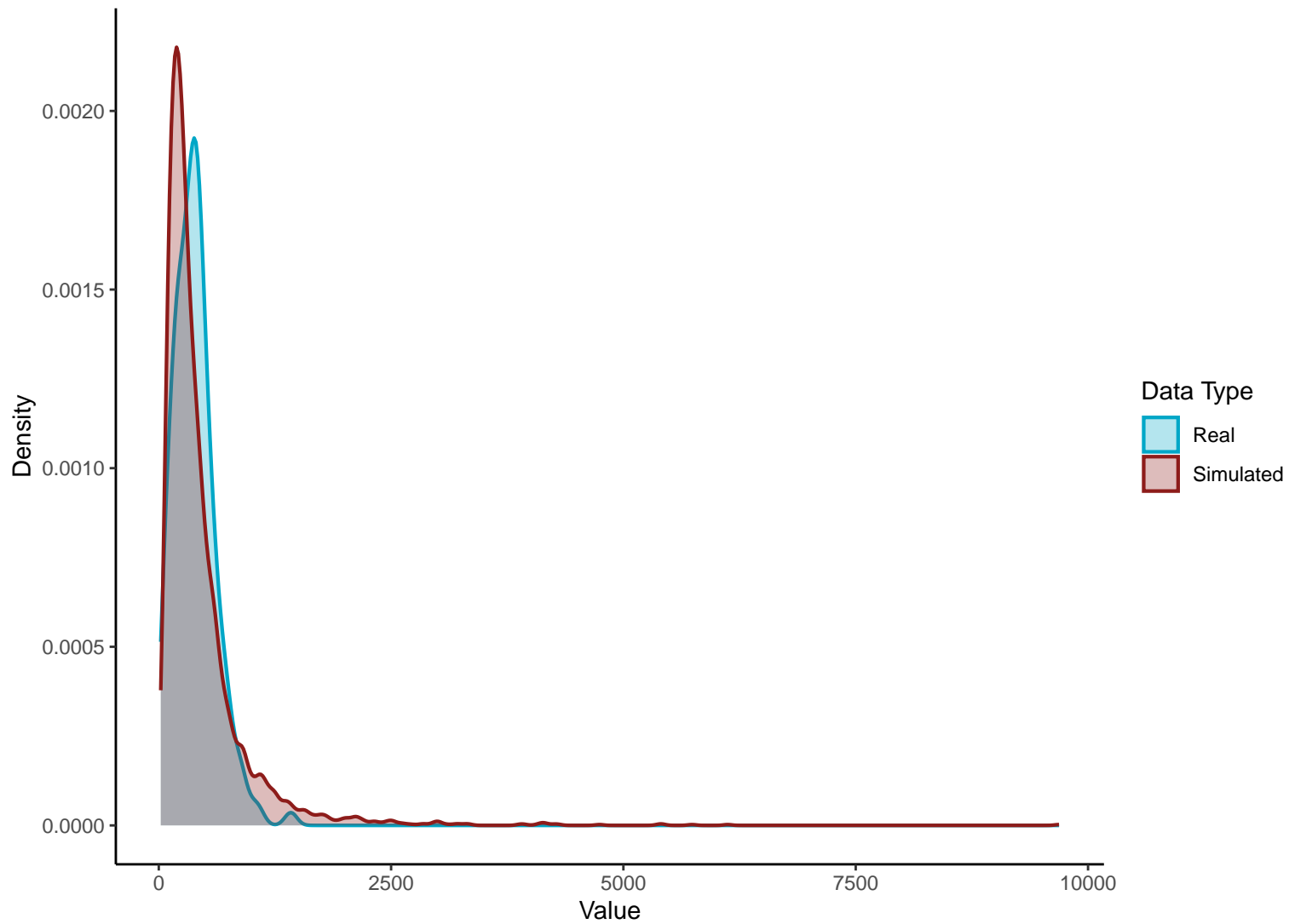
Dorea



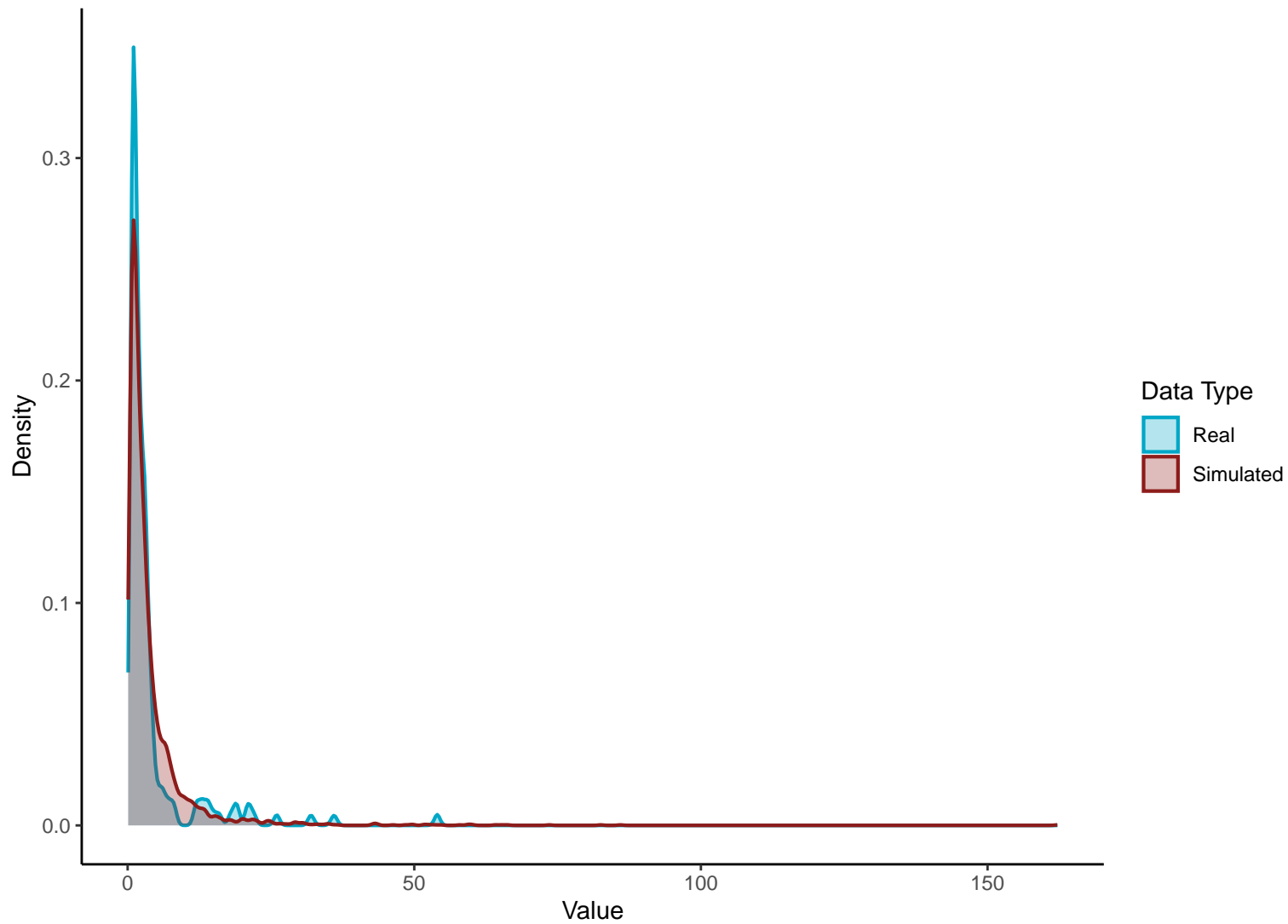
Candidatus.Soleaferrea



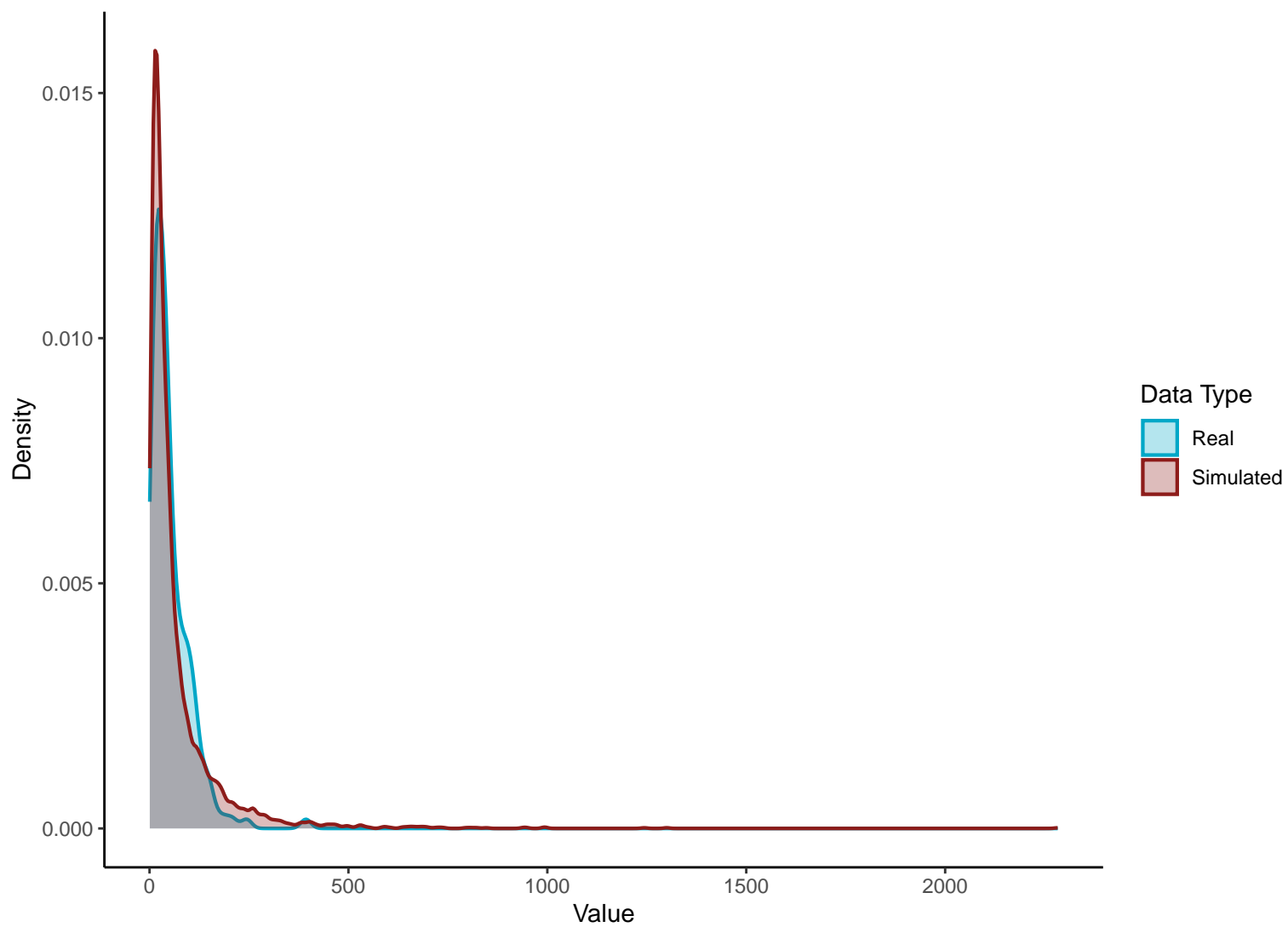
Oribacterium



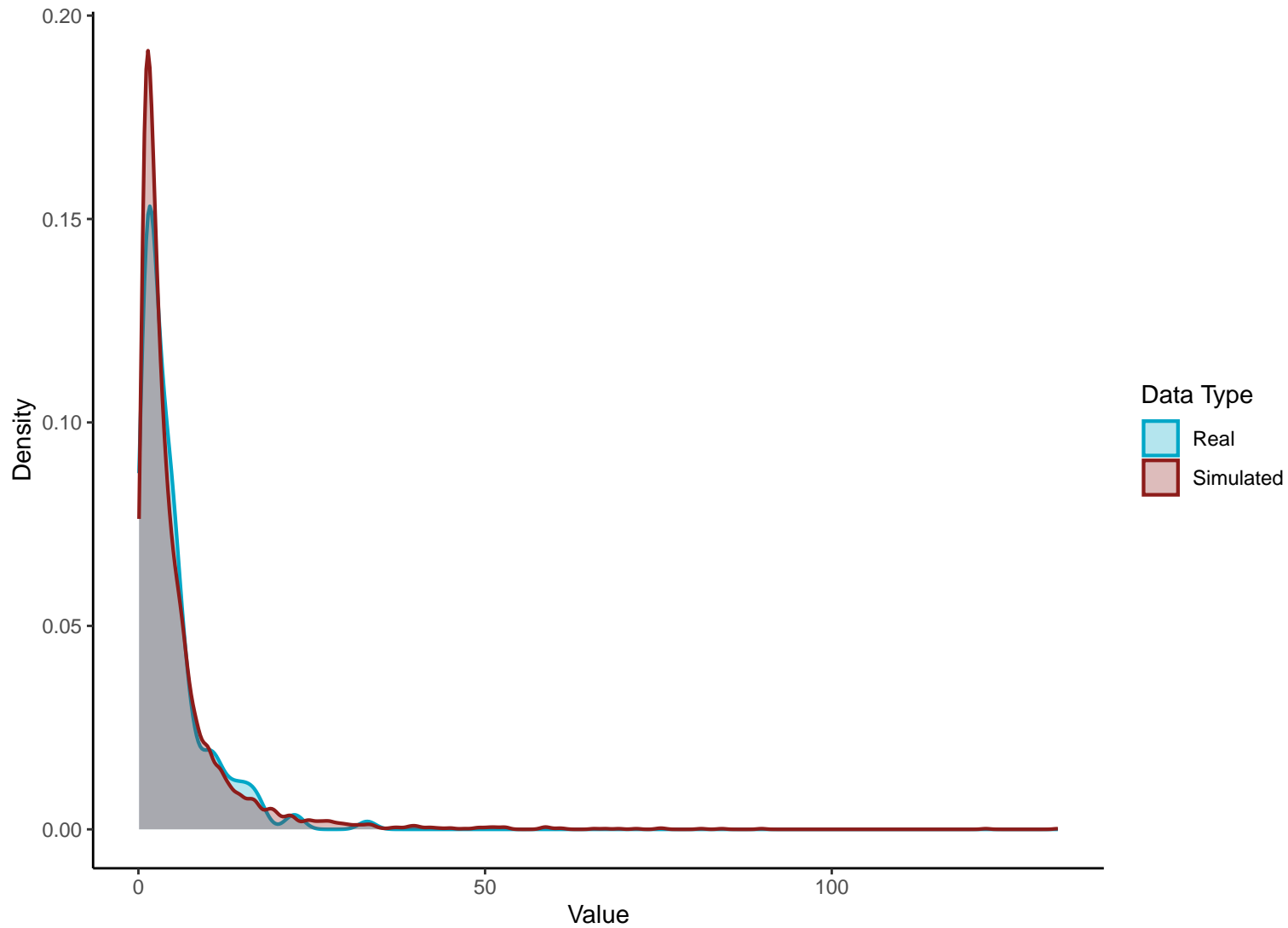
Helicobacter



Oscillospira

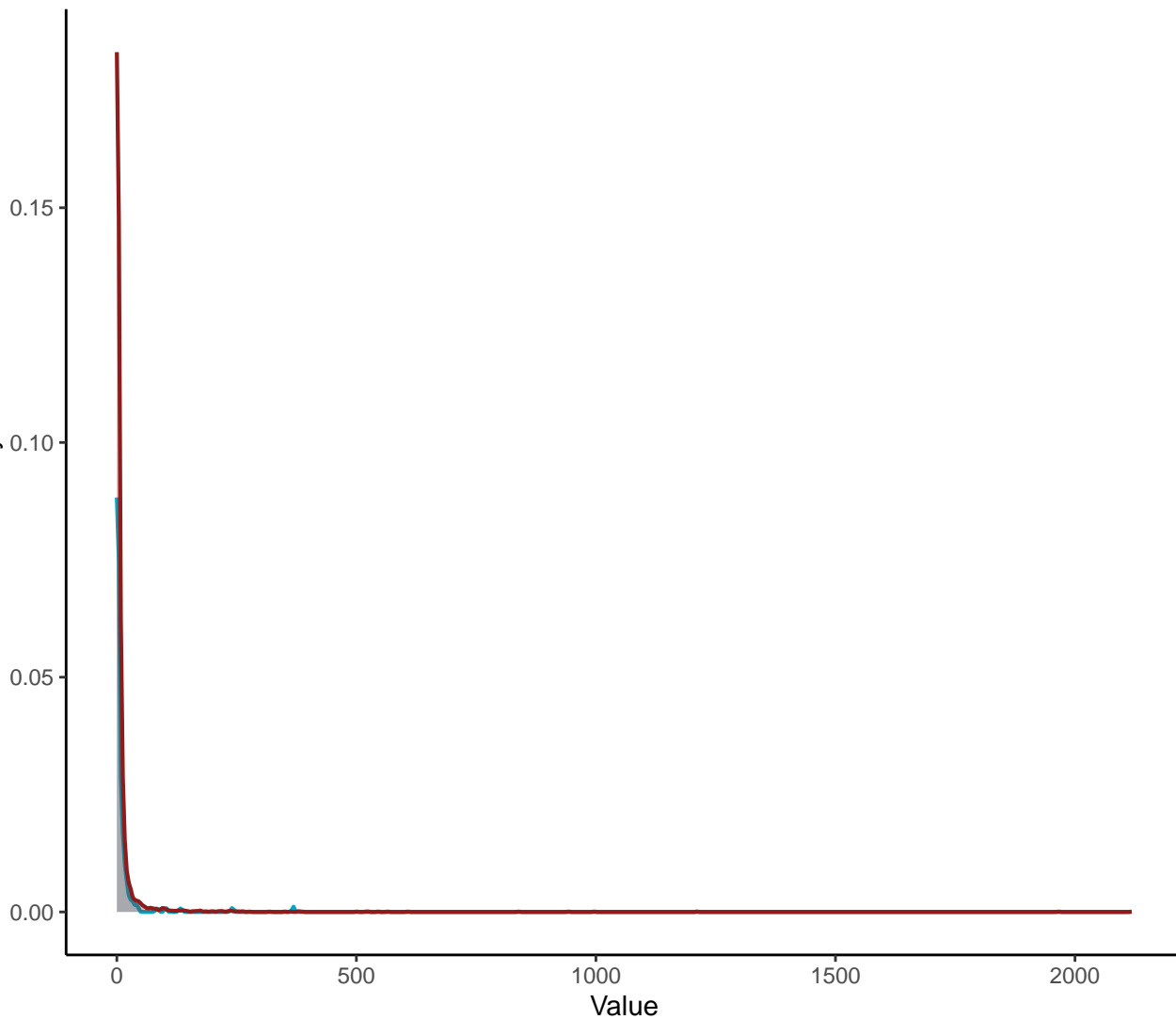


Mailhella



Negativibacillus

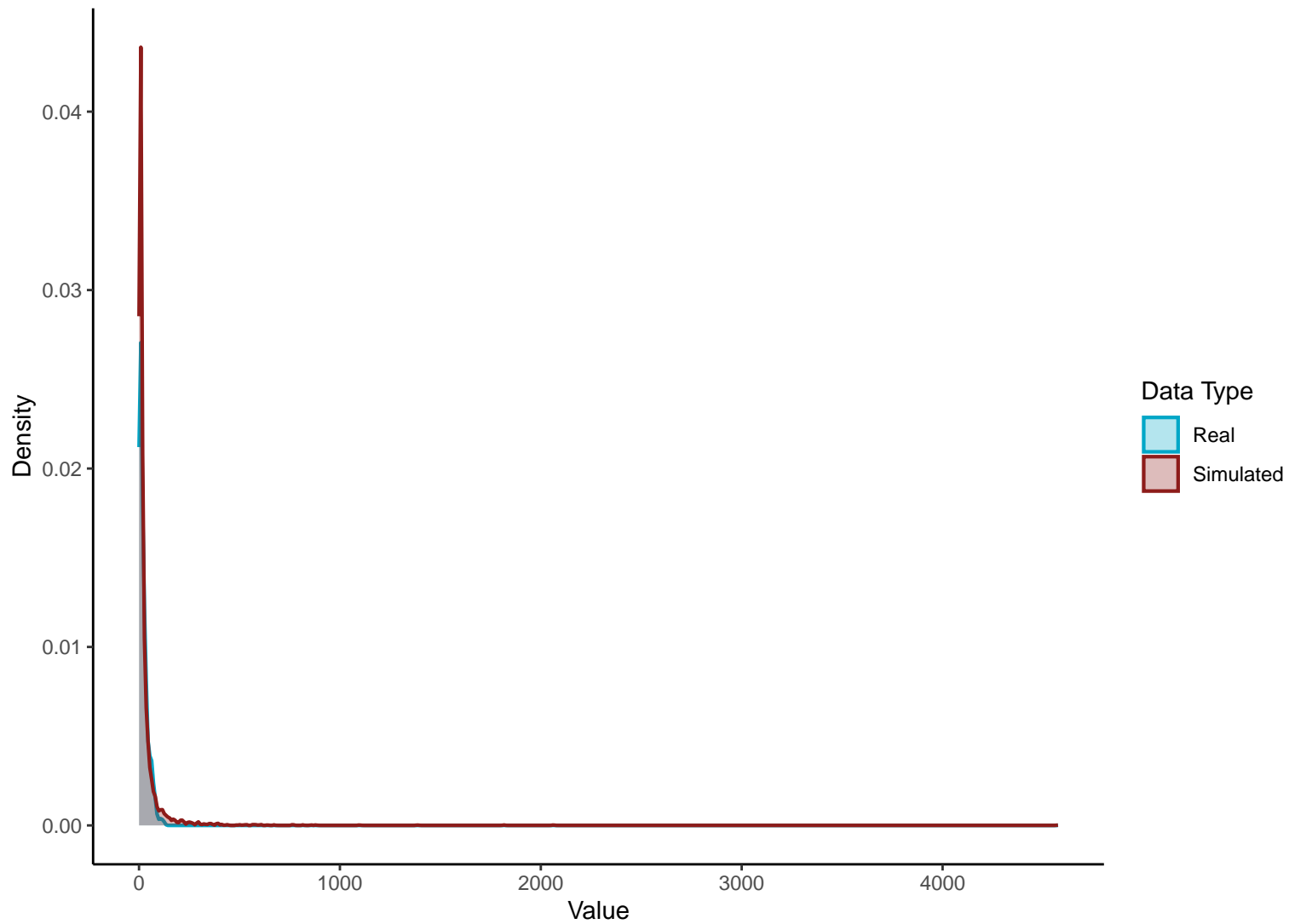
Density



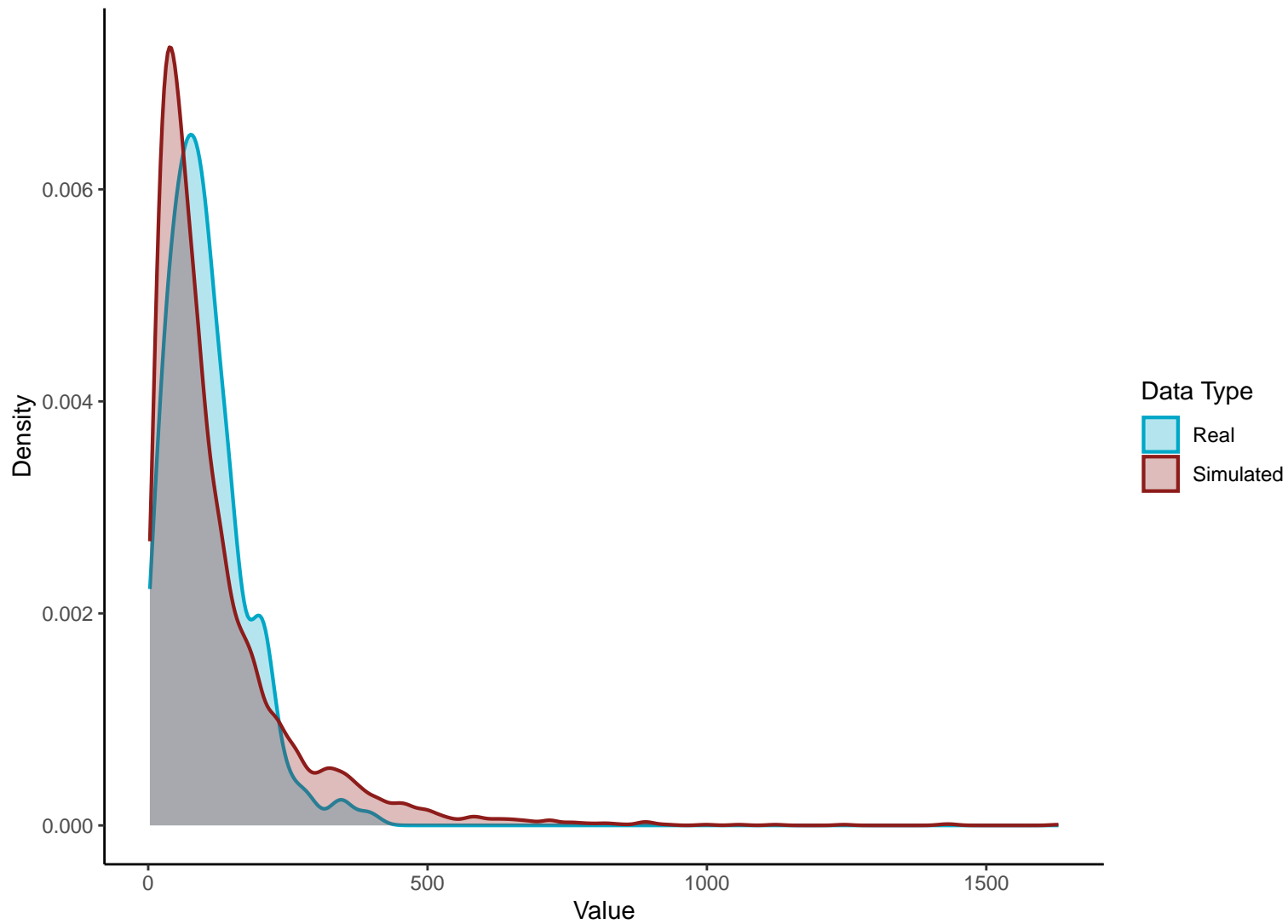
Data Type

- Real
- Simulated

Succinivibrio



Peptococcus



UCG.003

Density

0.08
0.06
0.04
0.02
0.00

0

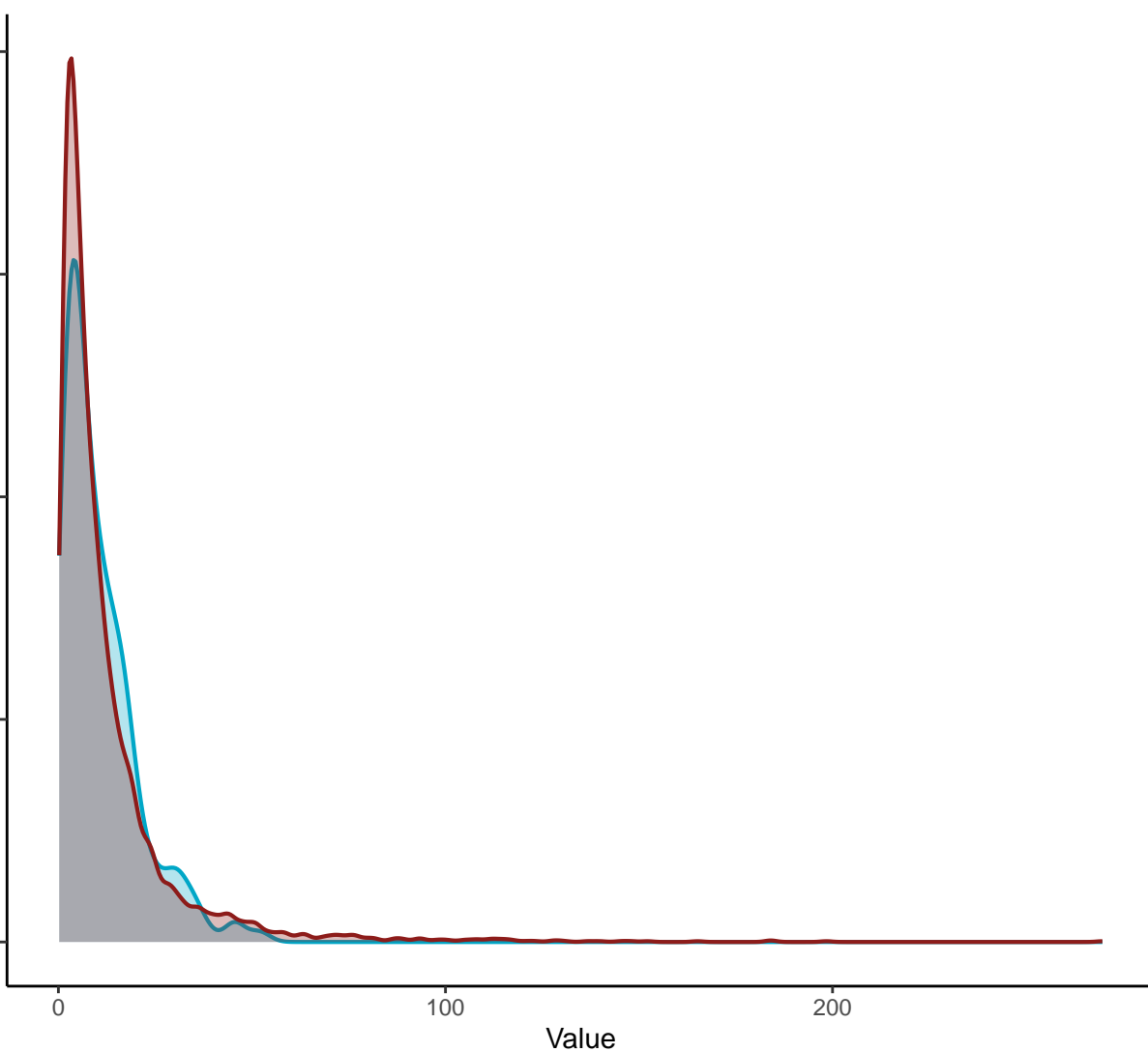
100

200

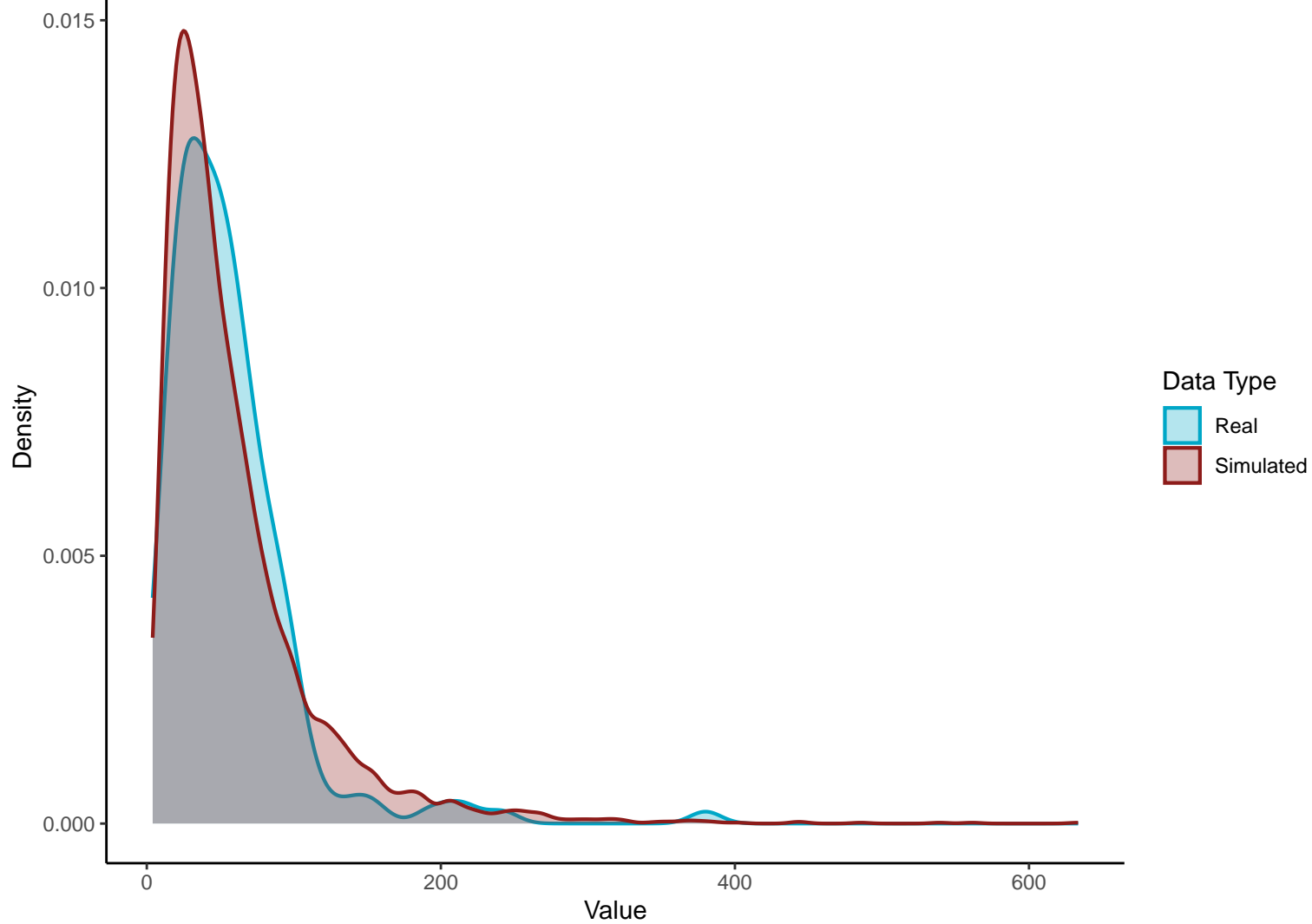
Value

Data Type

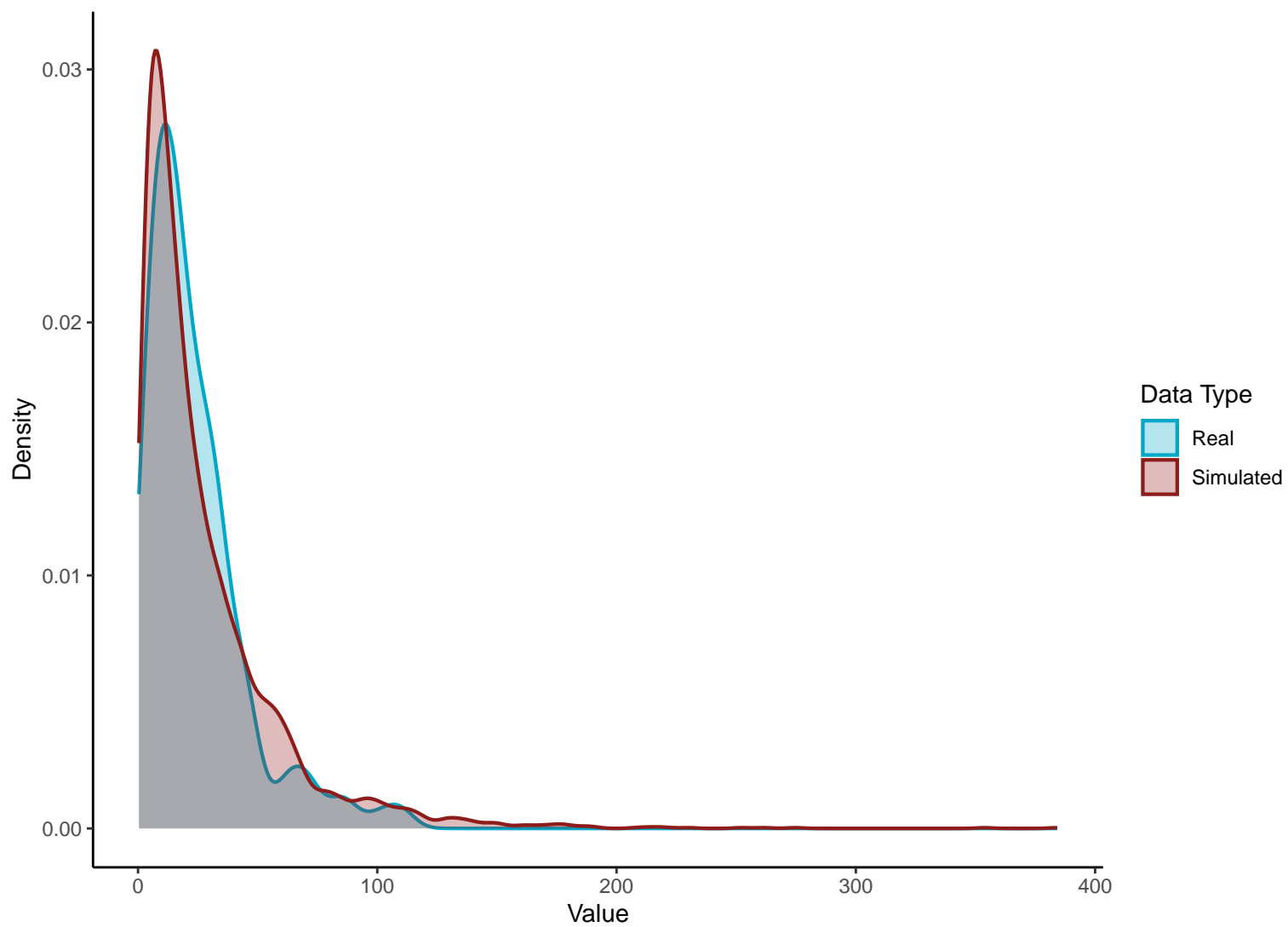
Real
Simulated



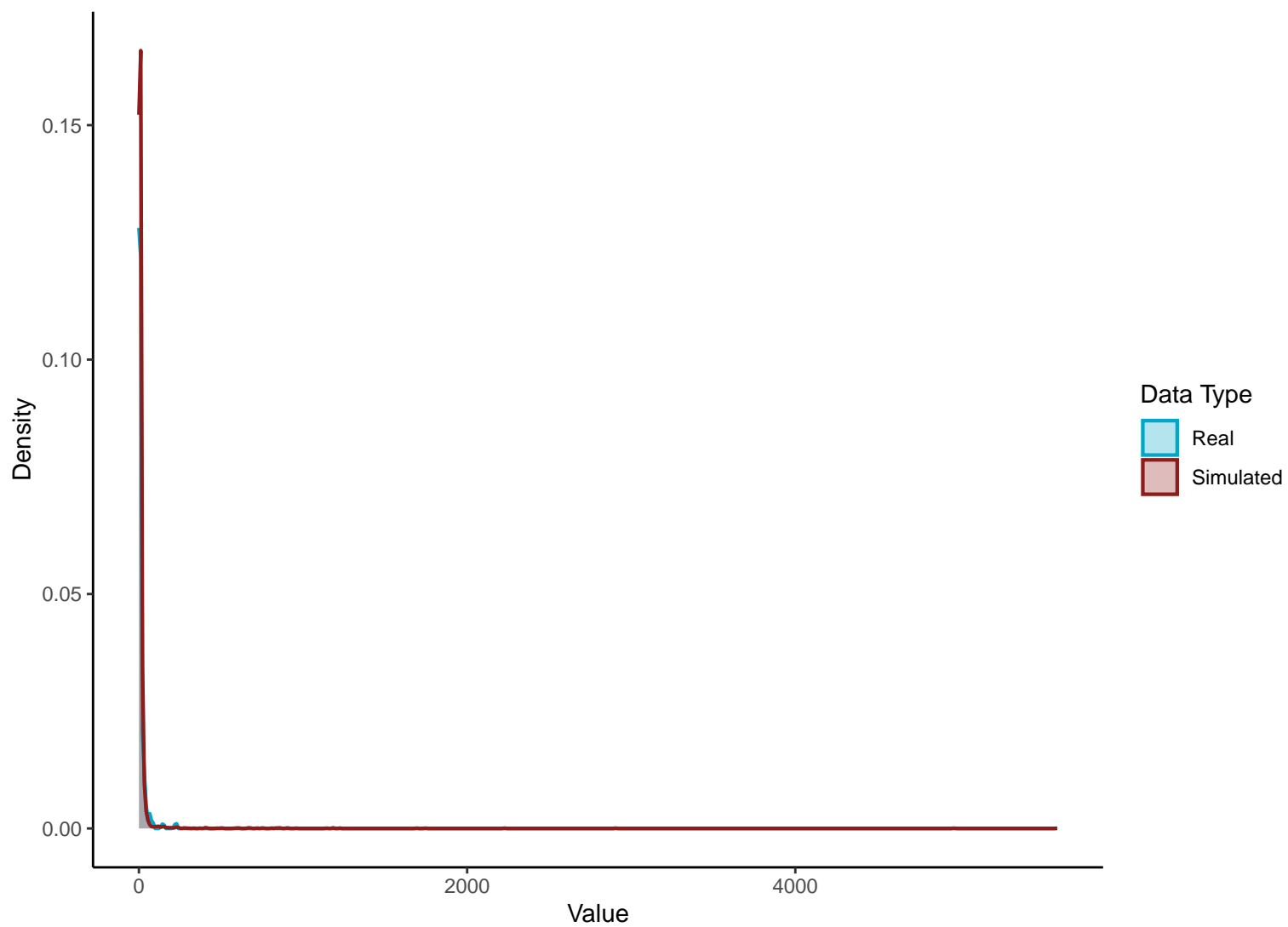
Lachnoclostridium



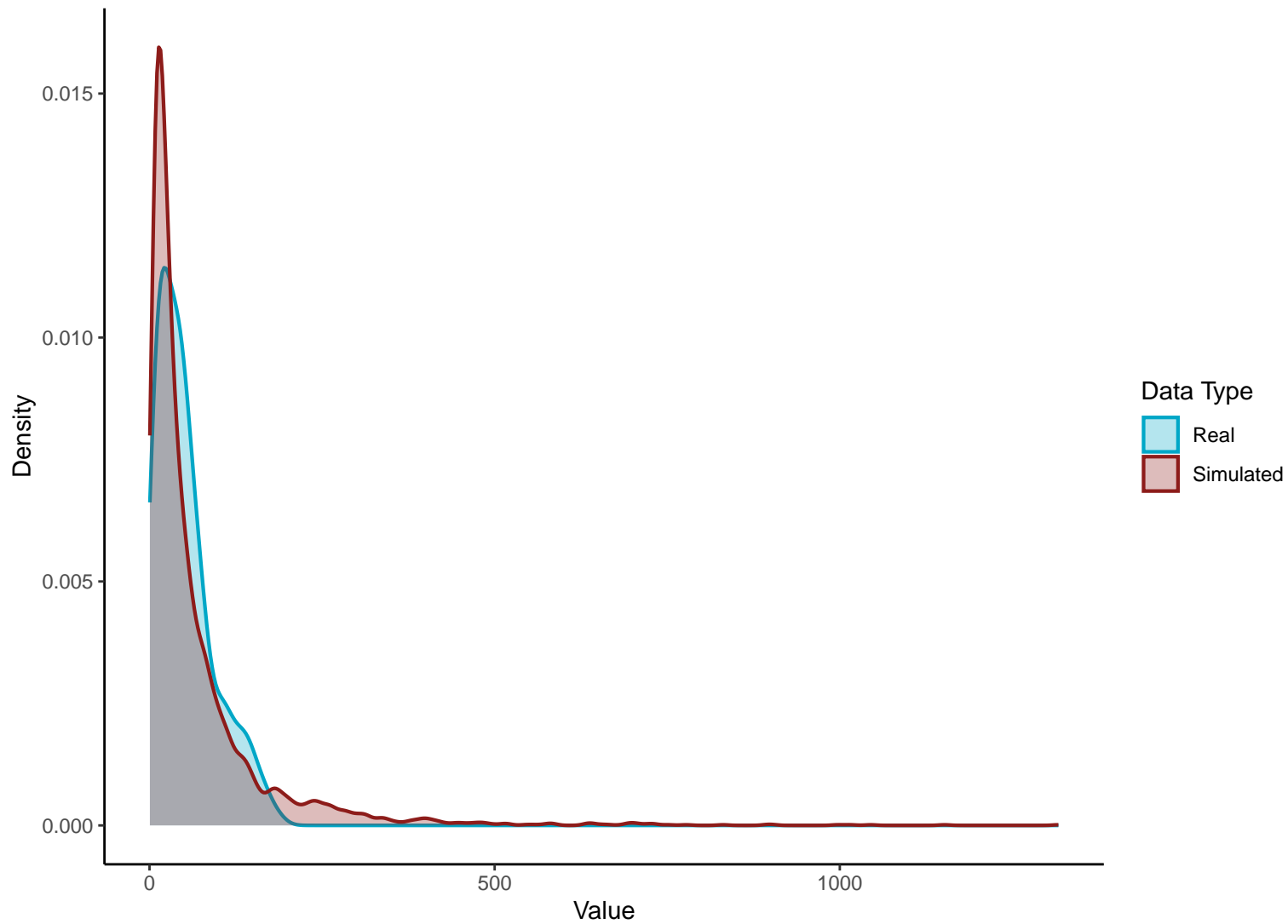
X.Eubacterium..ventriosum.group



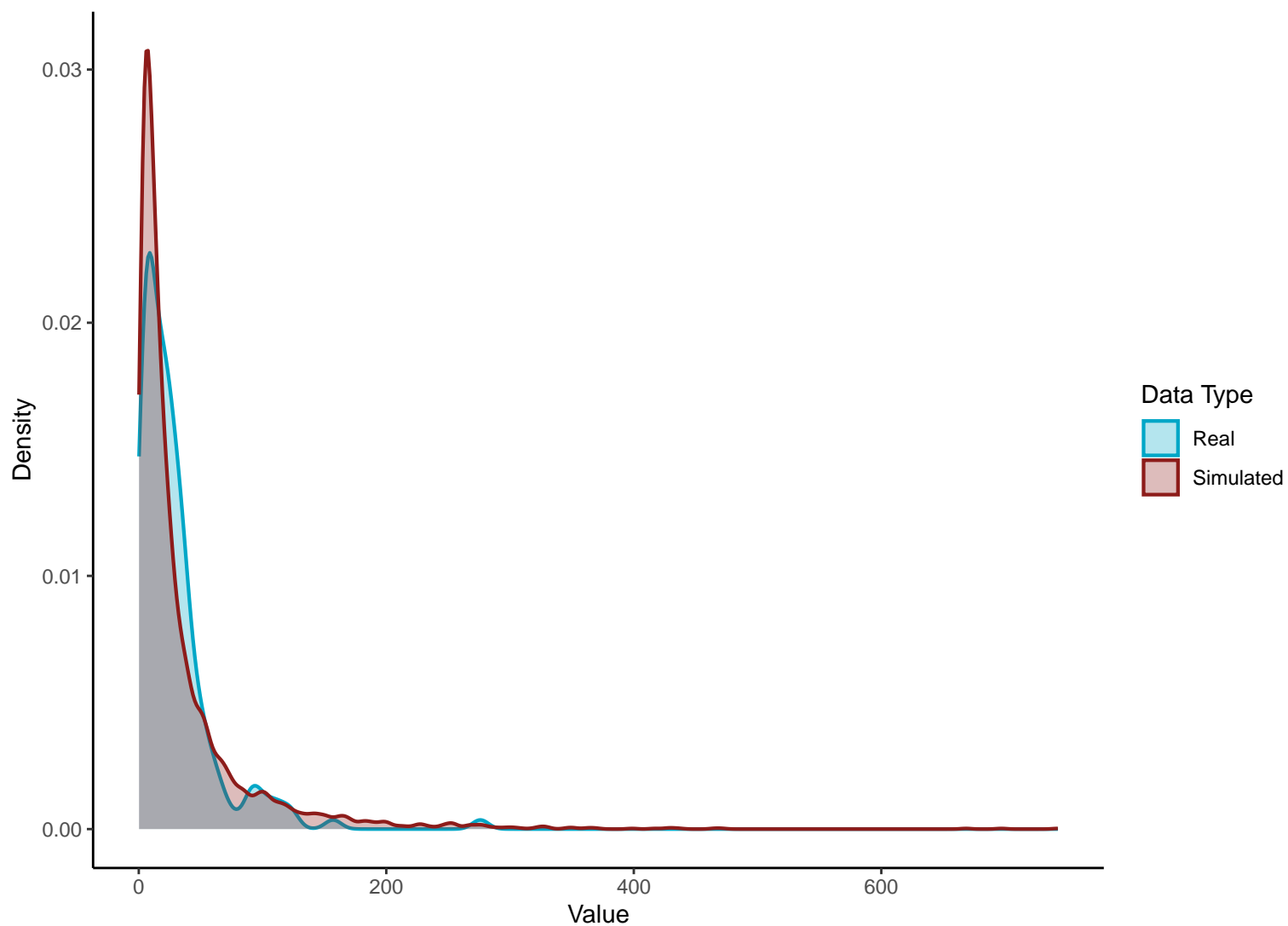
Anaerococcus



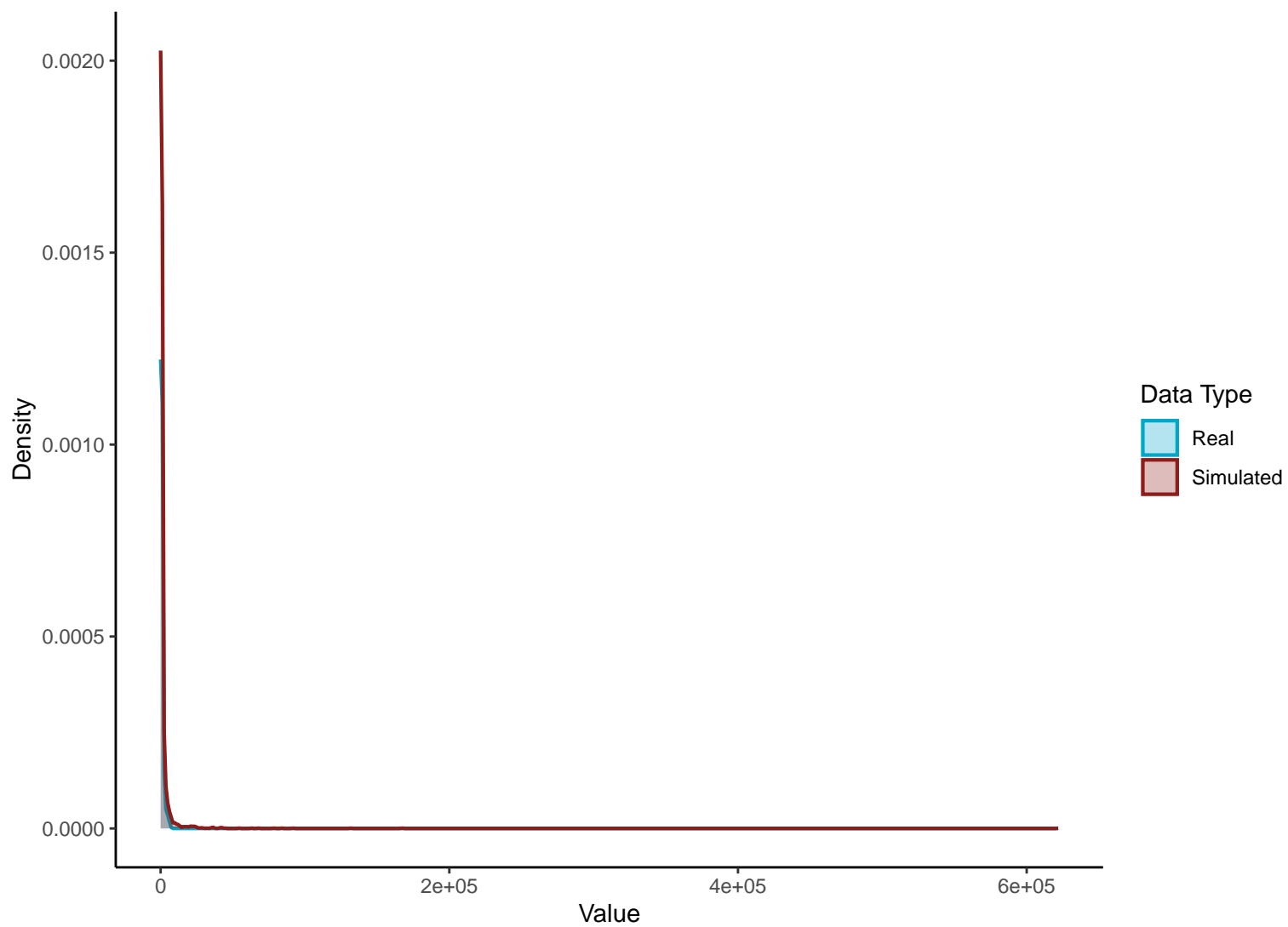
Enterorhabdus



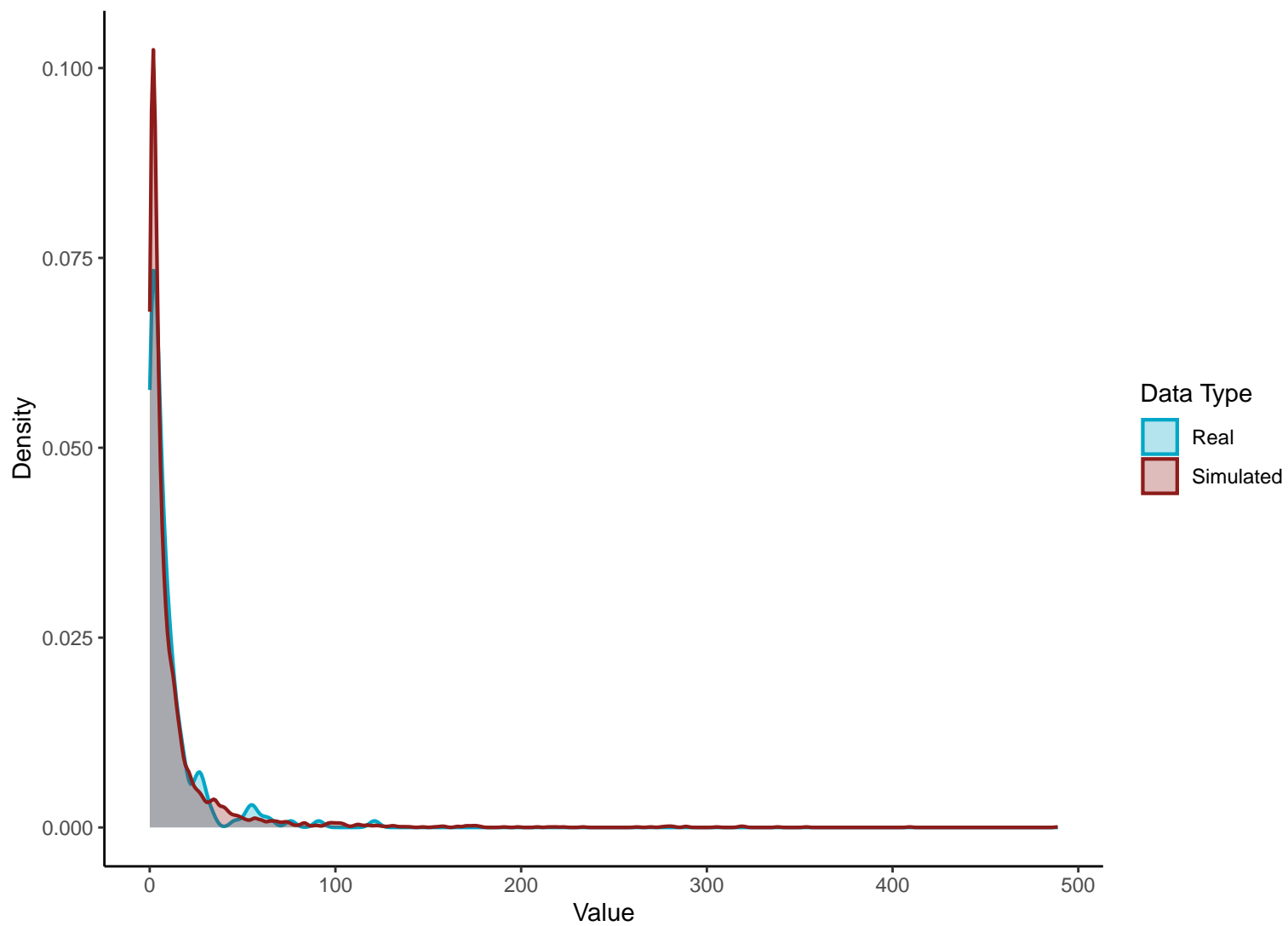
Libanicoccus



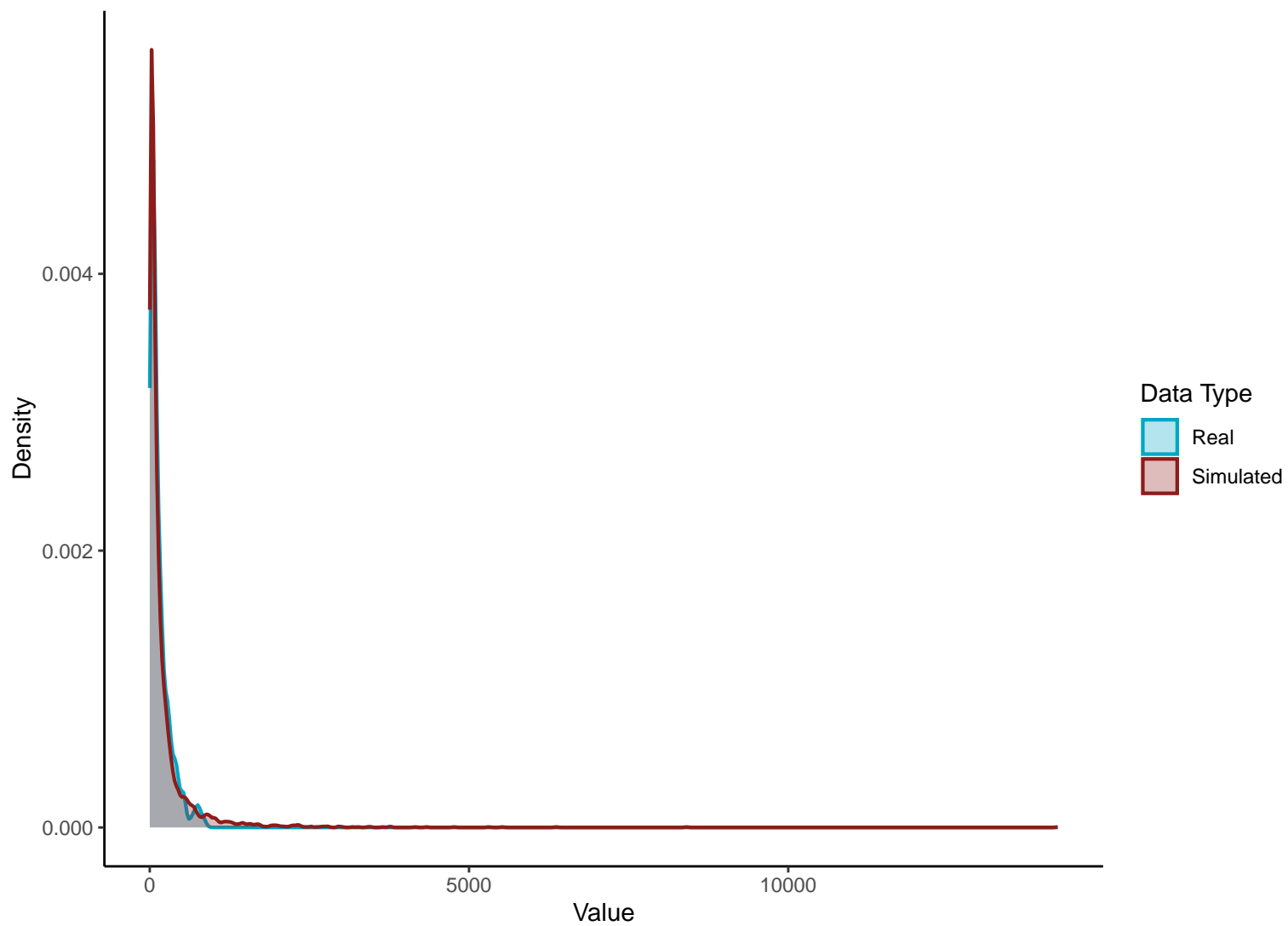
Turicibacter



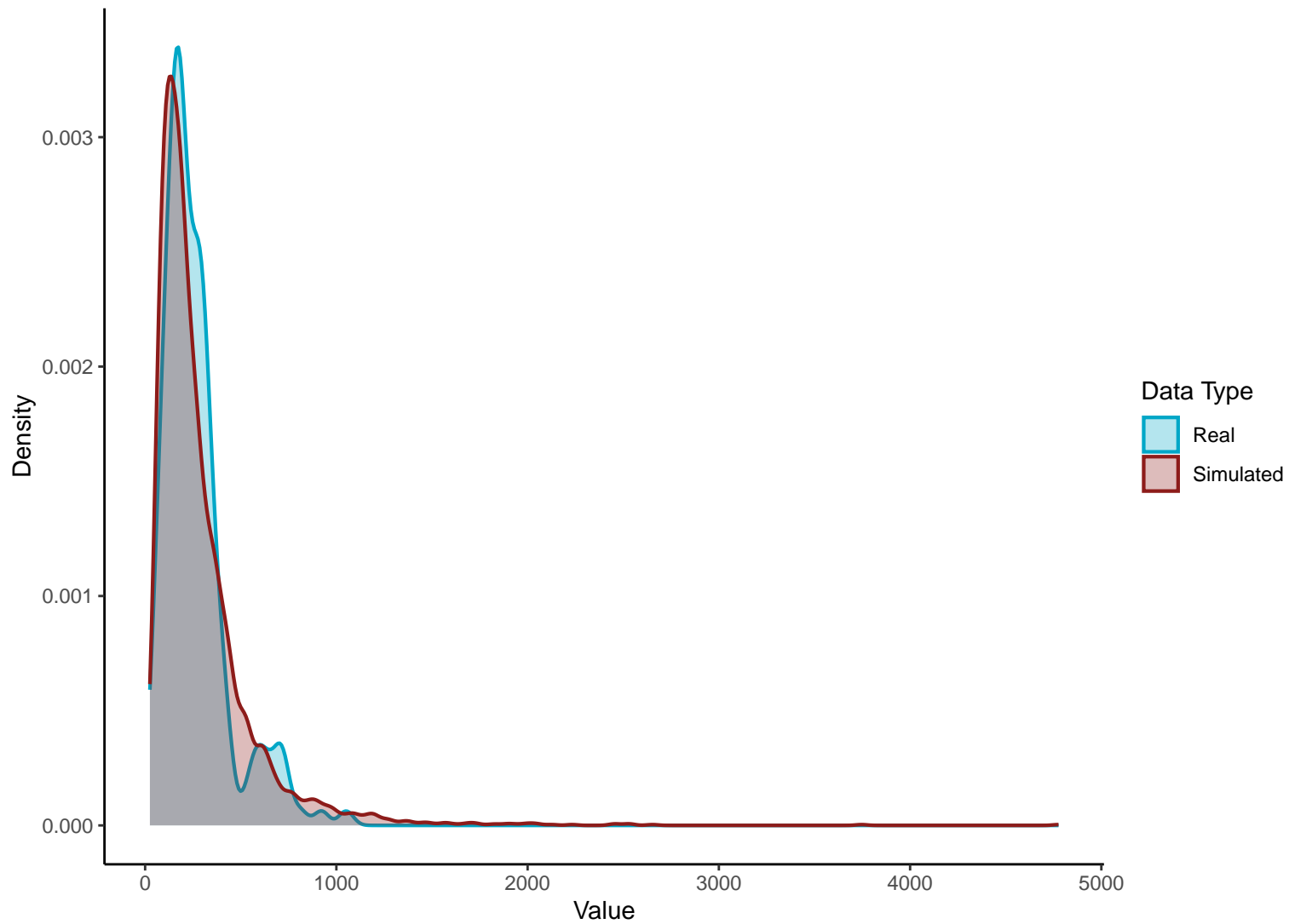
XBB1006



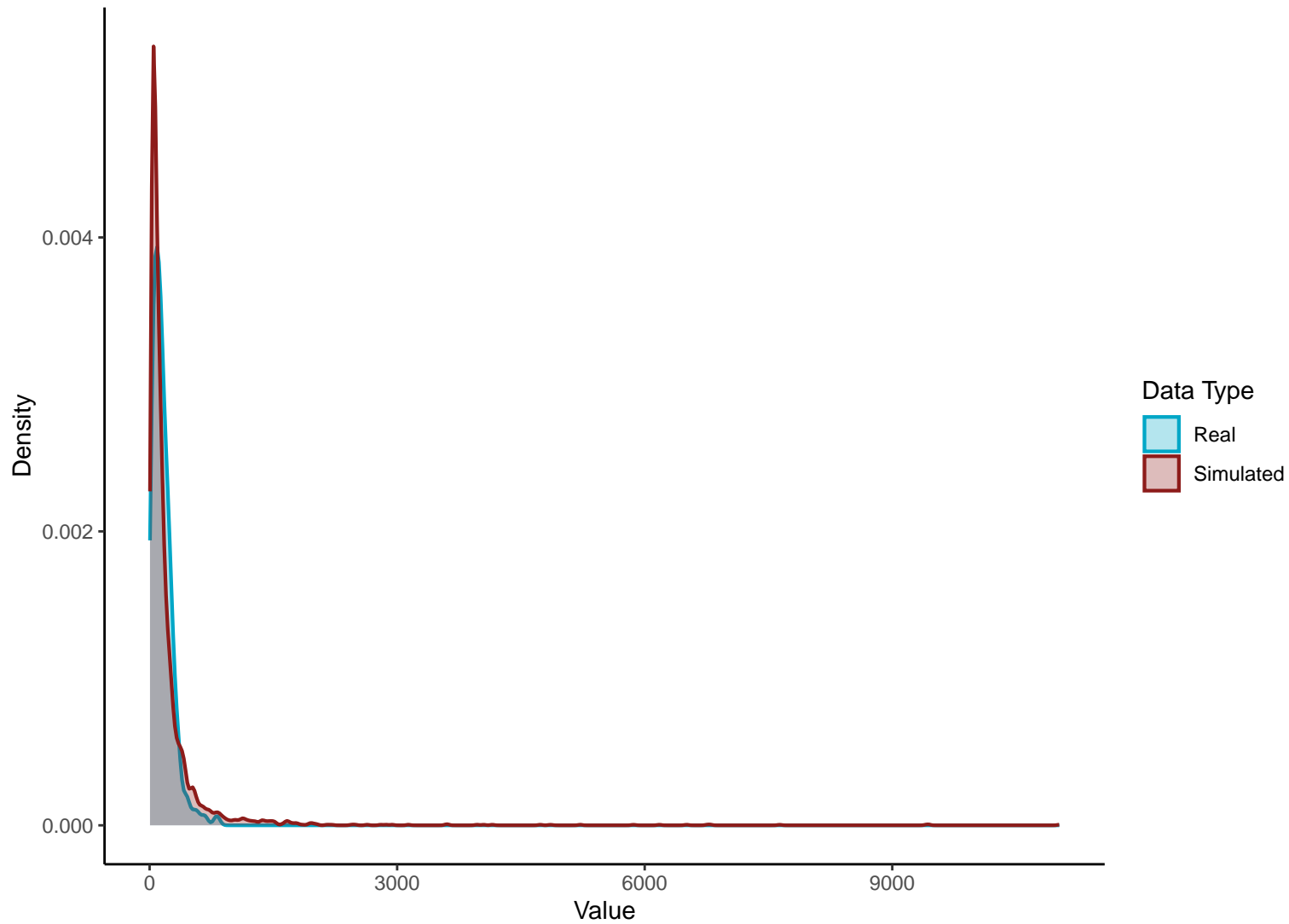
UCG.008



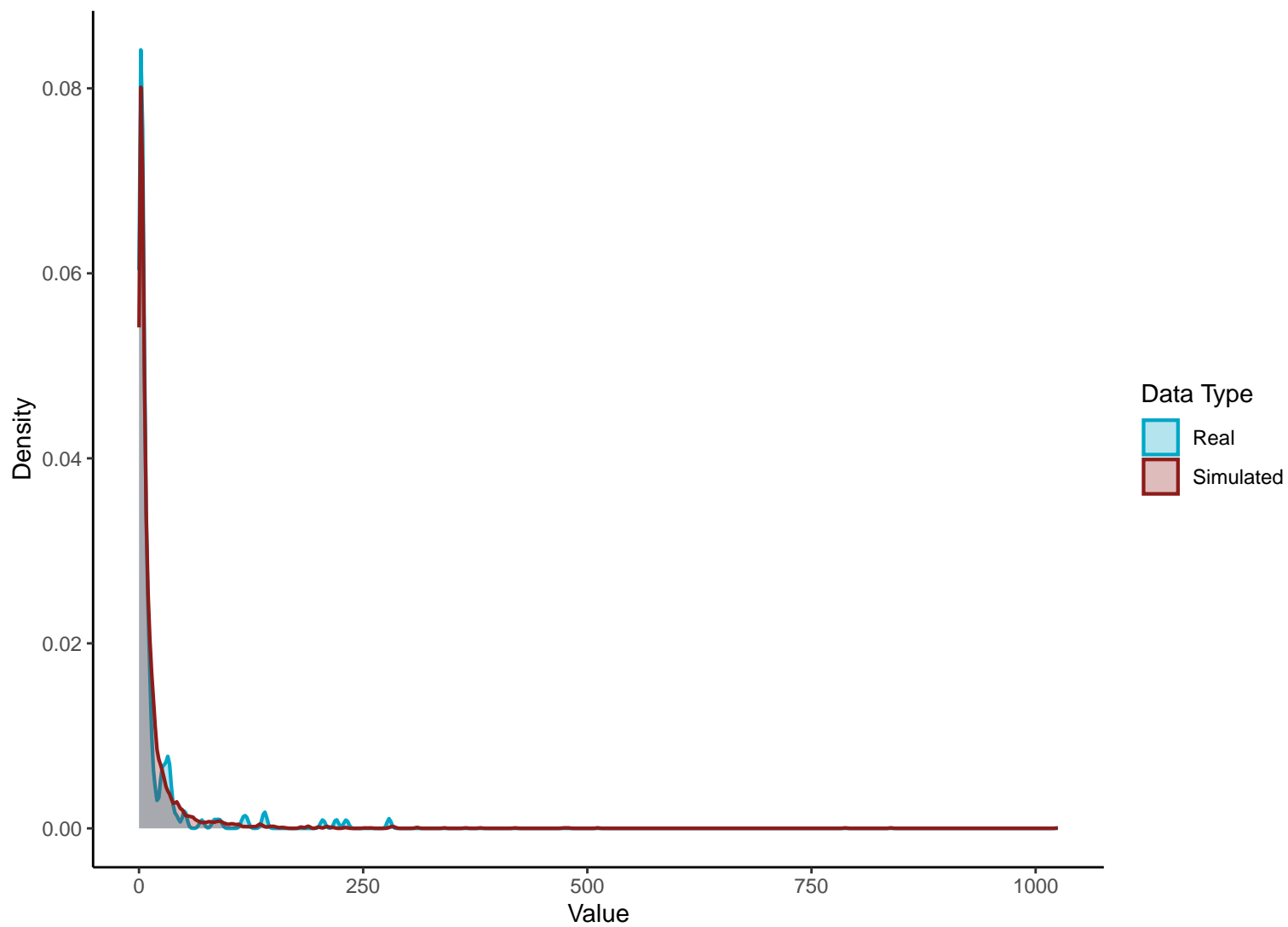
Intestinibacter



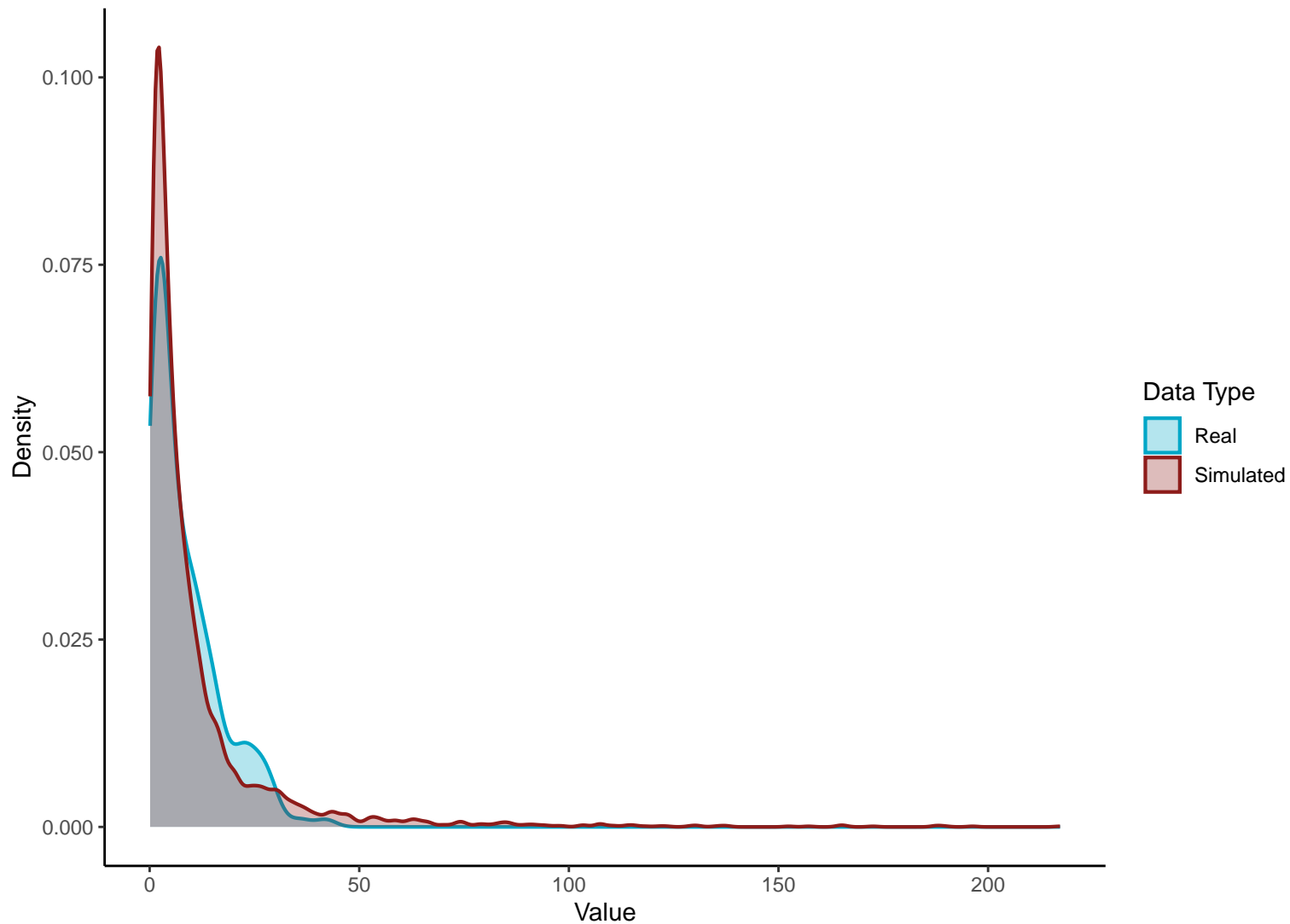
Fusicatenibacter



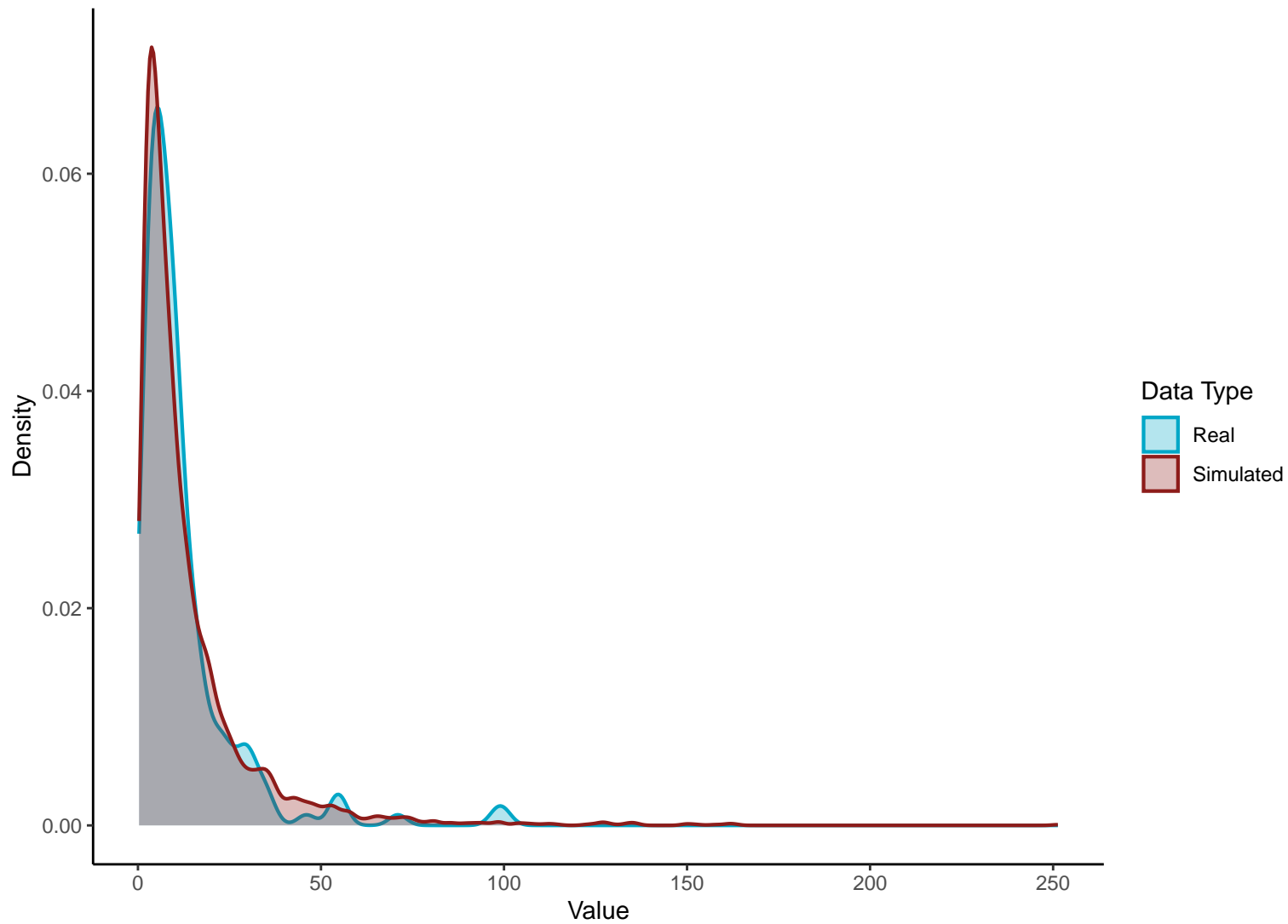
X28.4



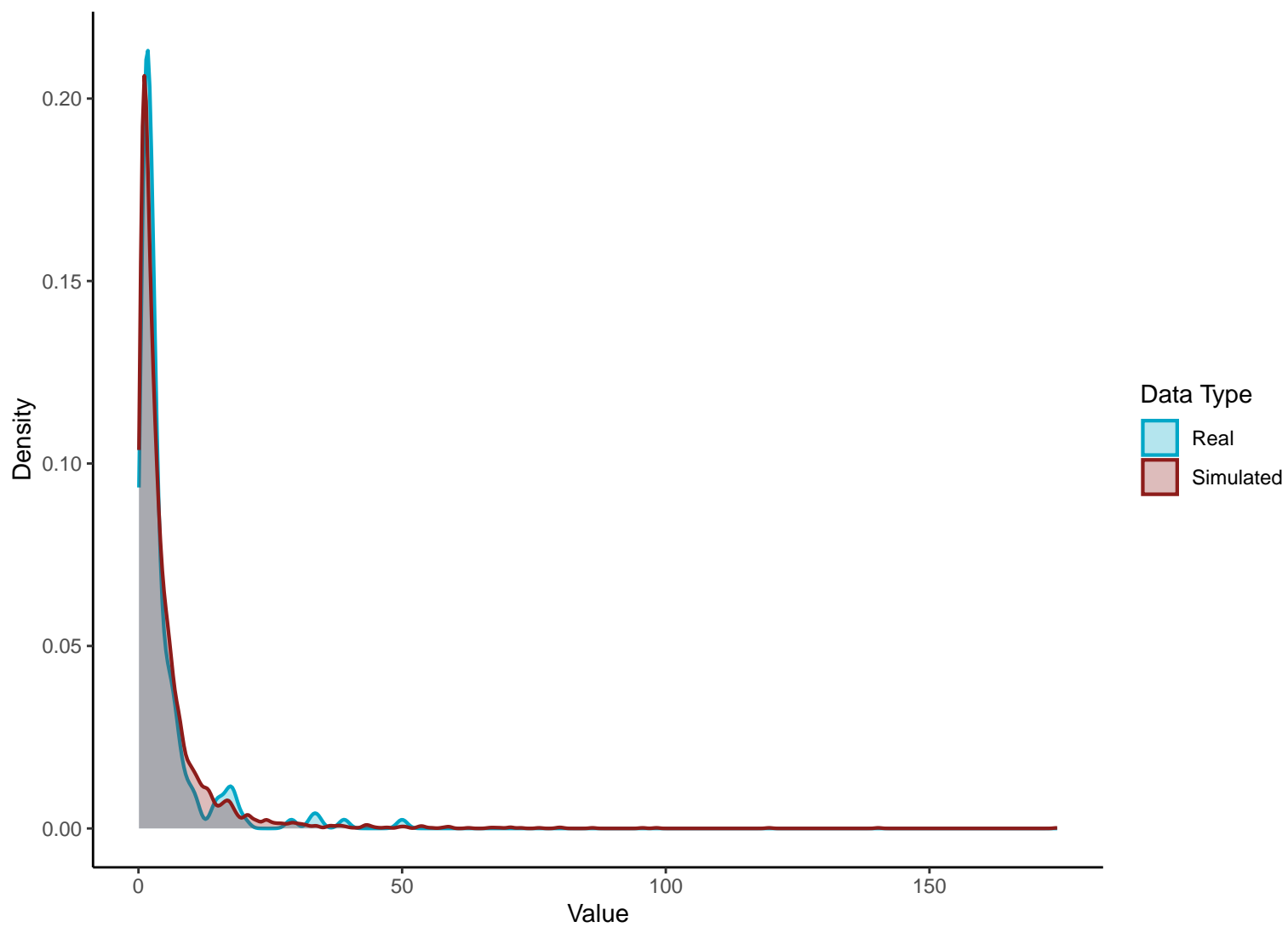
Howardella



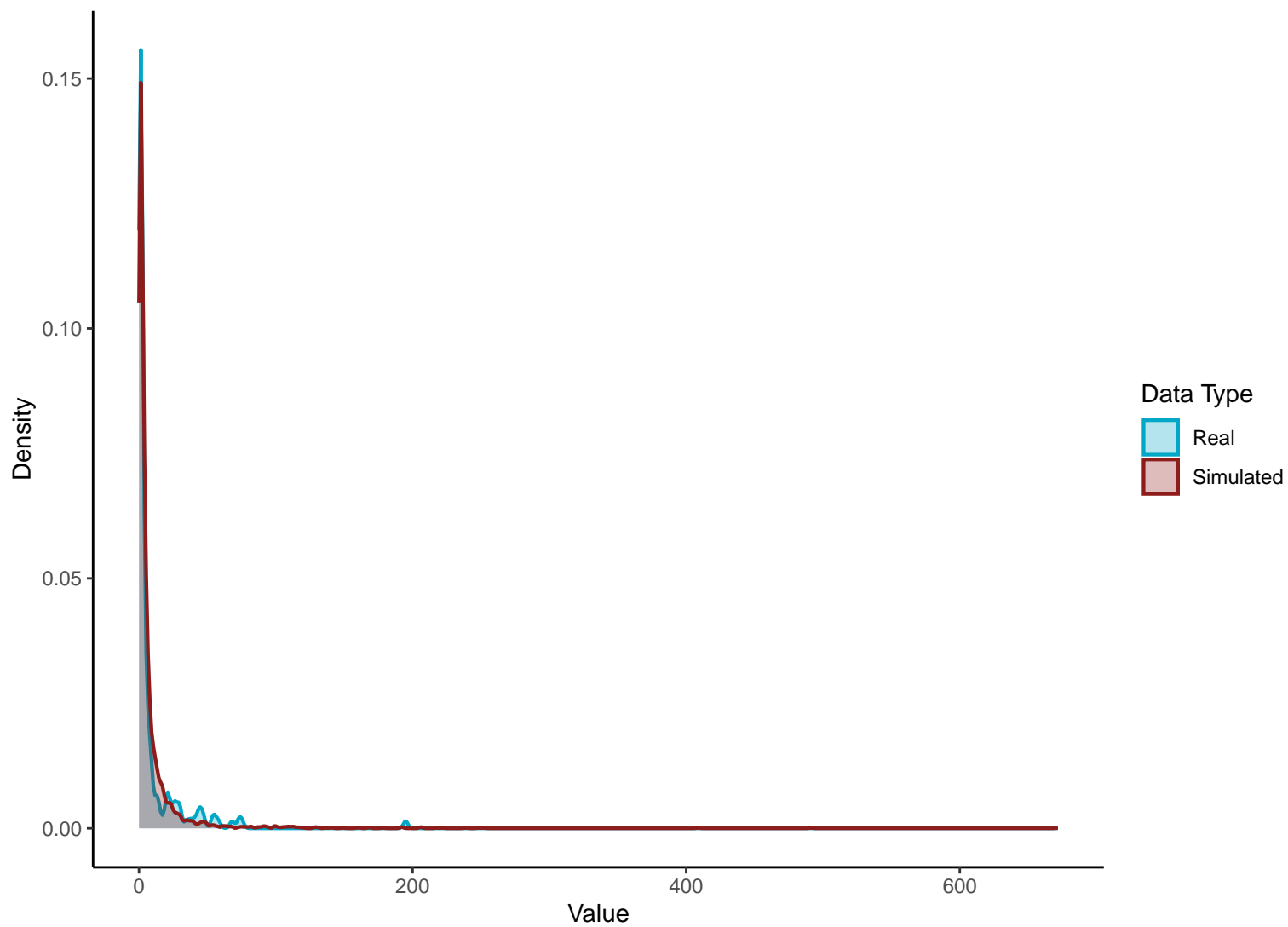
Paludicola



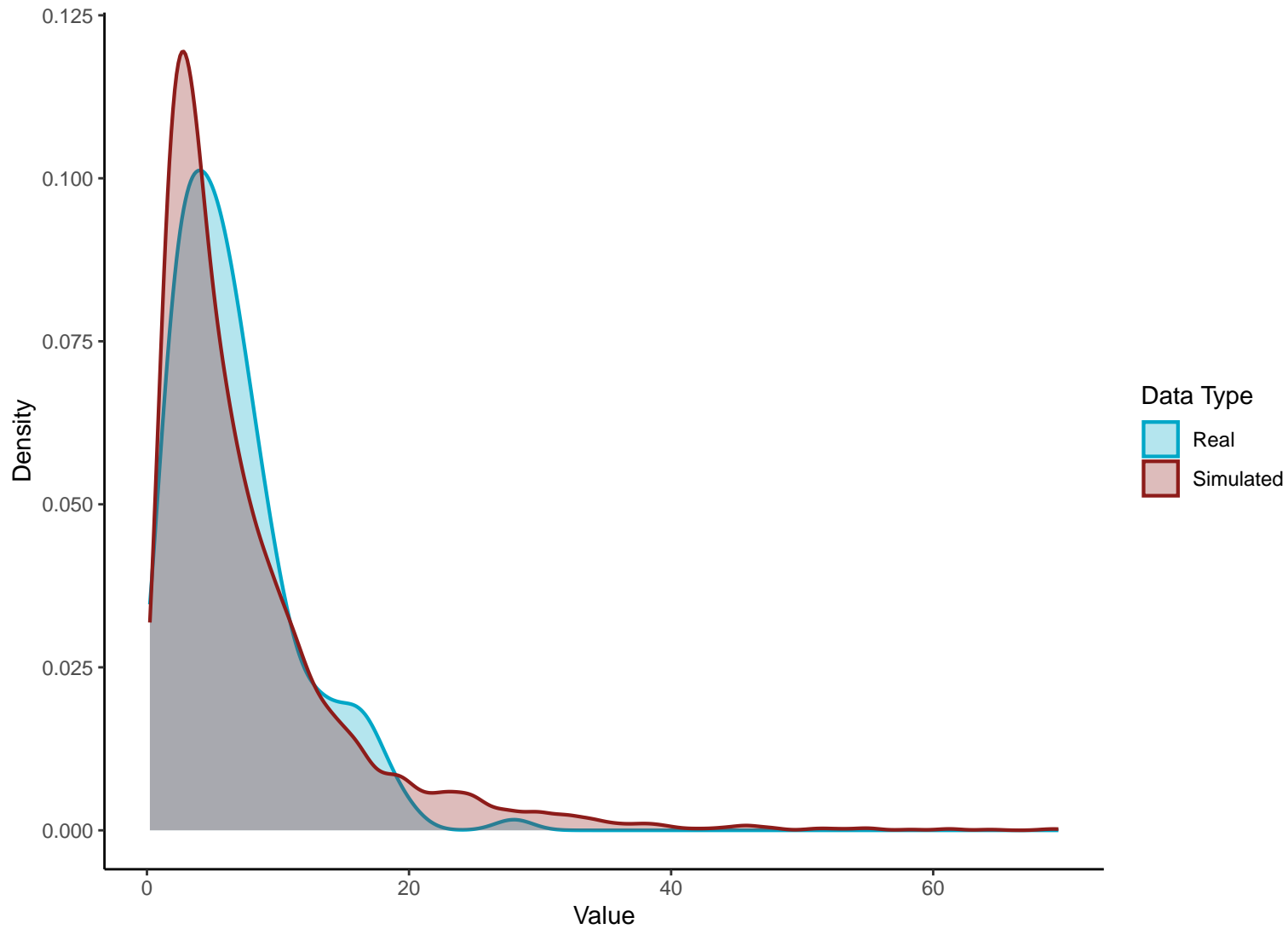
Tyzzerella



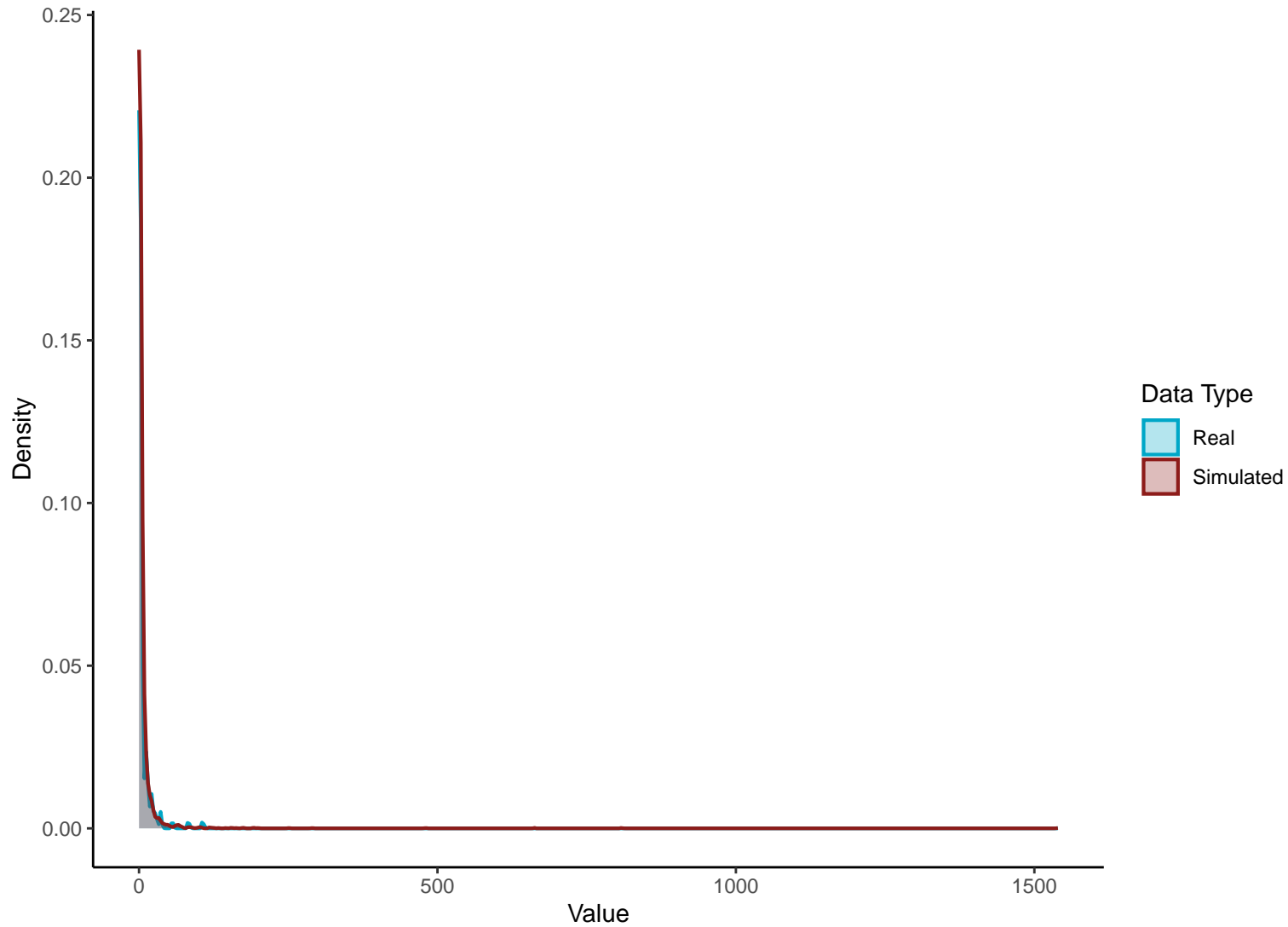
UCG.001



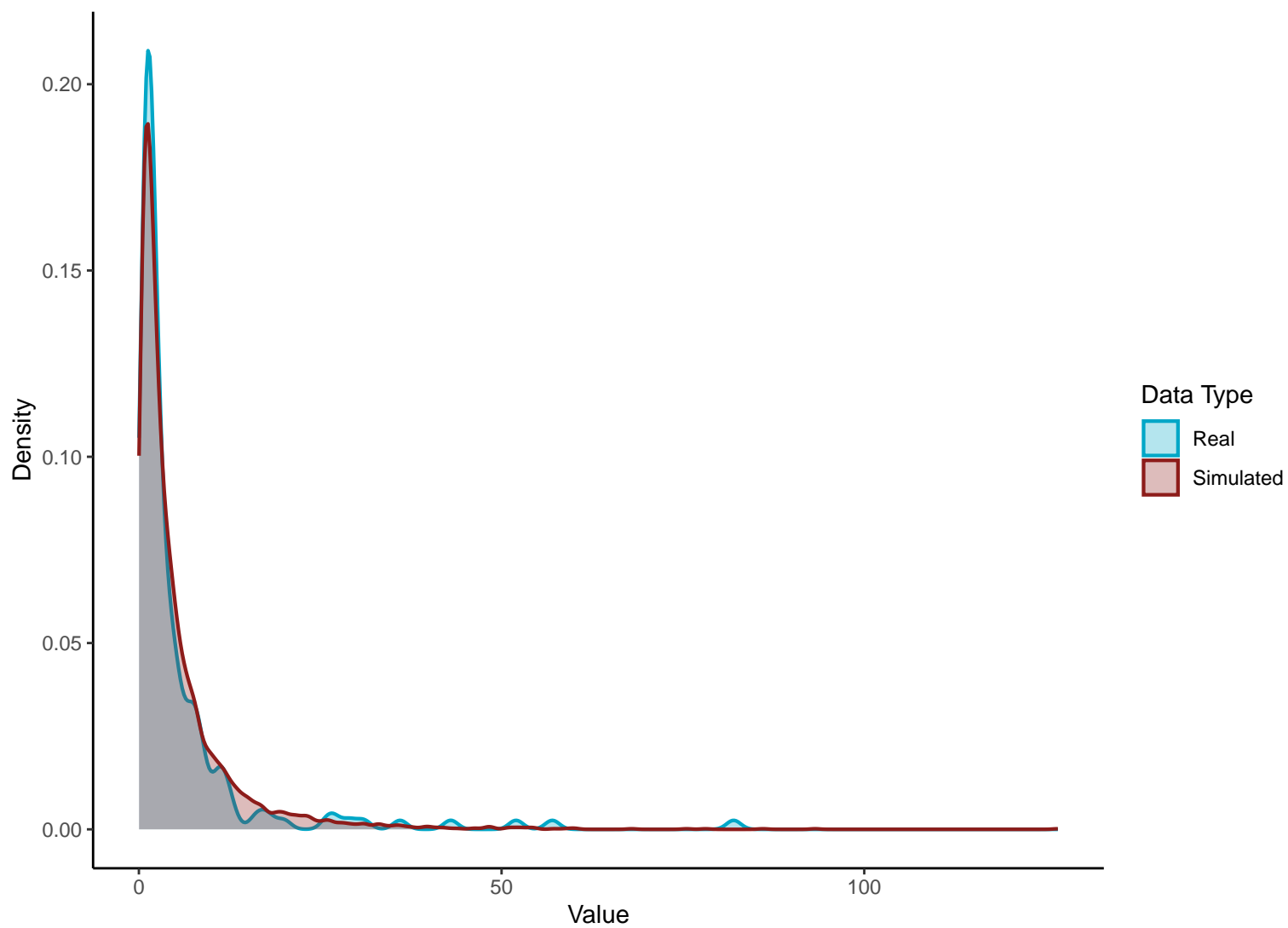
Lachnospiraceae.UGC.002



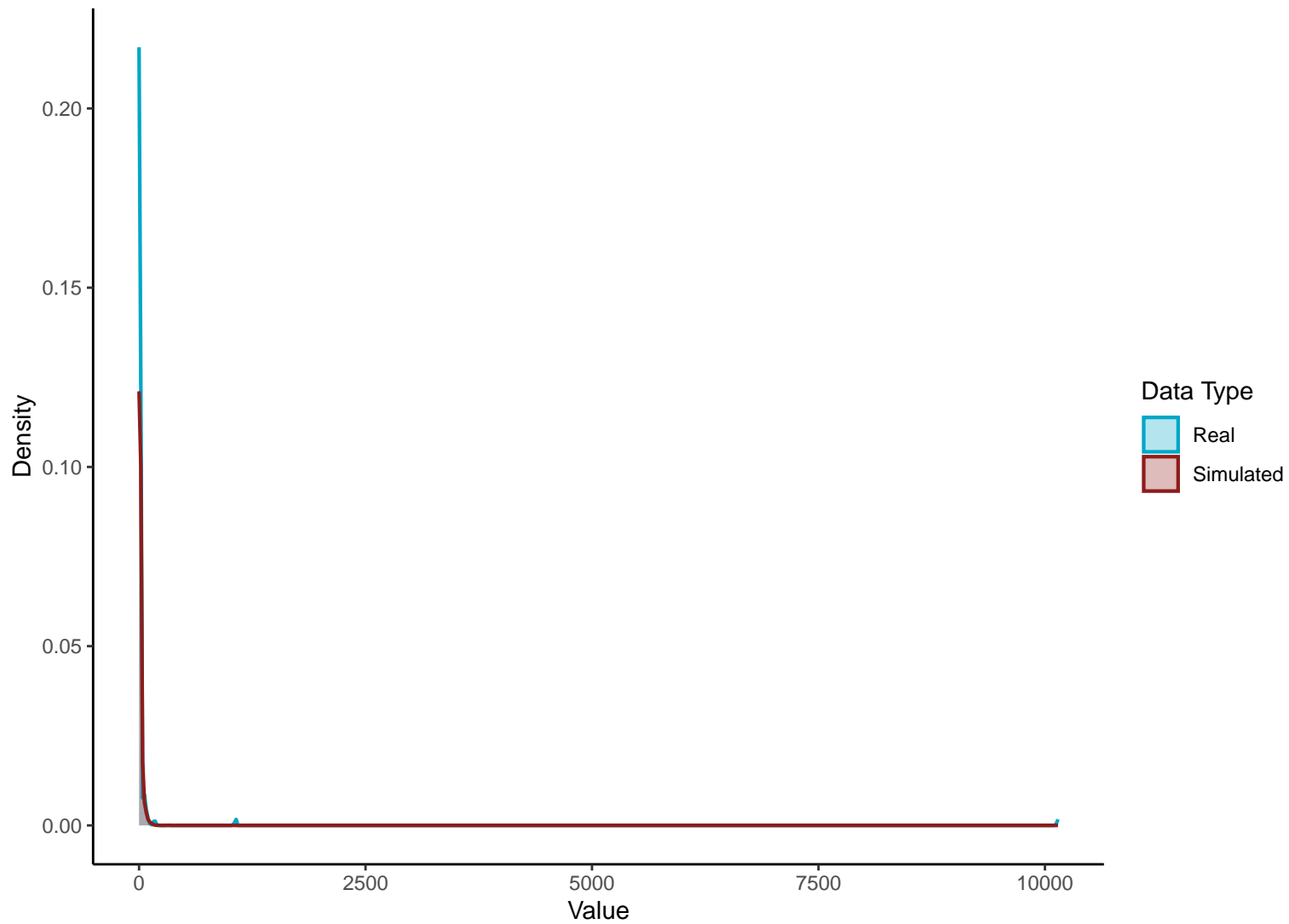
Lachnospiraceae.UCG.007



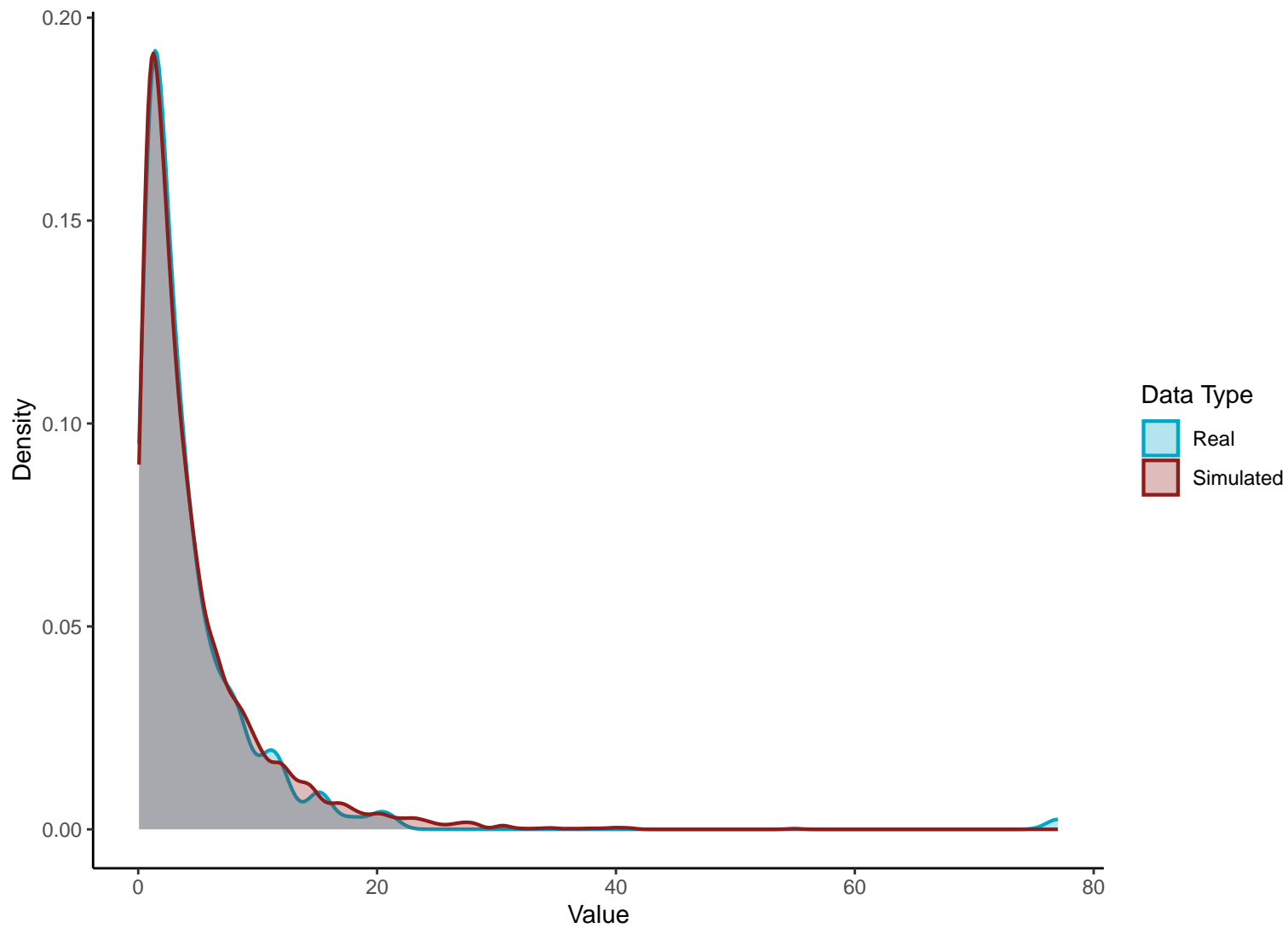
Lachnospiraceae.UGC.003



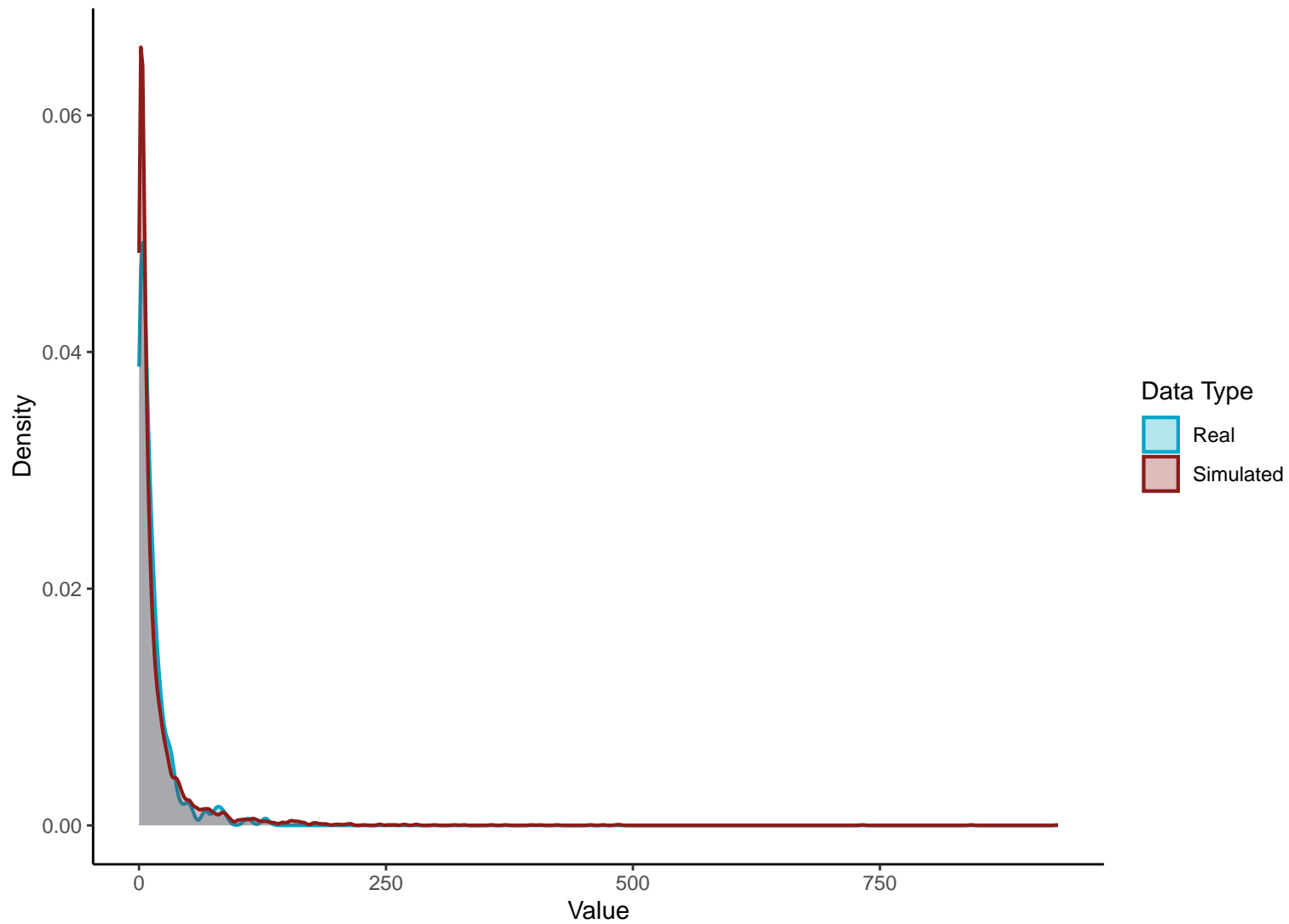
Bifidobacterium



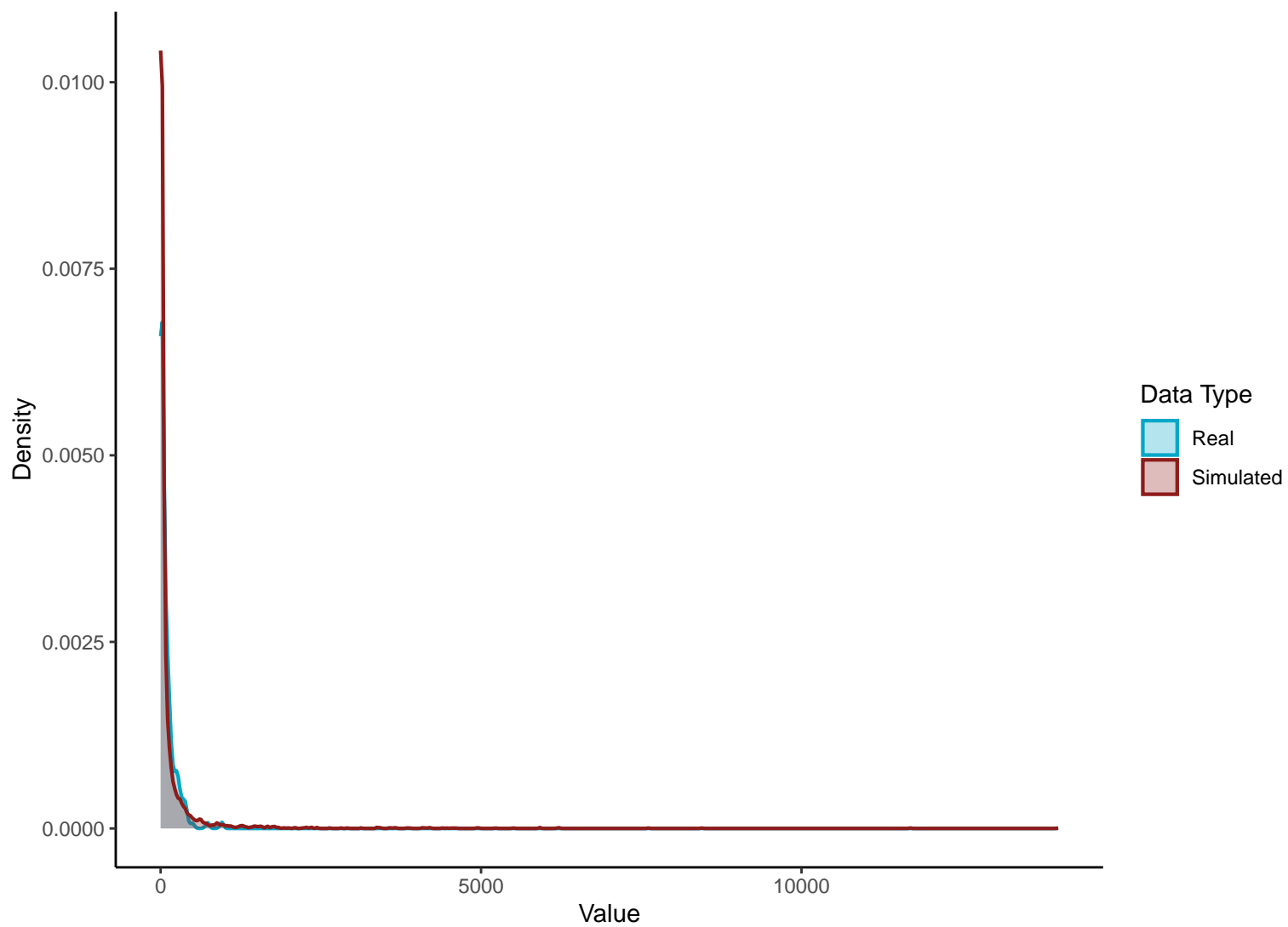
Butyrivibrio



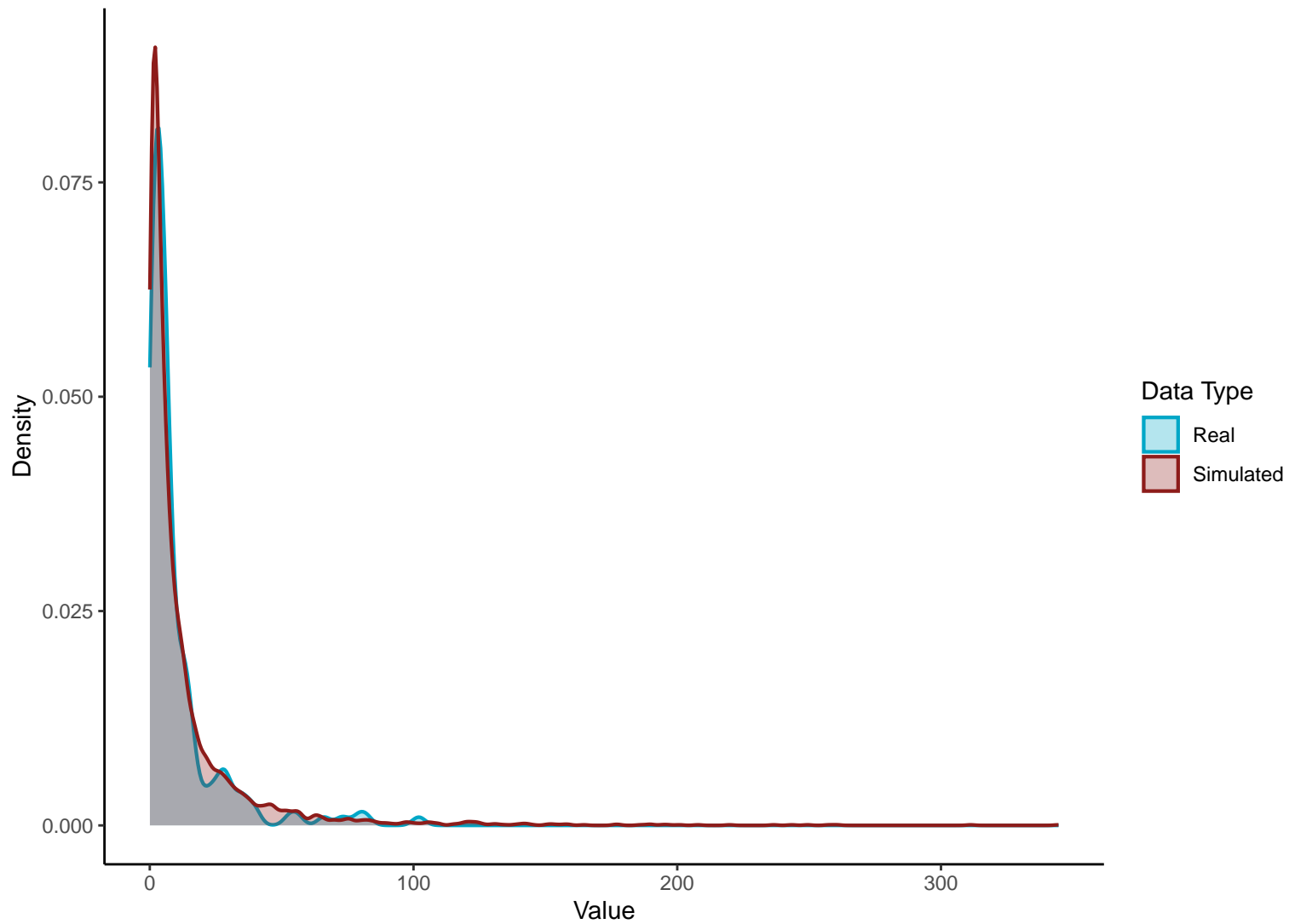
Pseudobutyrvibrio



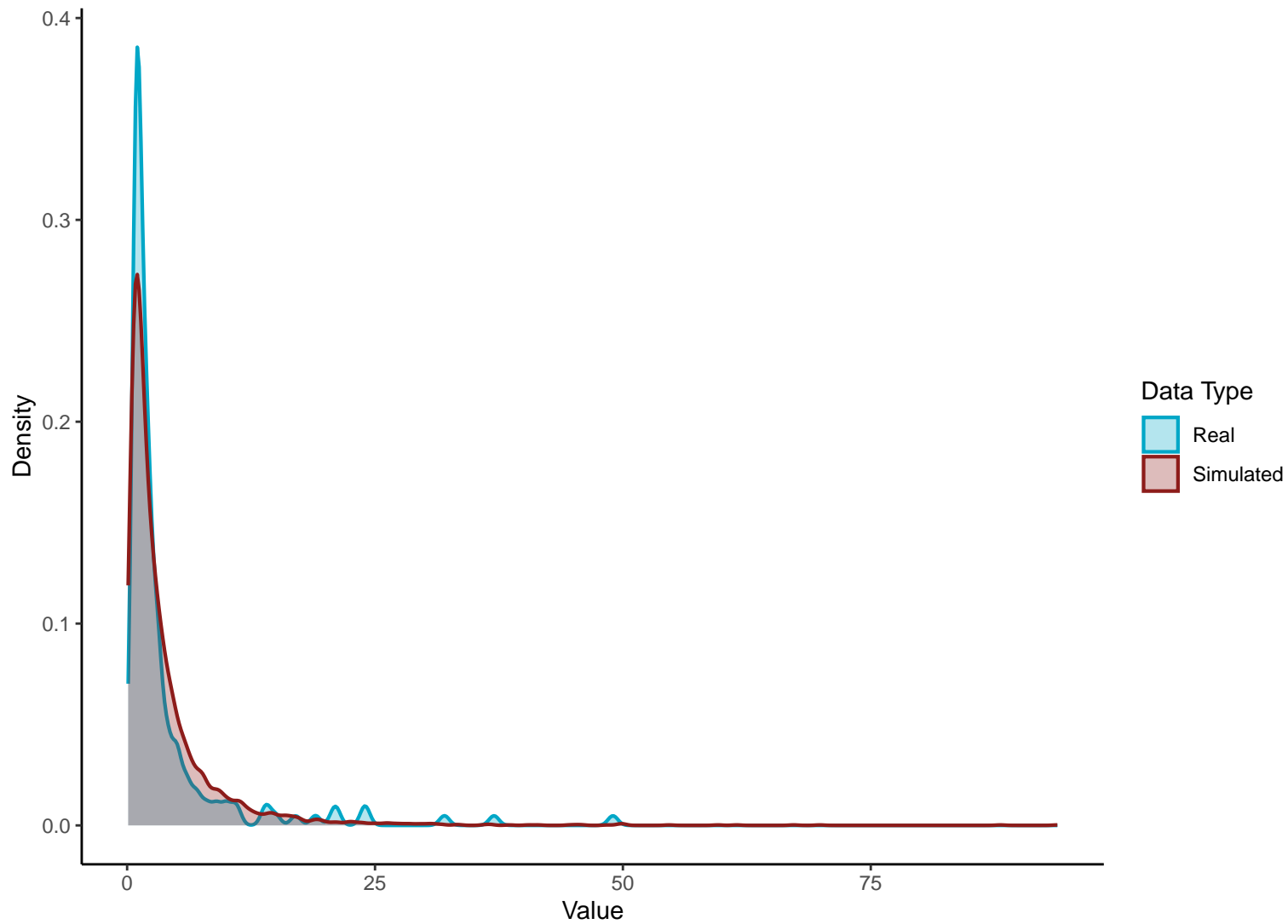
Catenisphaera



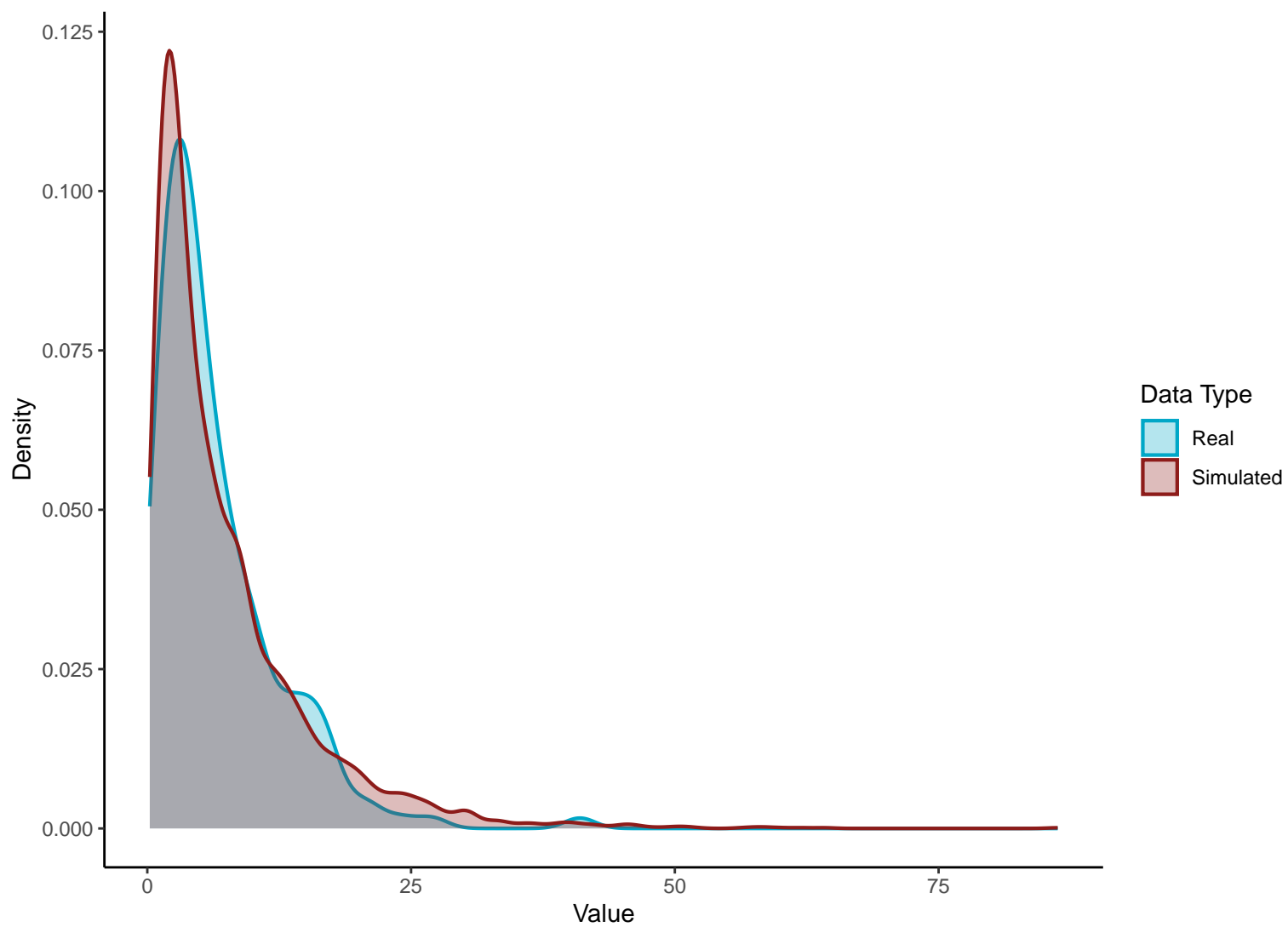
Prevotellaceae.UGC.004



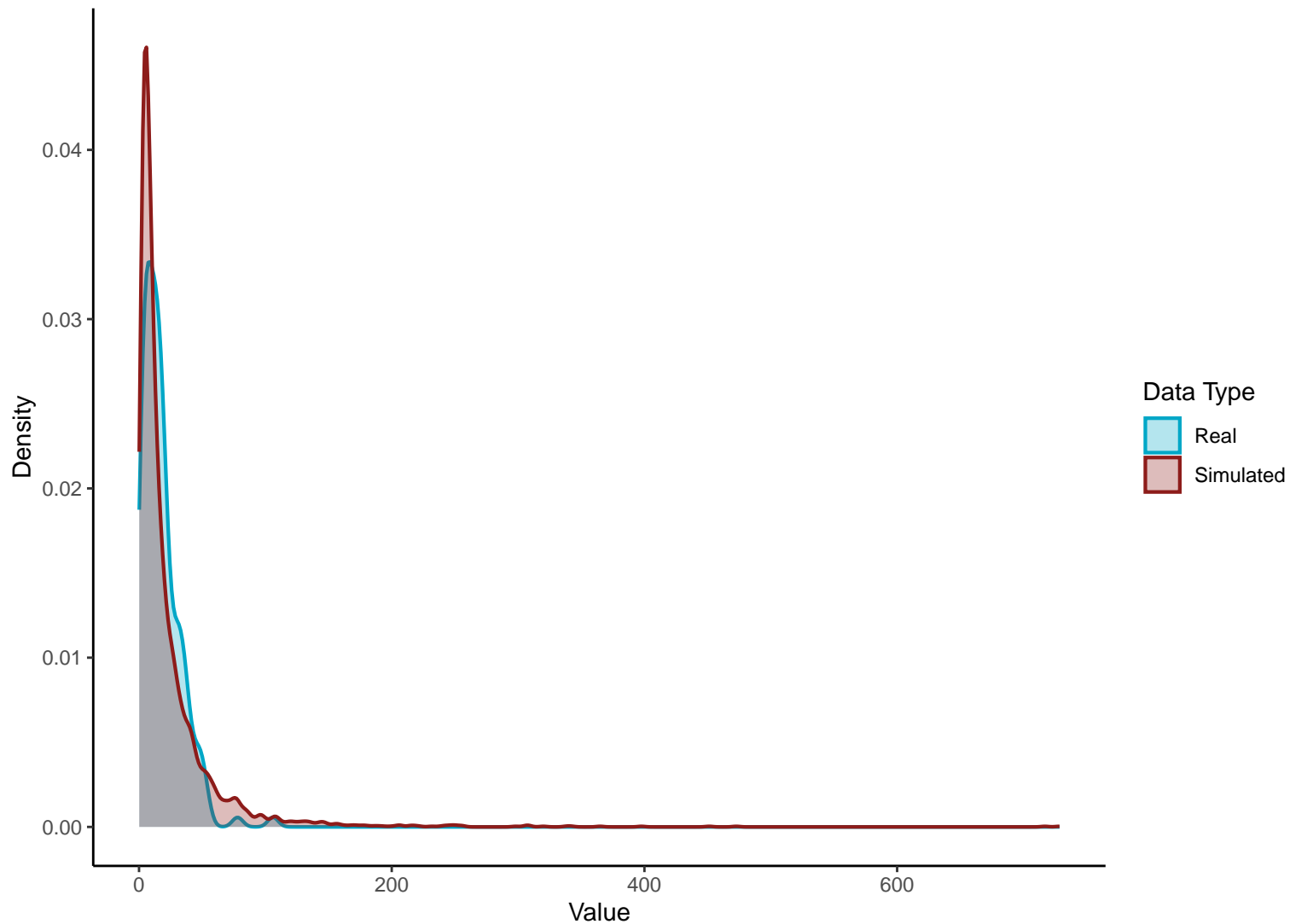
X.Eubacterium..brachy.group



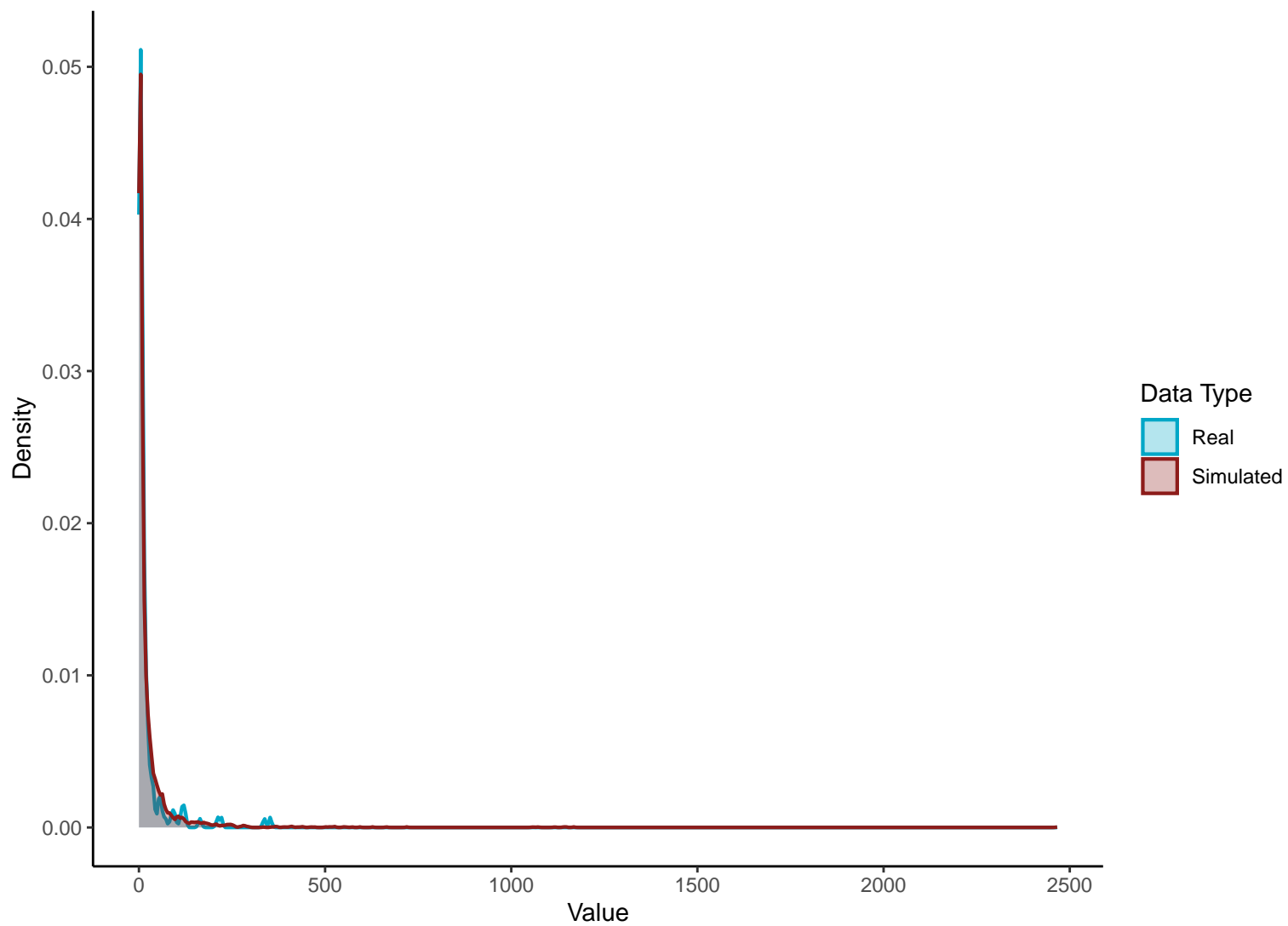
GCA.900066575



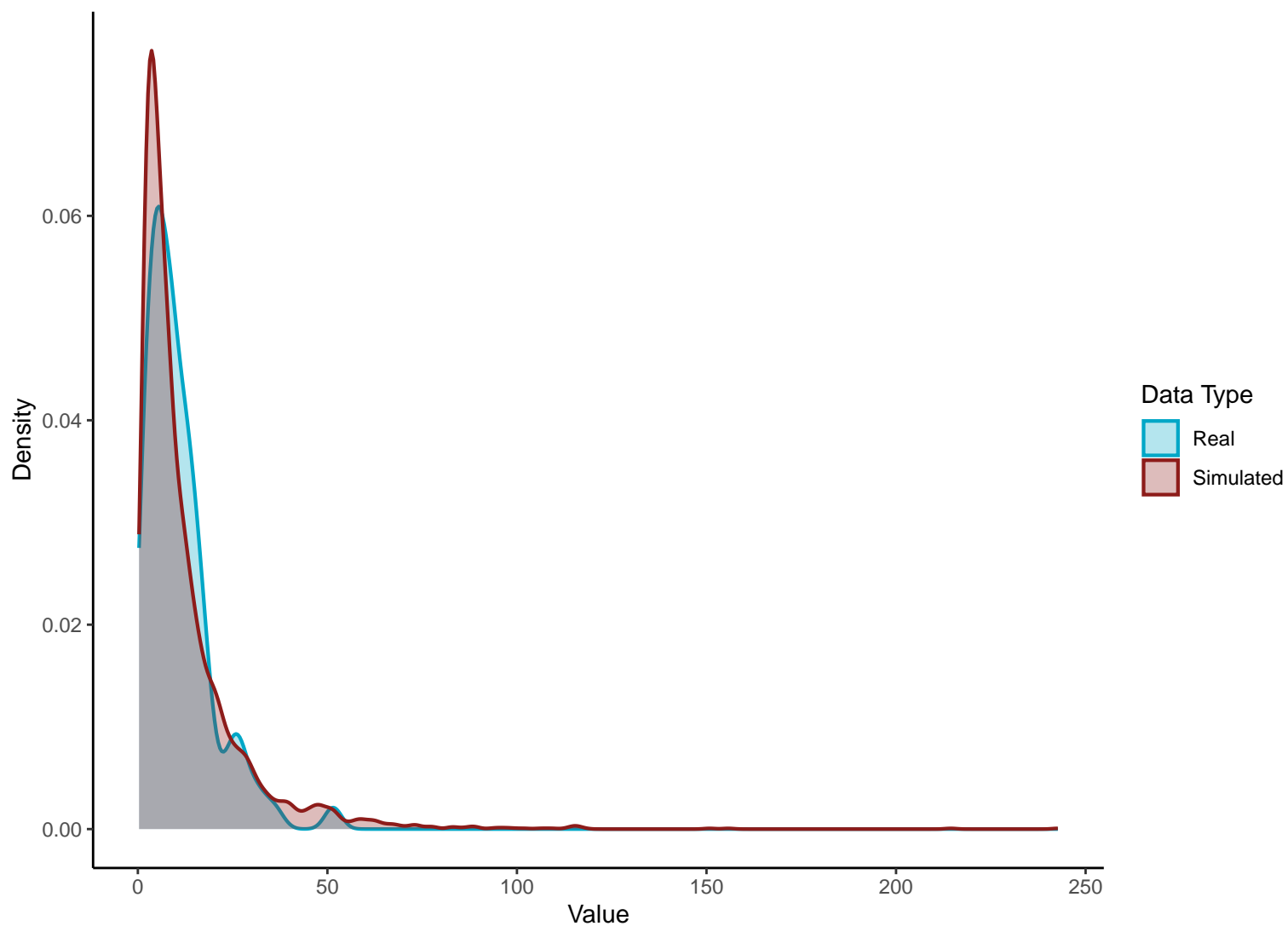
Lachnospiraceae.UGC.004



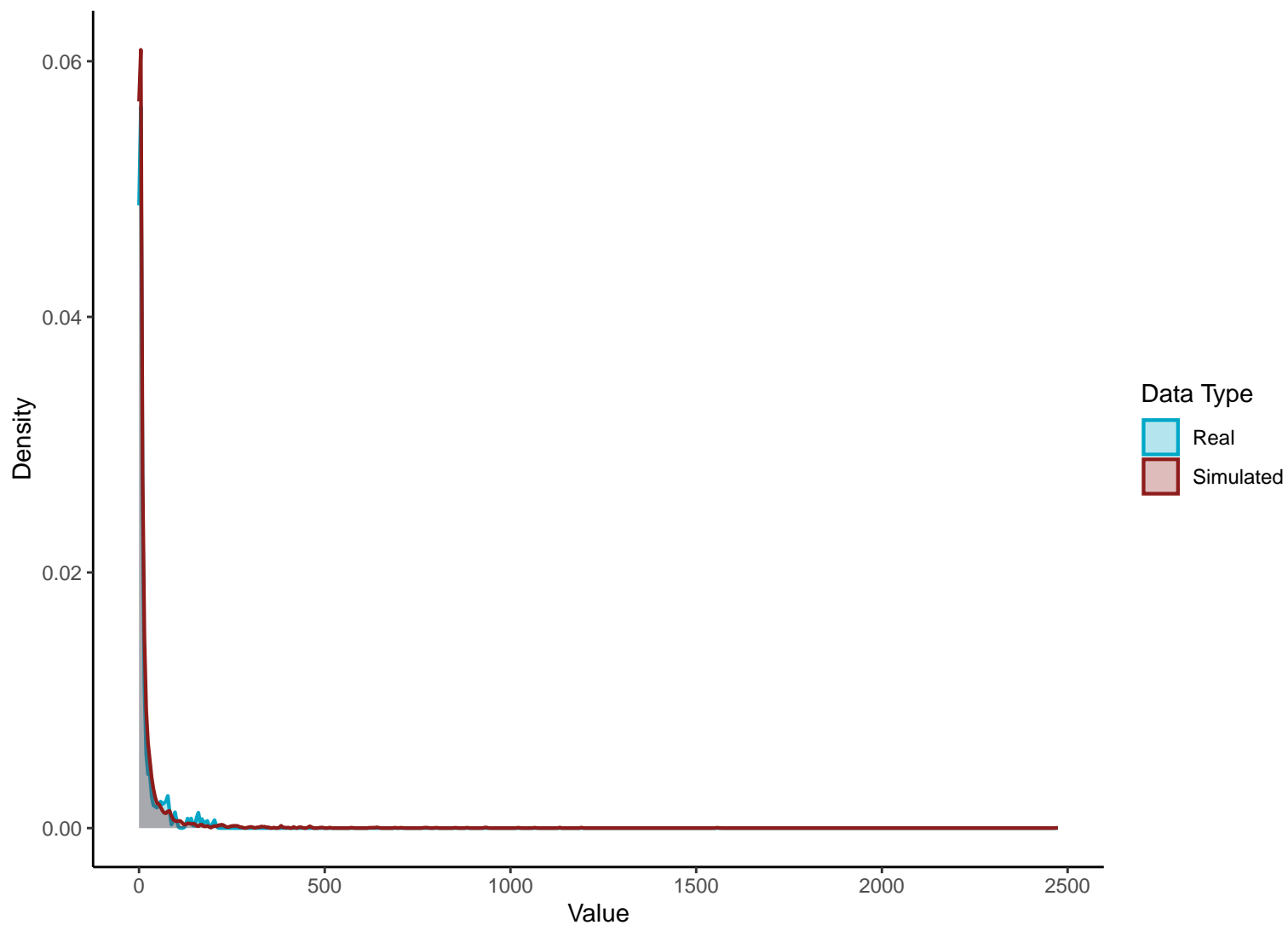
dgA.11.gut.group



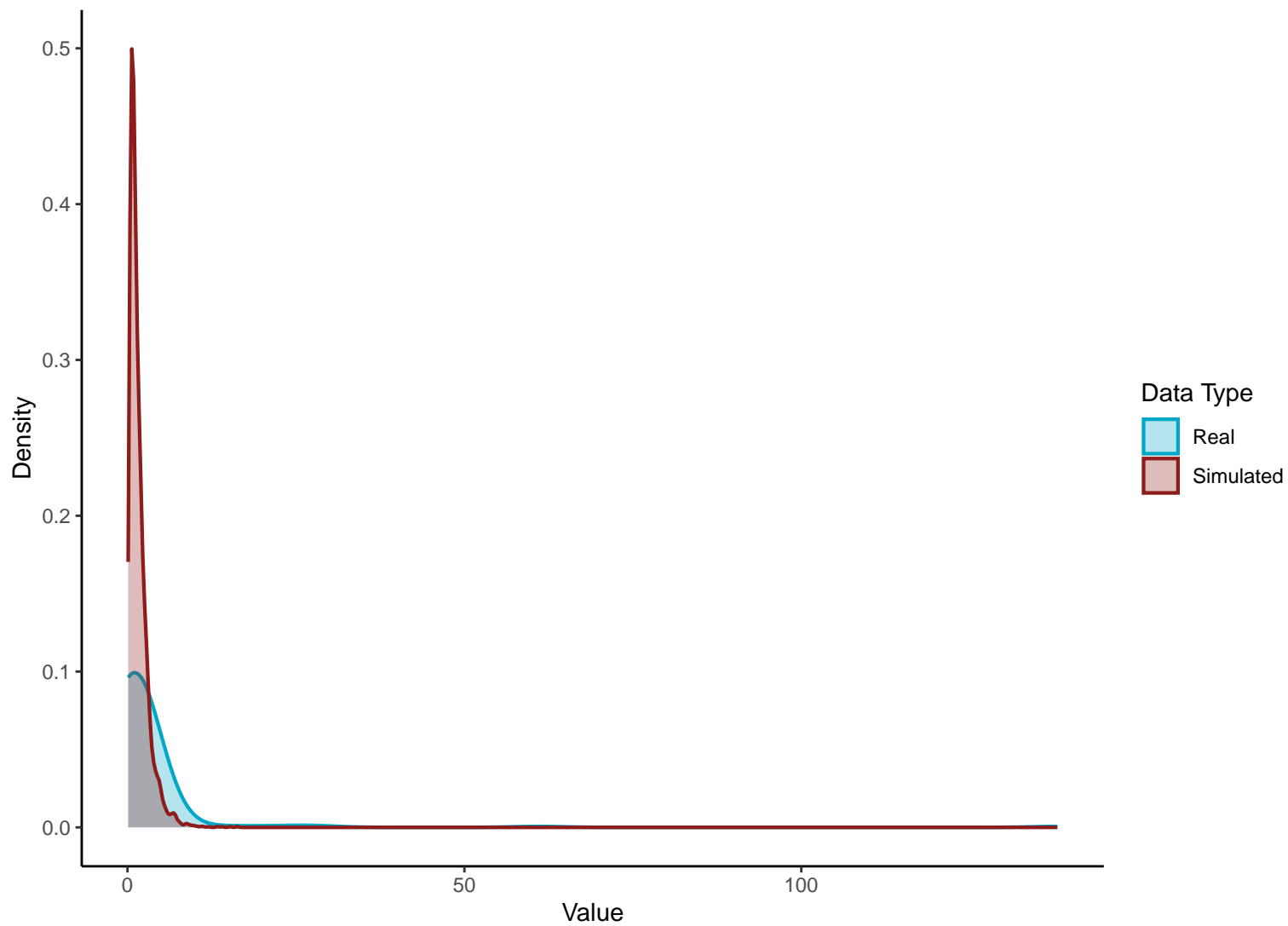
Erysipelotrichaceae.UGC.006



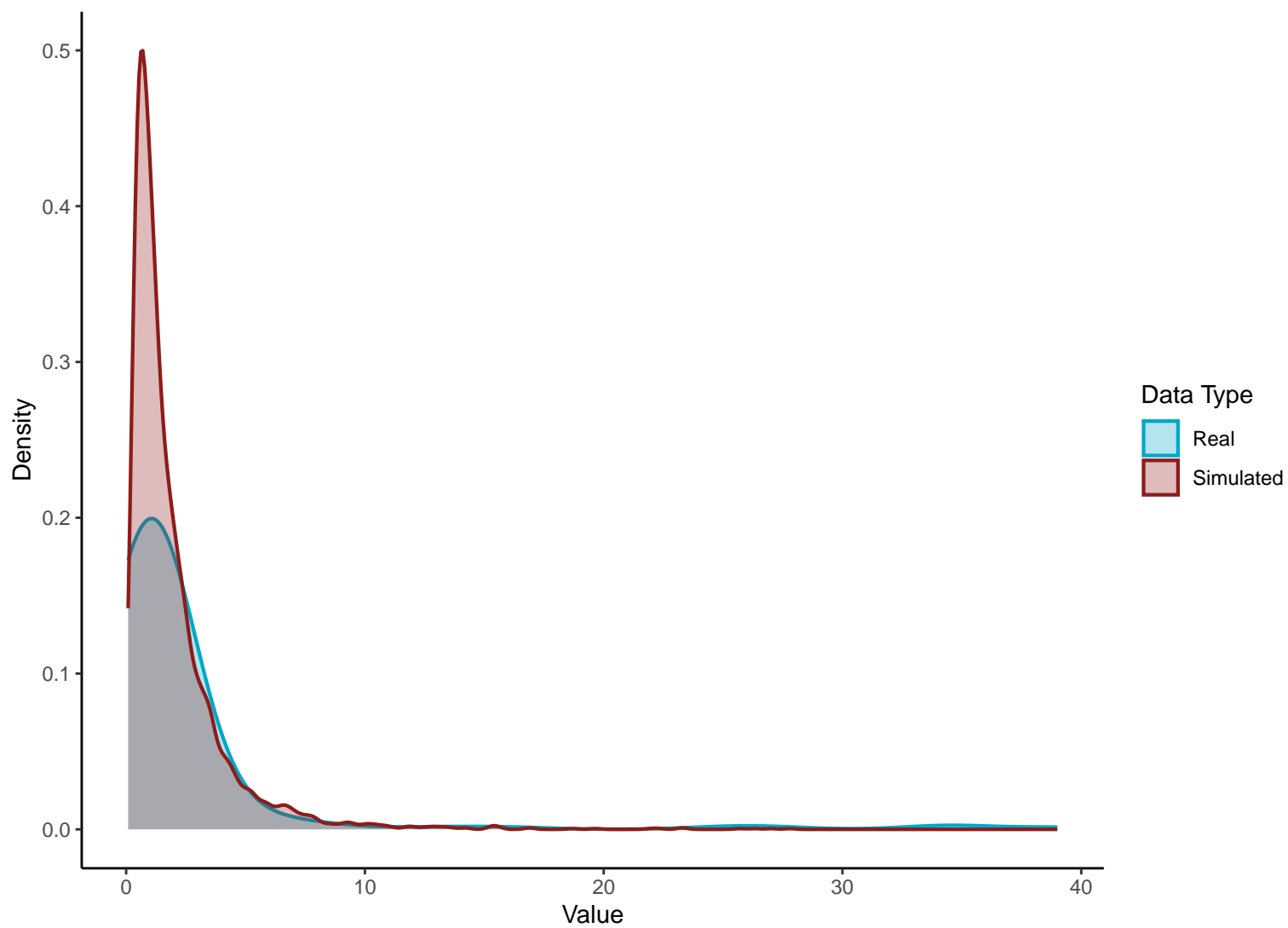
Erysipelotrichaceae.UGC.003



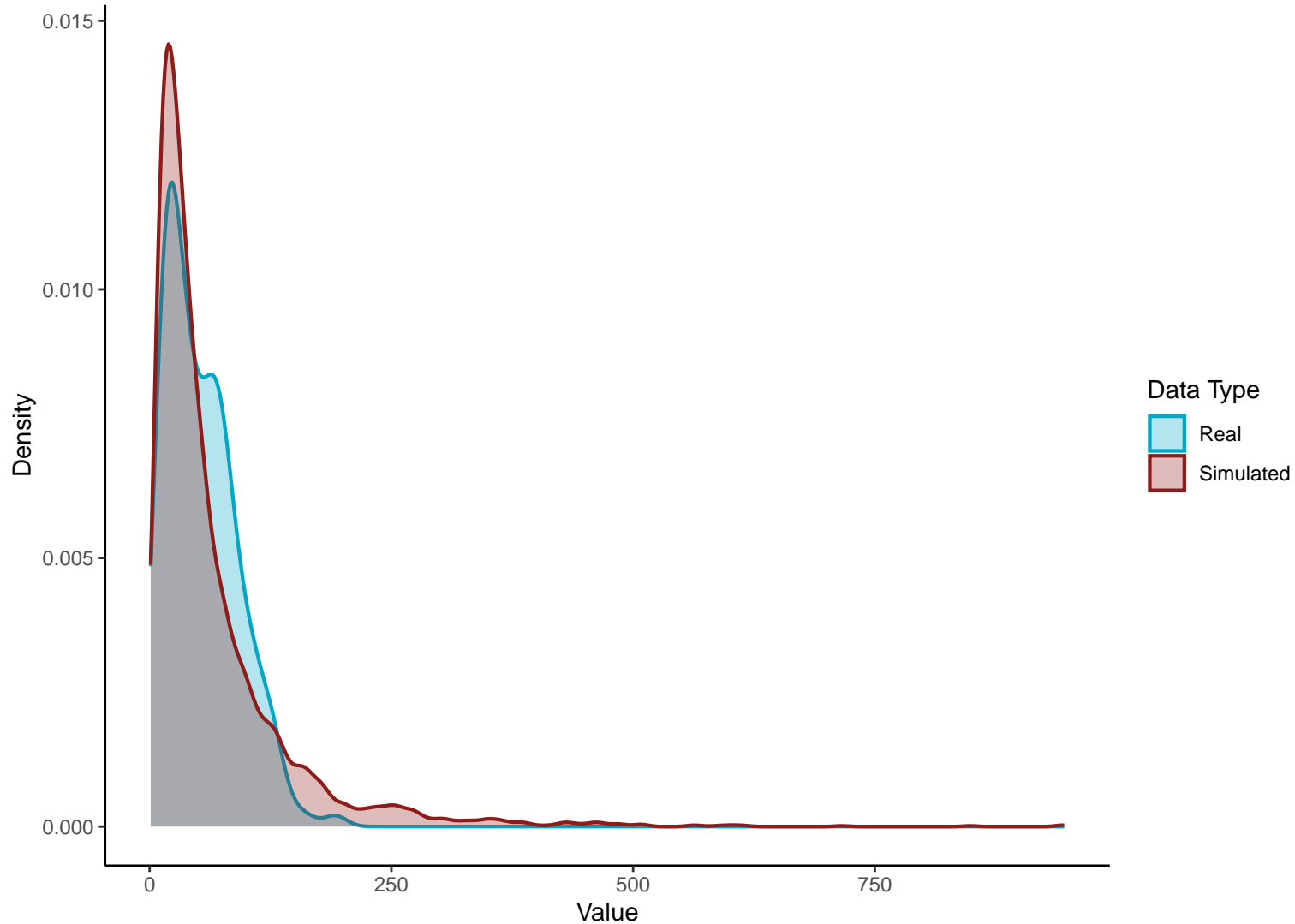
X.Eubacterium..saphenum.group



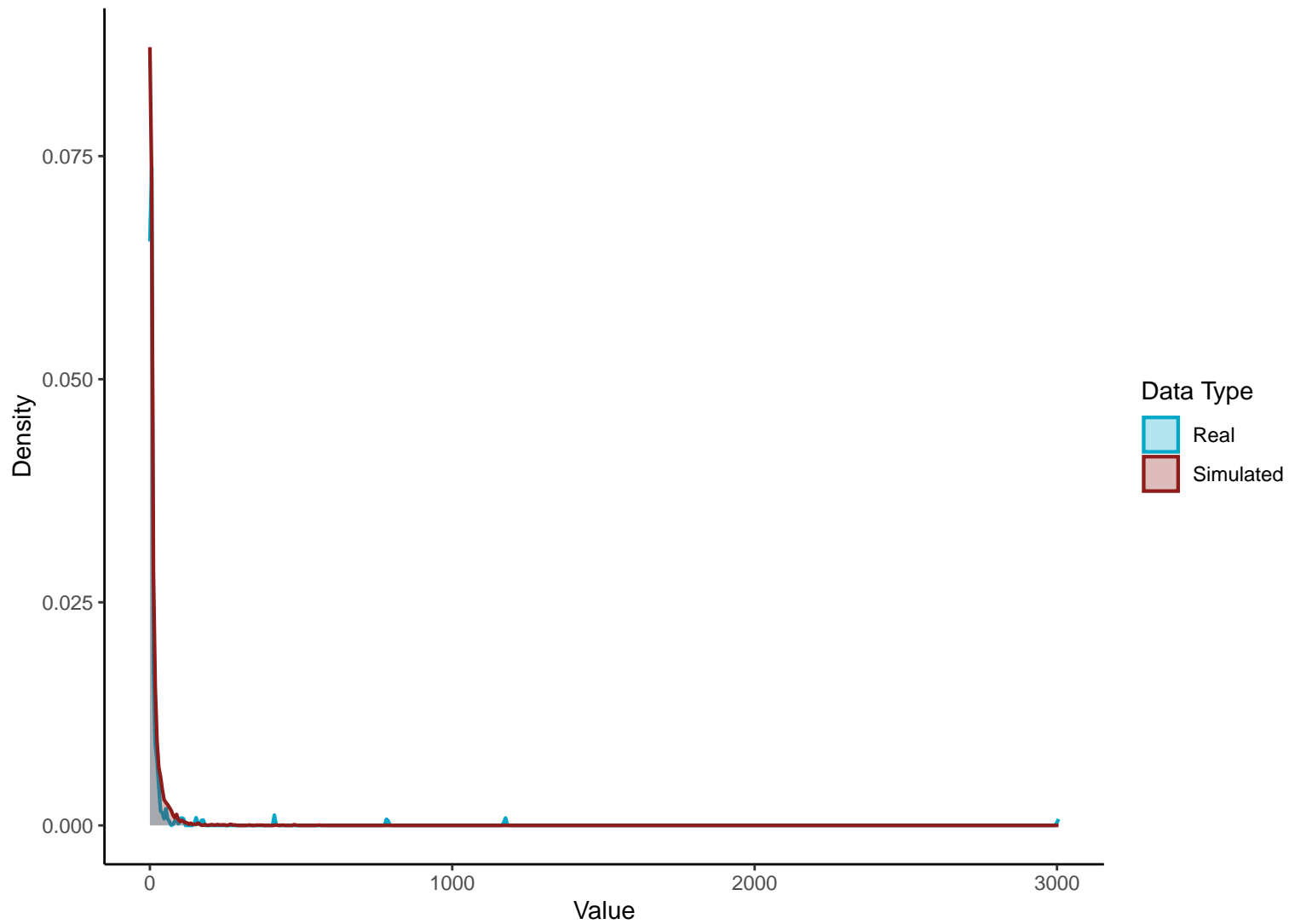
X.Ruminococcus..gnavus.group



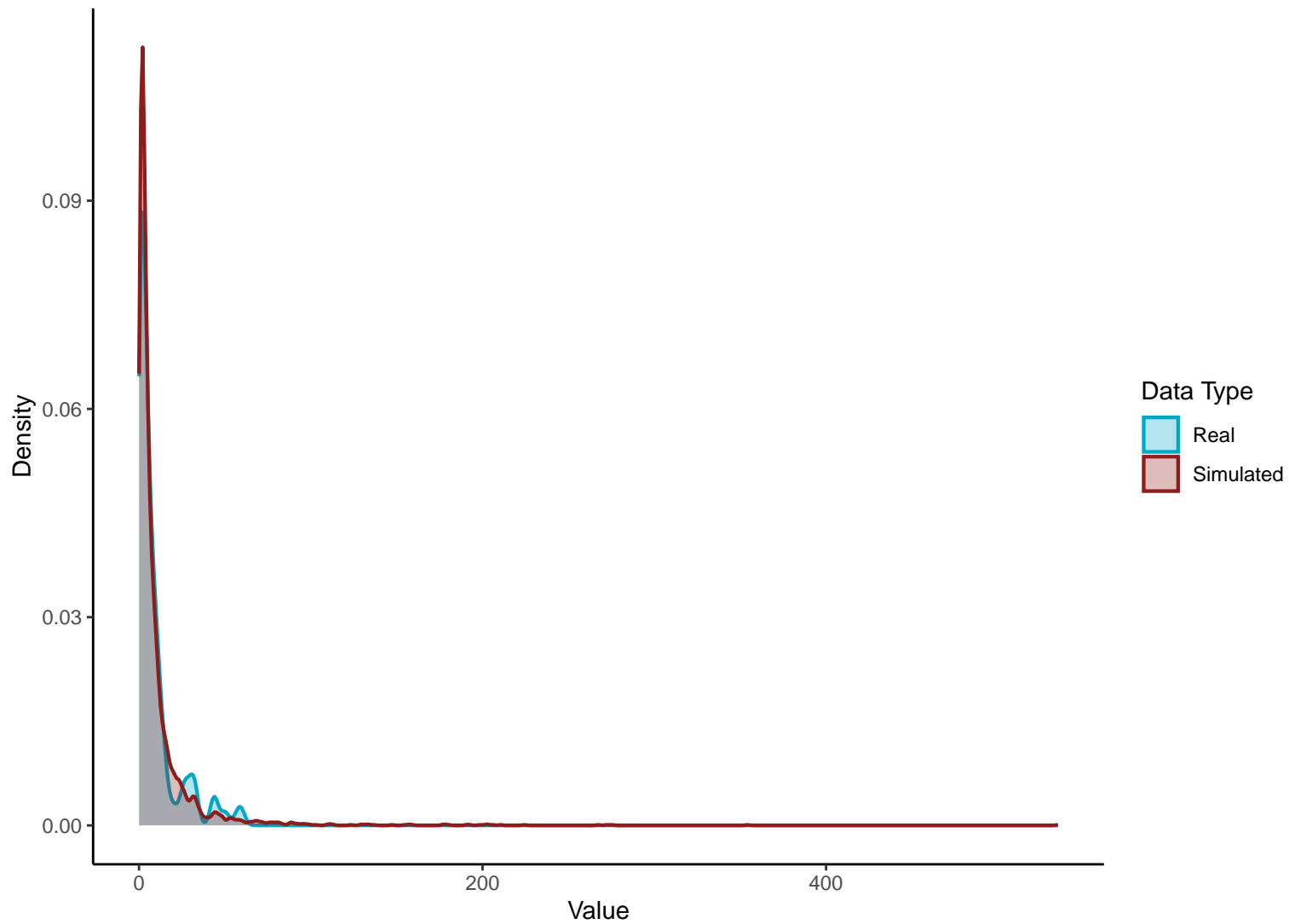
Fournierella



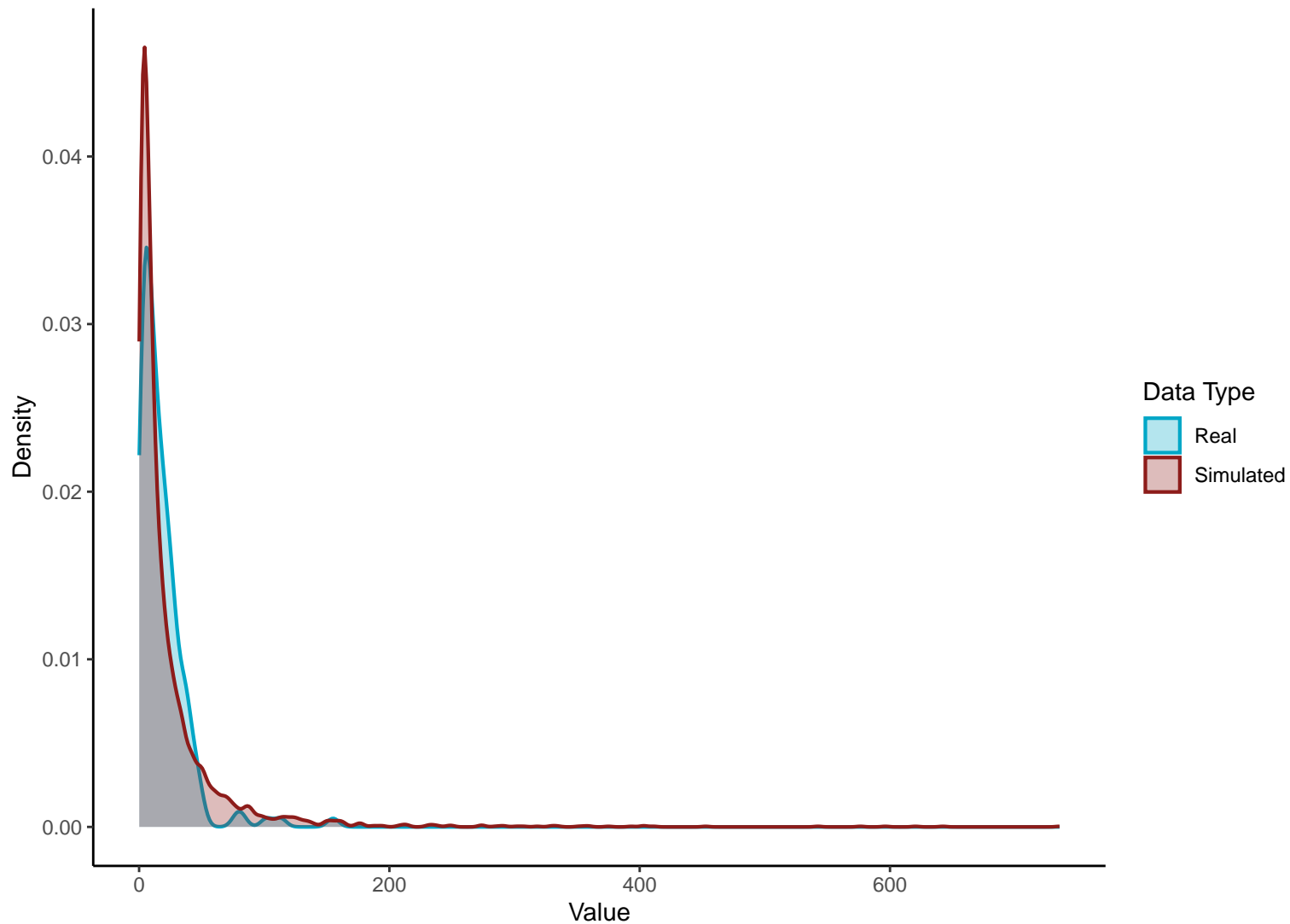
Escherichia.Shigella



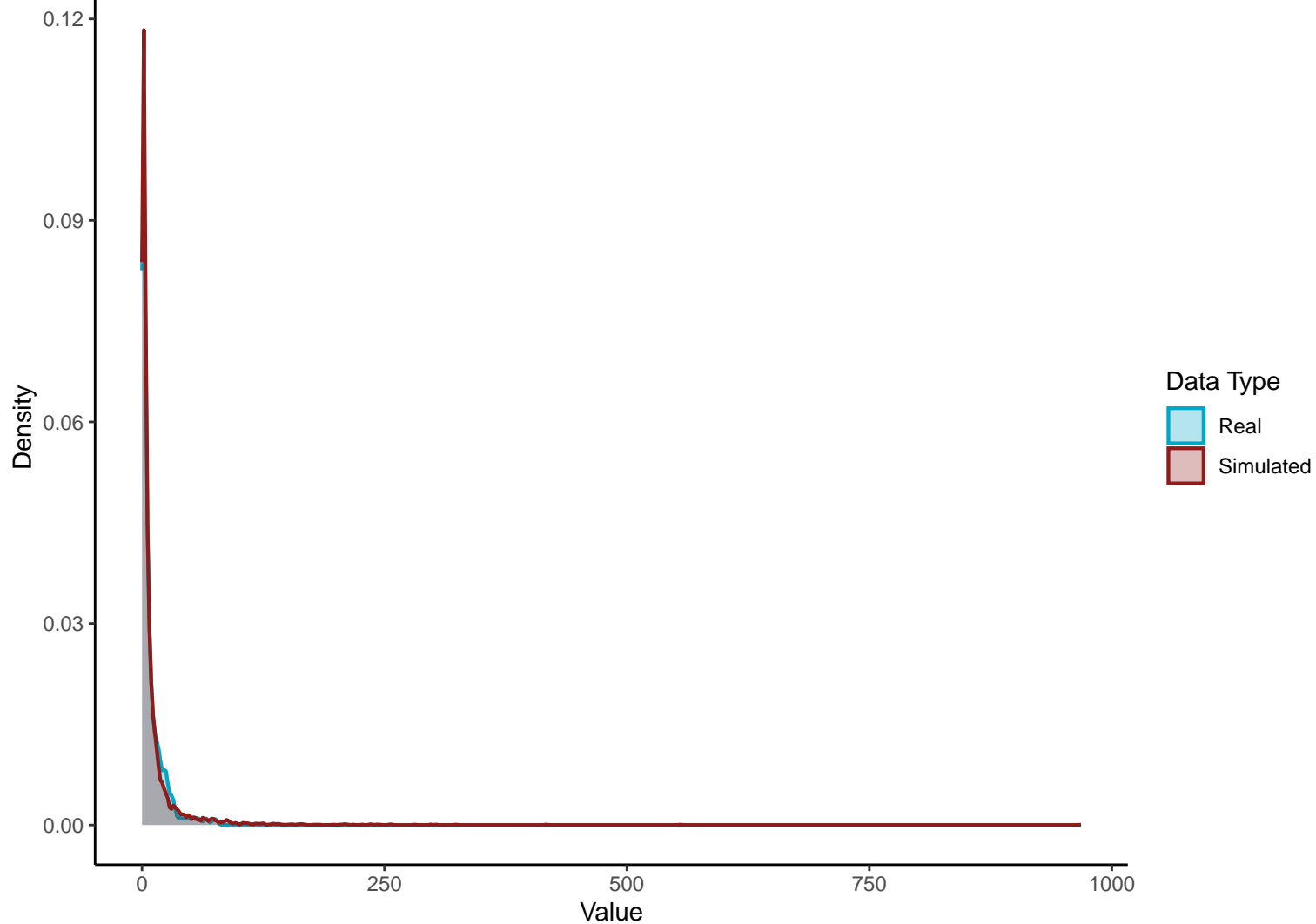
X.Eubacterium..fissicatena.group



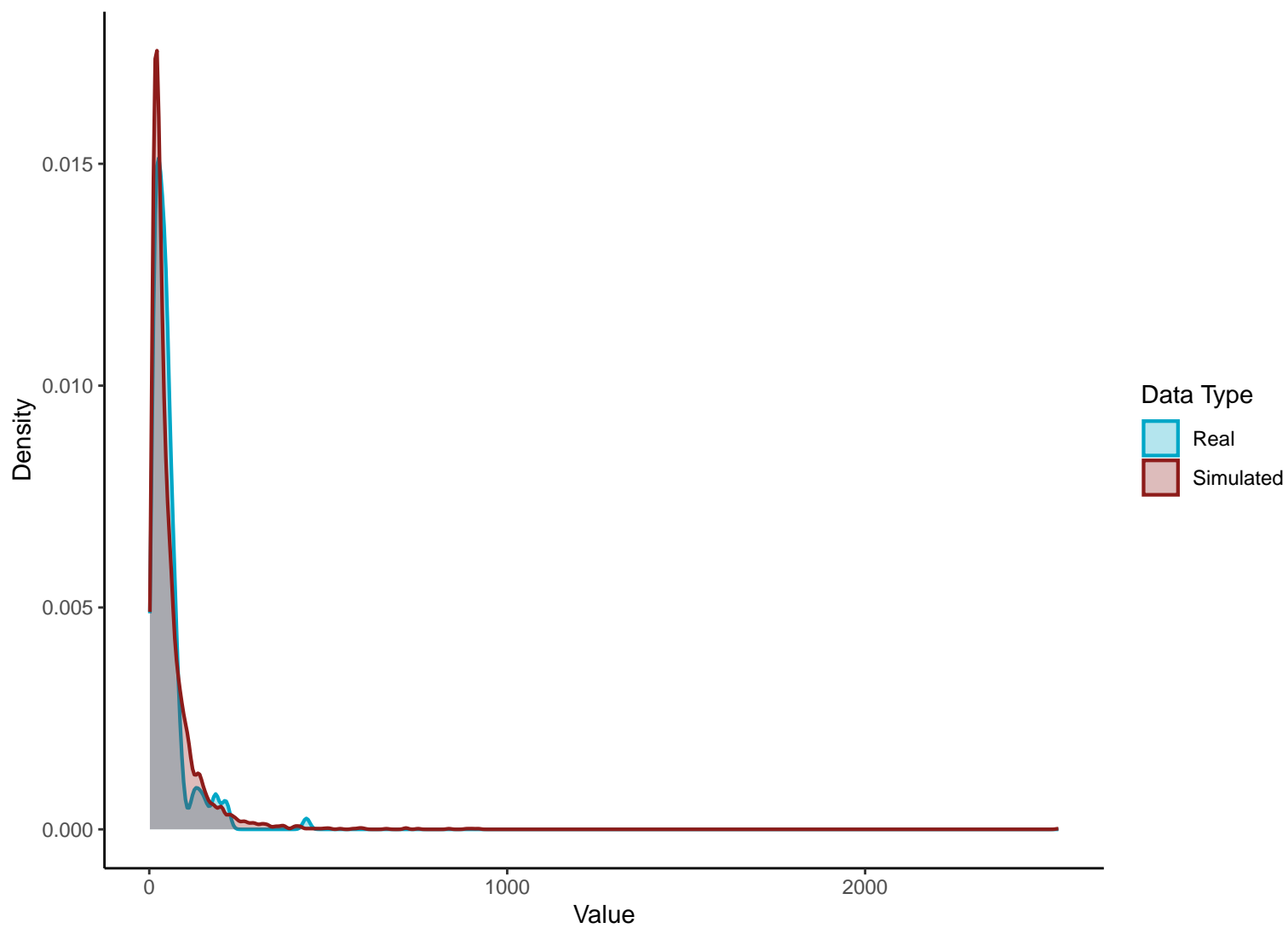
X.Anaerorhabdus.furcosa.group



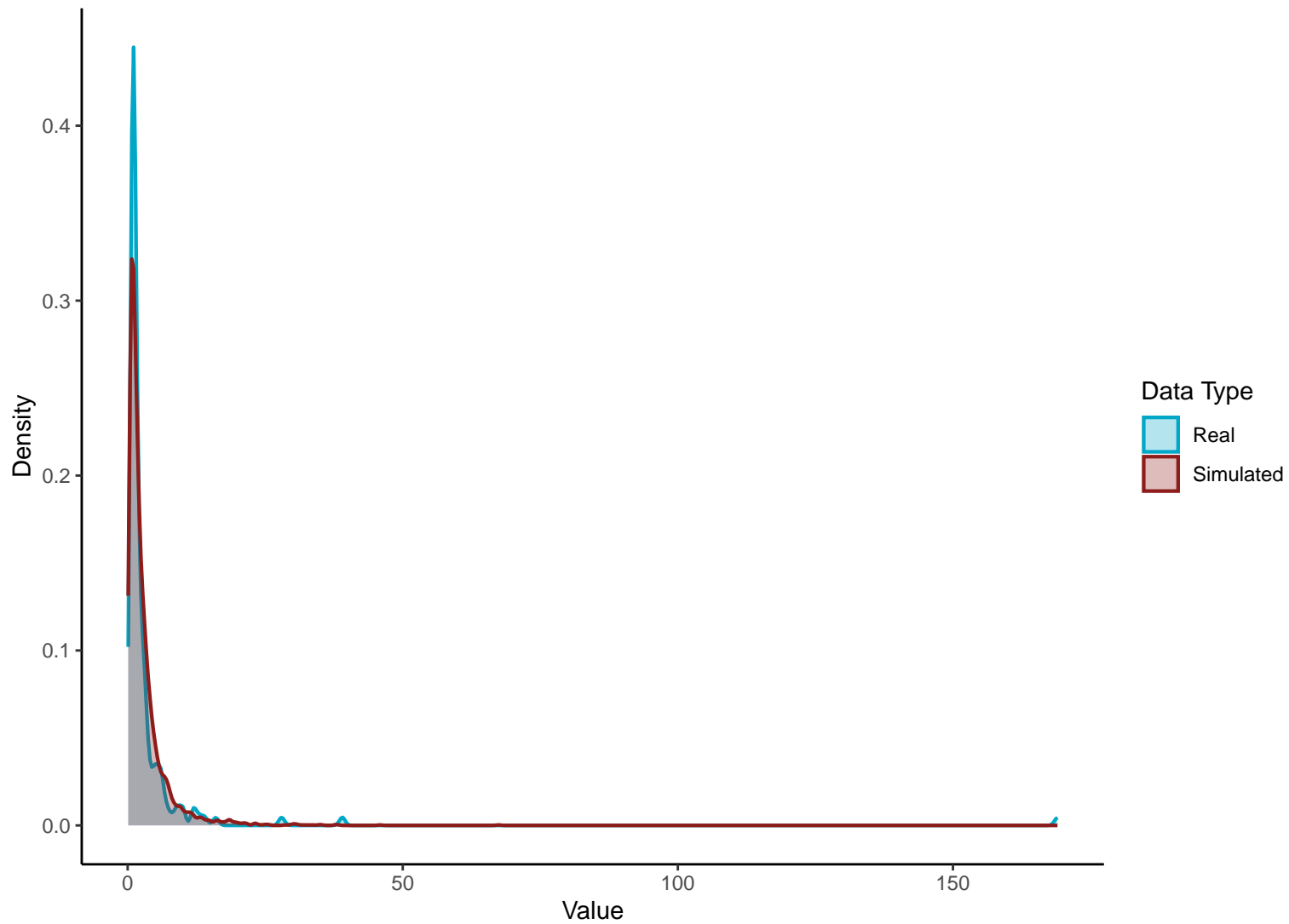
Lachnospiraceae.UGC.009



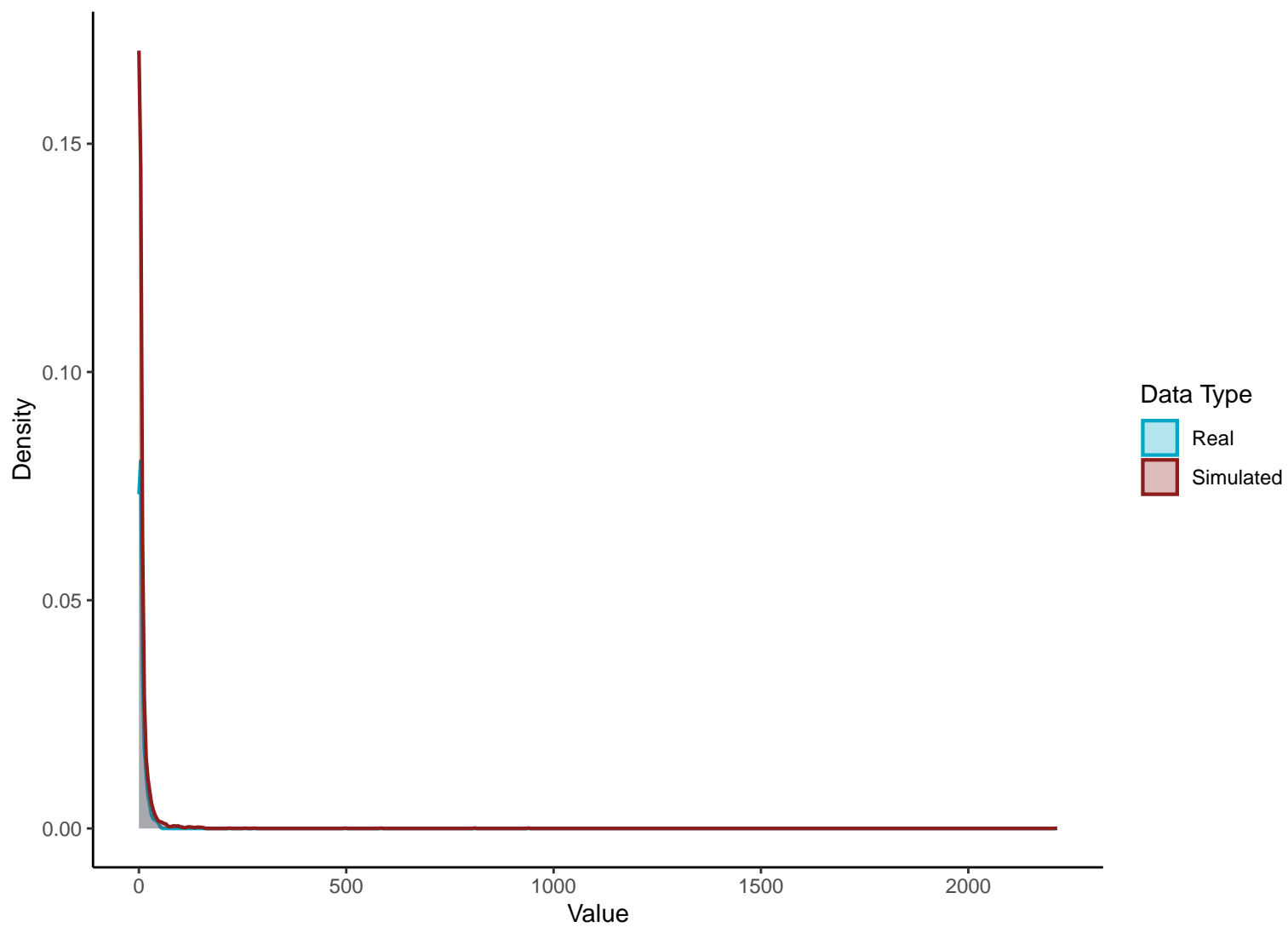
Paraeggerthella



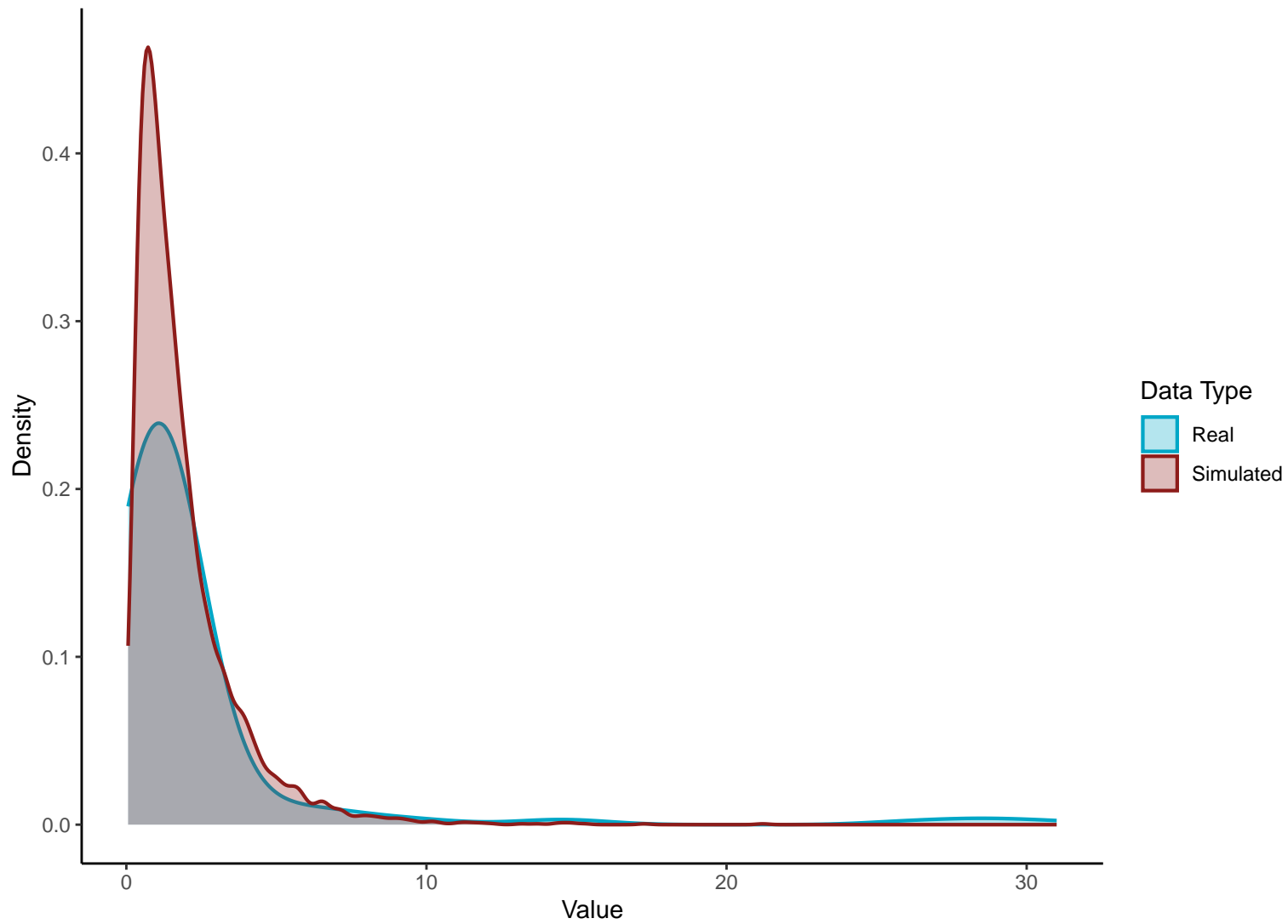
Selenomonas



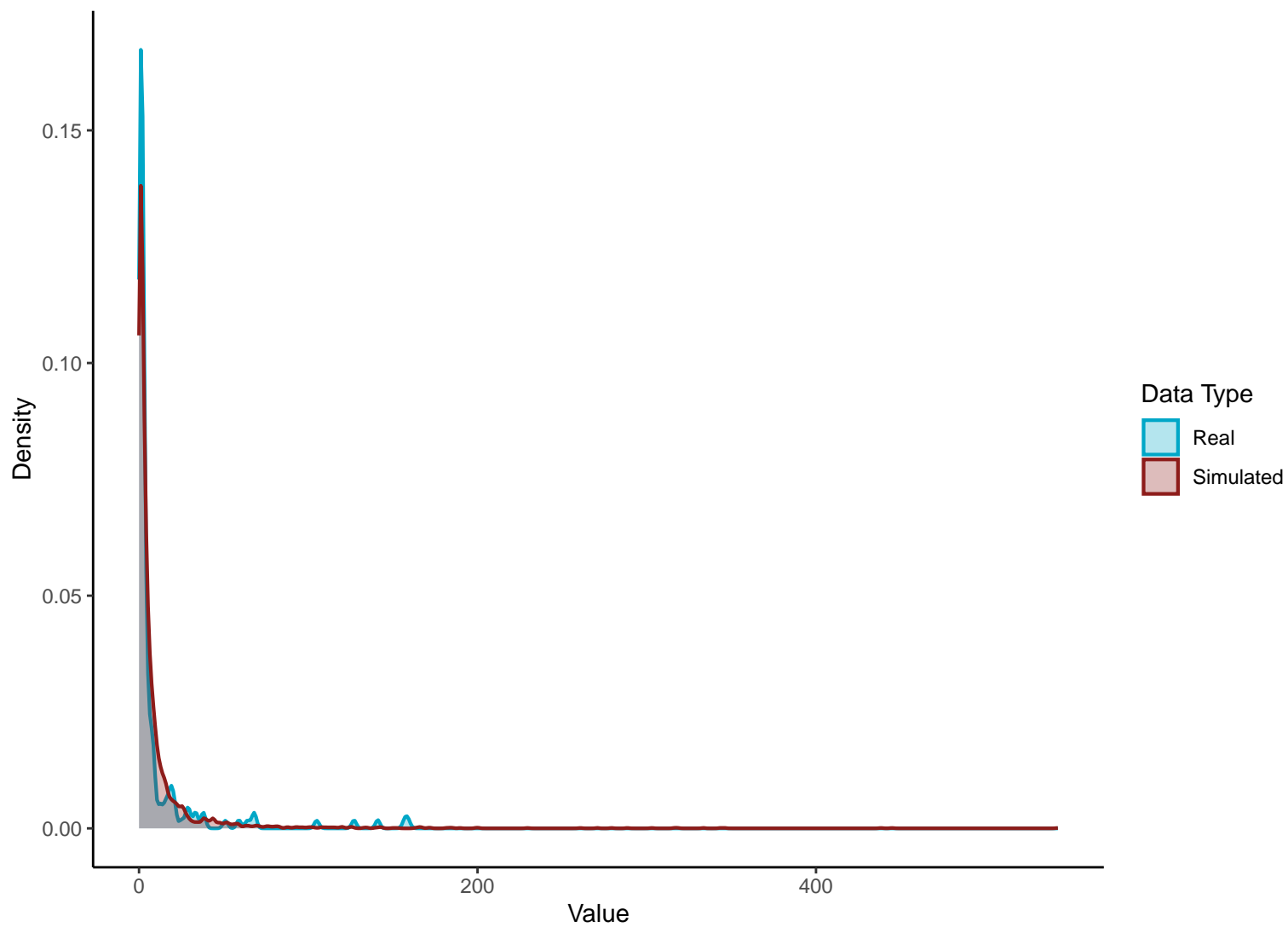
Senegalimassilia



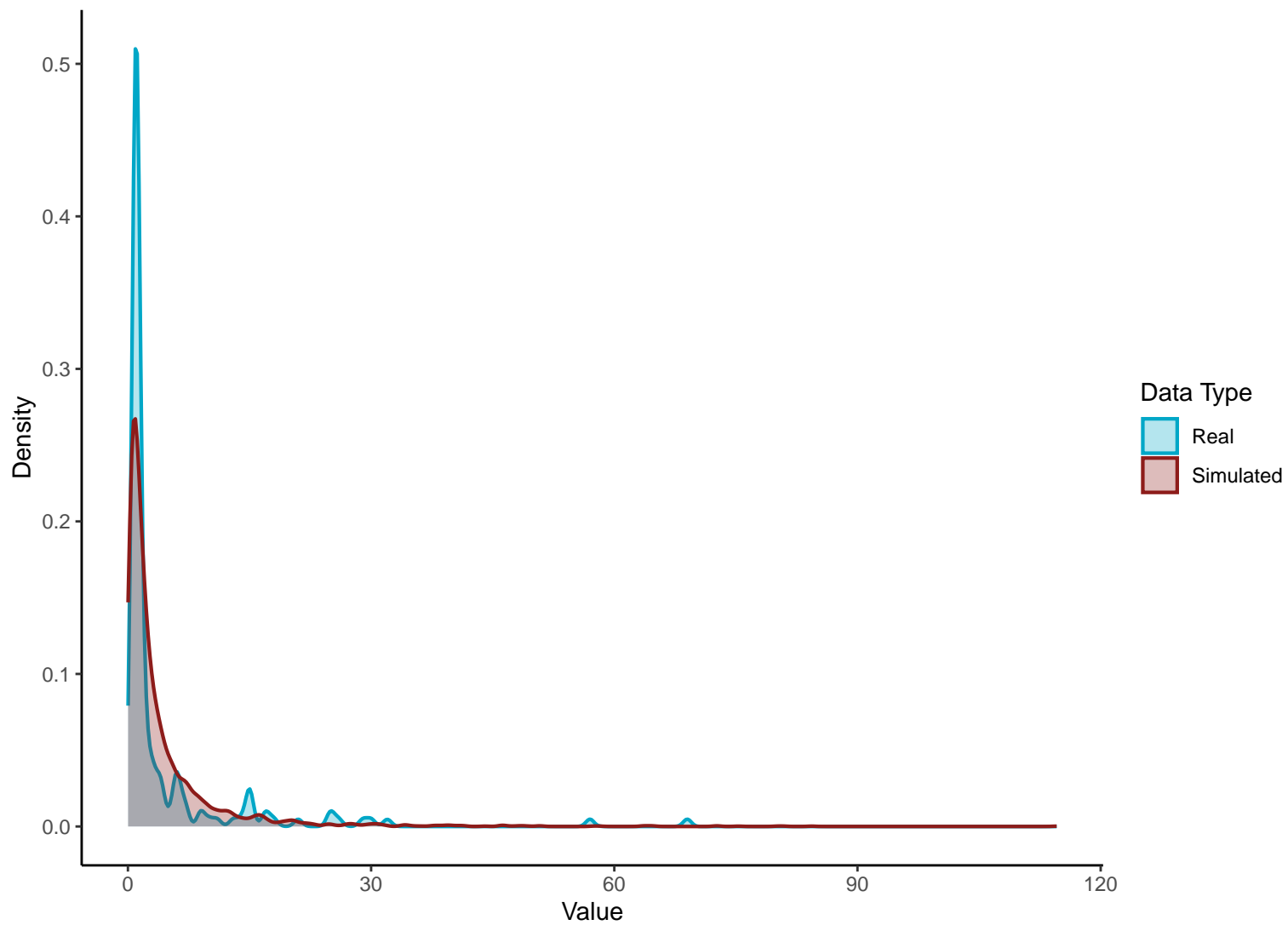
FD2005



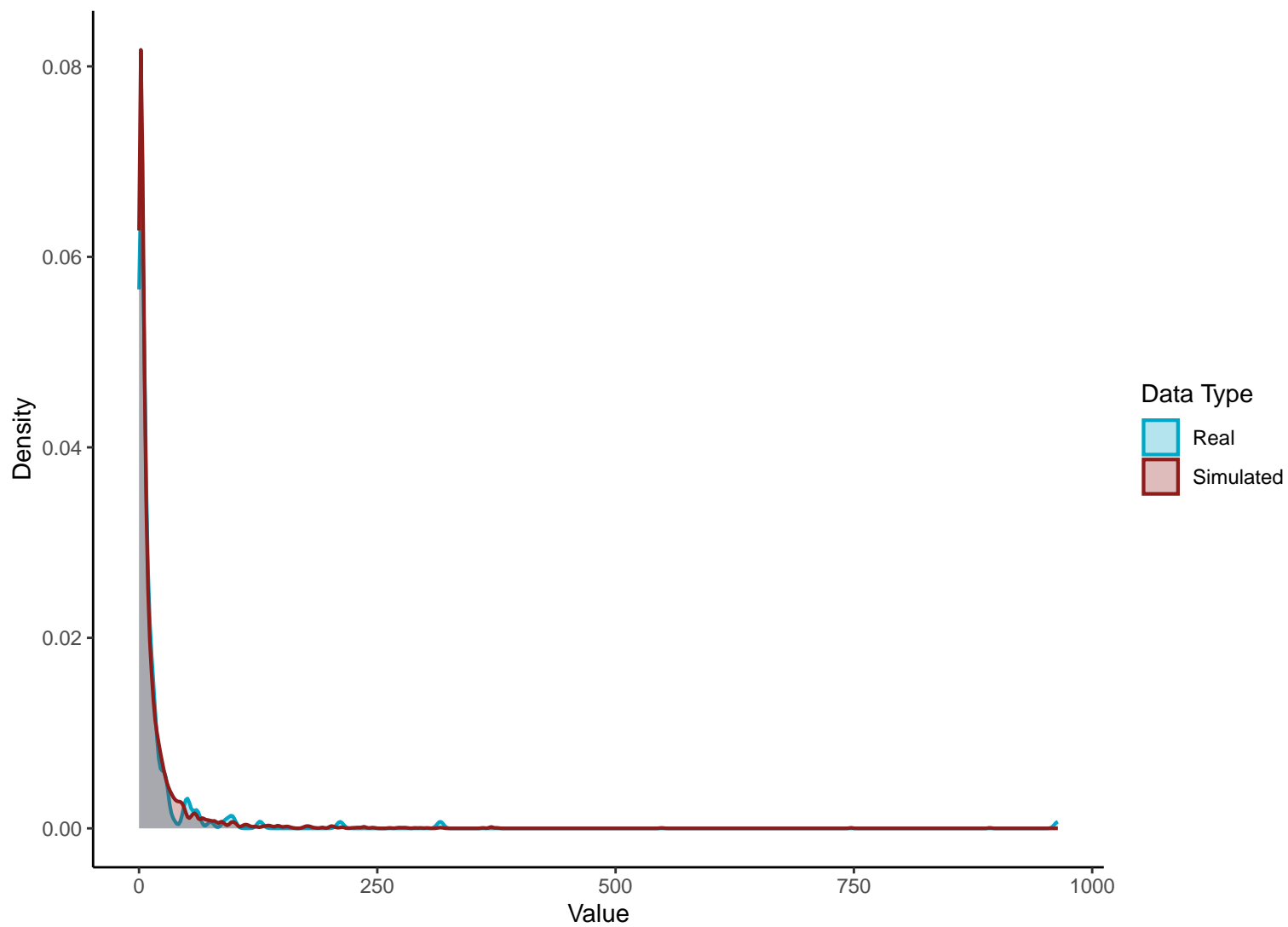
Veillonella



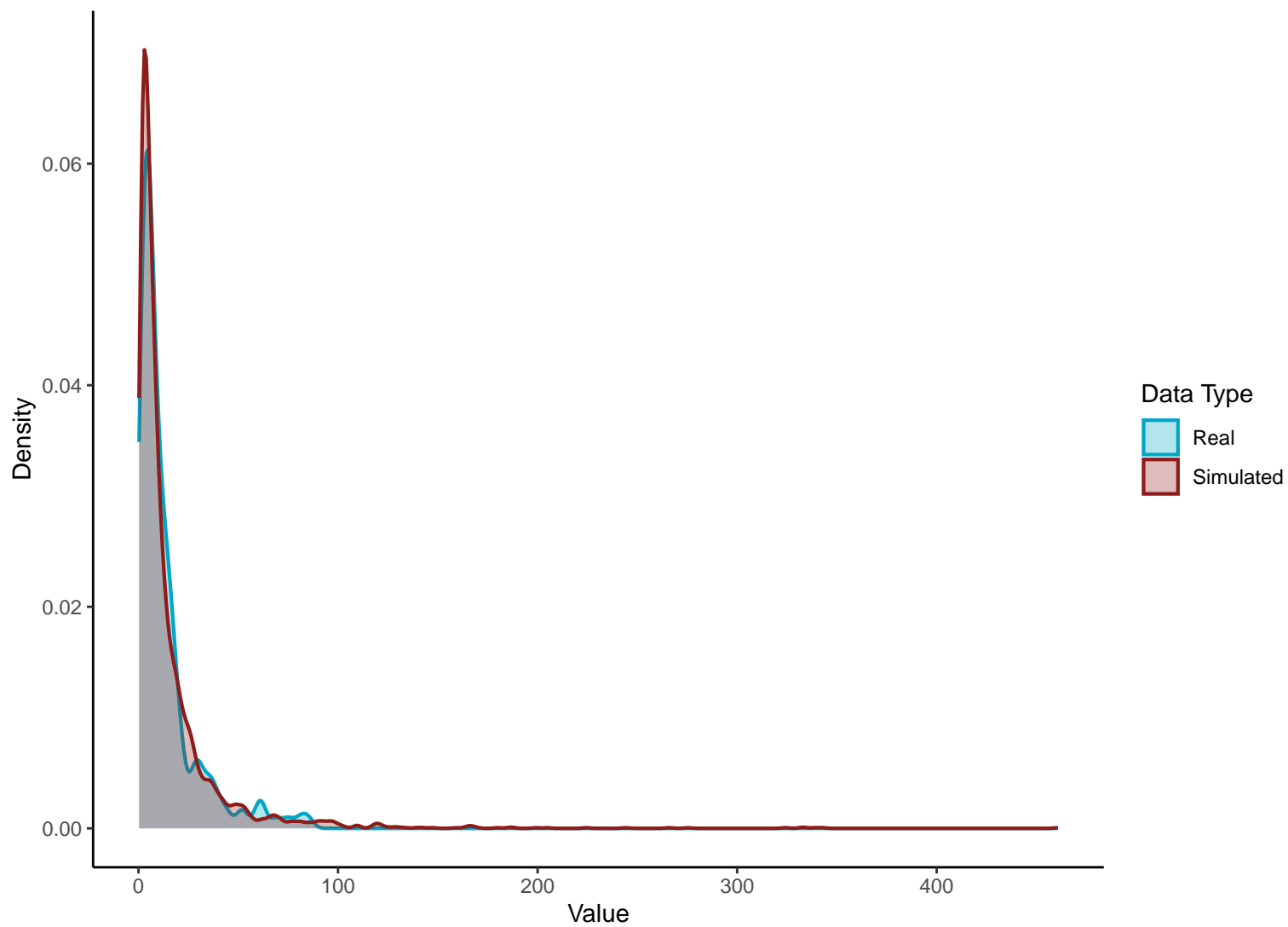
Clostridium.sensu.stricto.6



CAG.352



CAG.56



Candidatus.Stoquefichus

