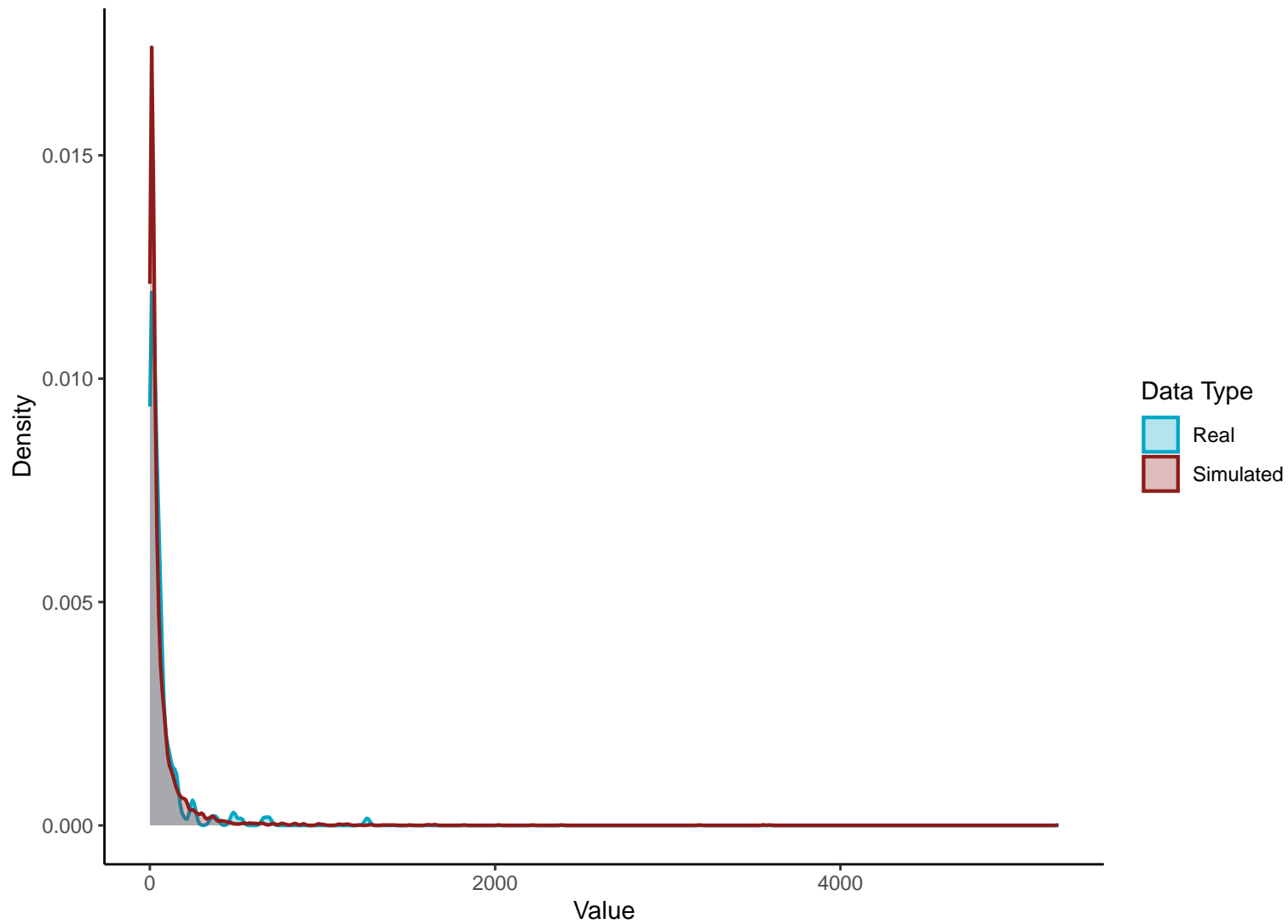
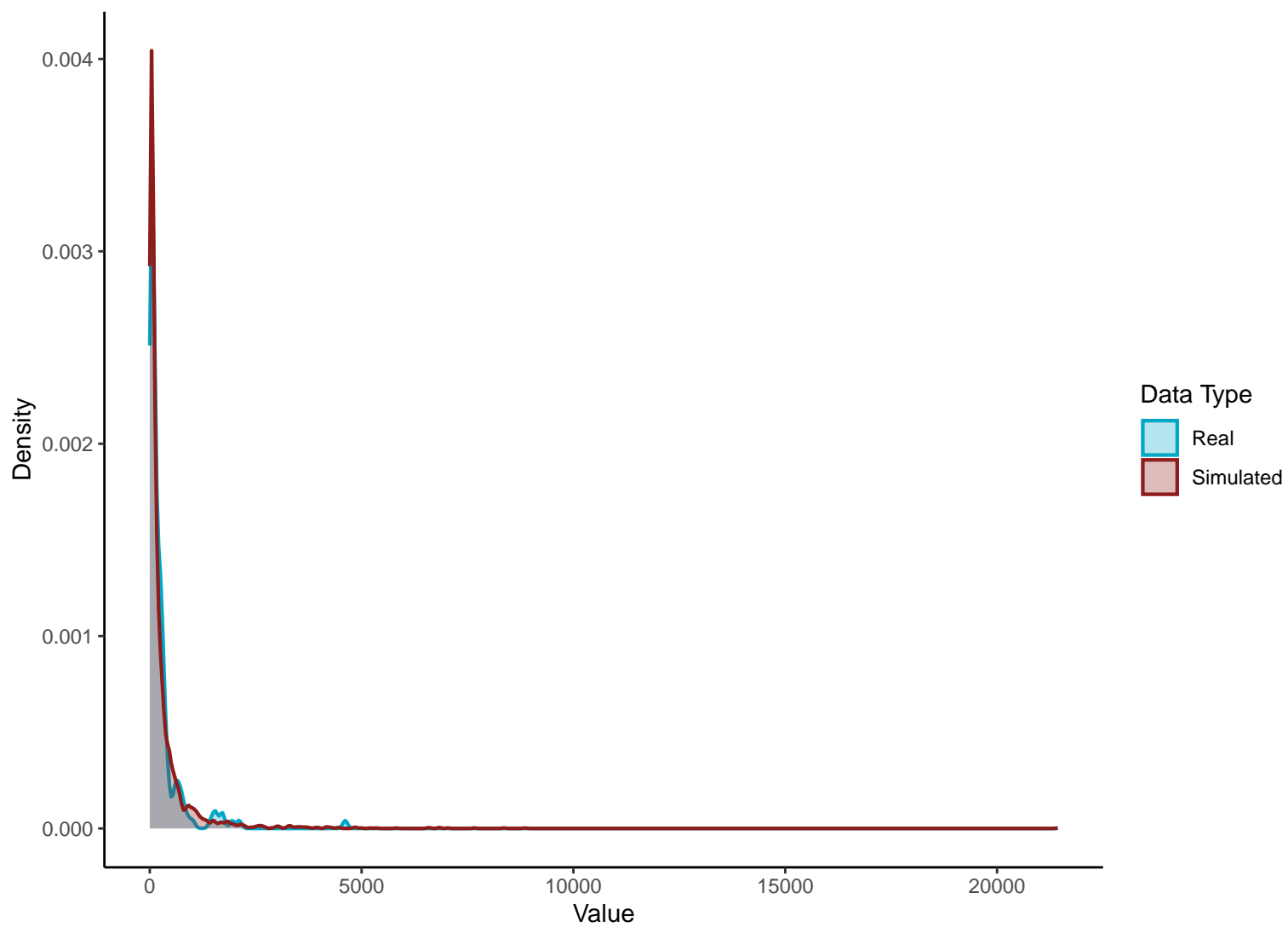


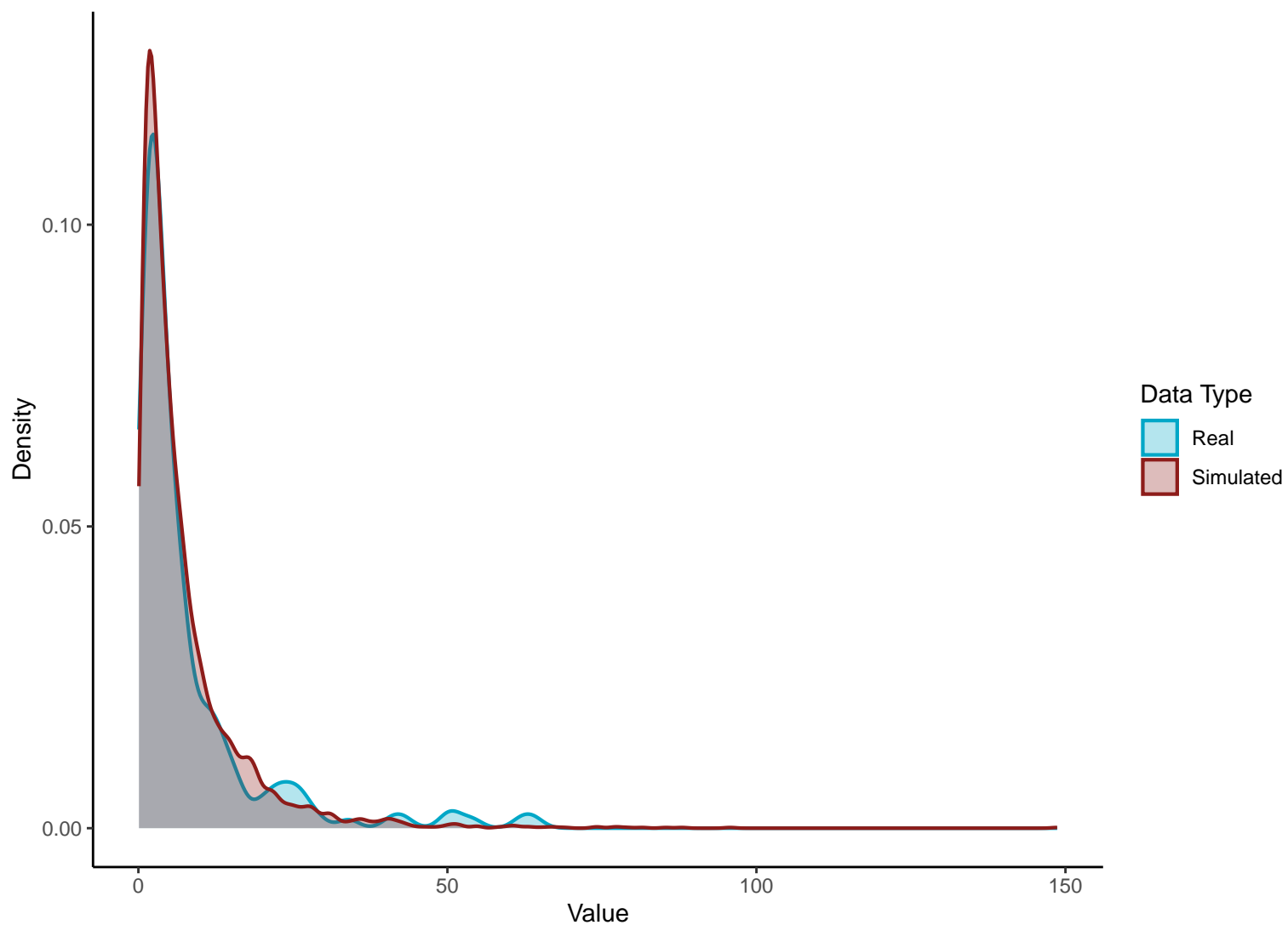
Prevotellaceae.UGC.003



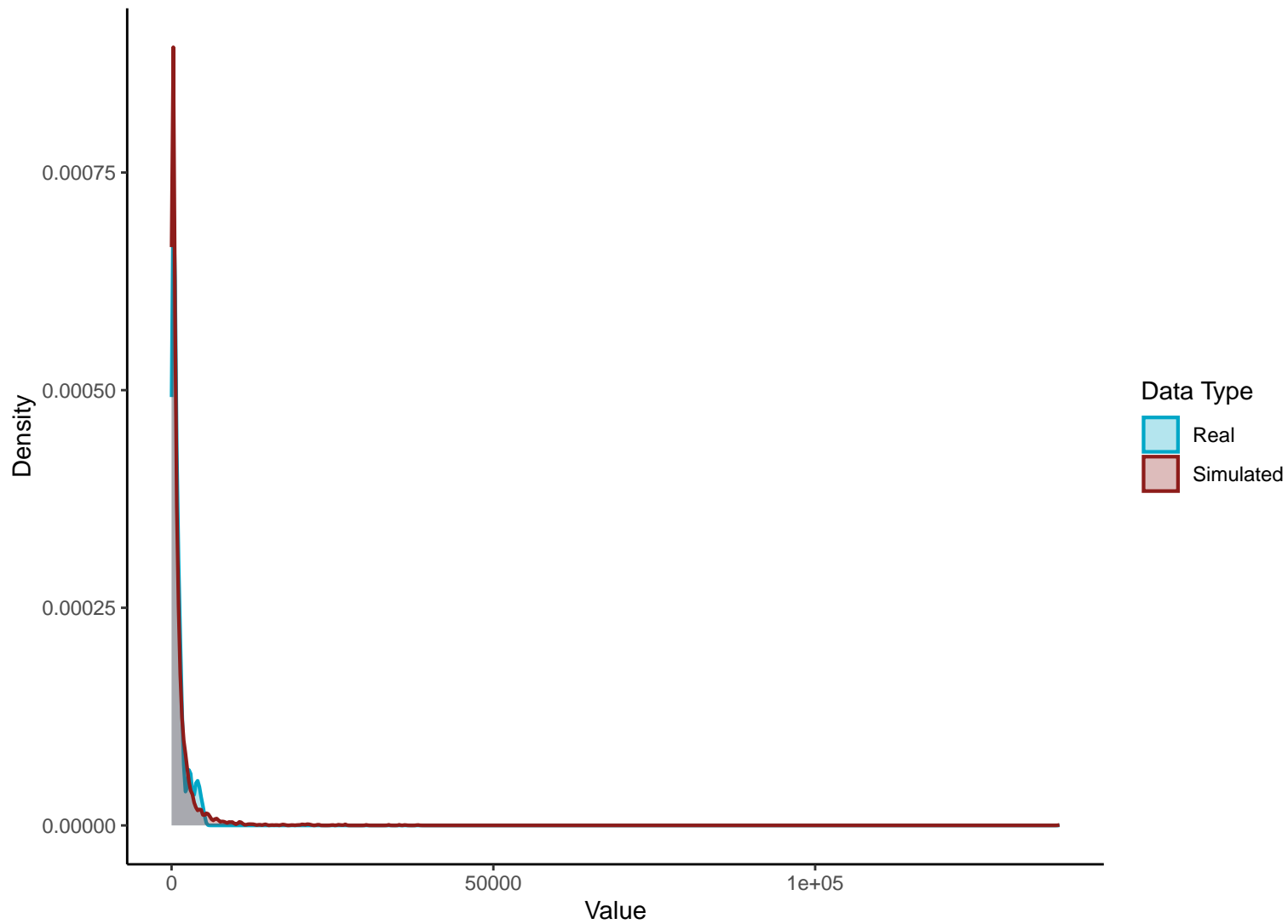
Prevotellaceae.NK3B31.group



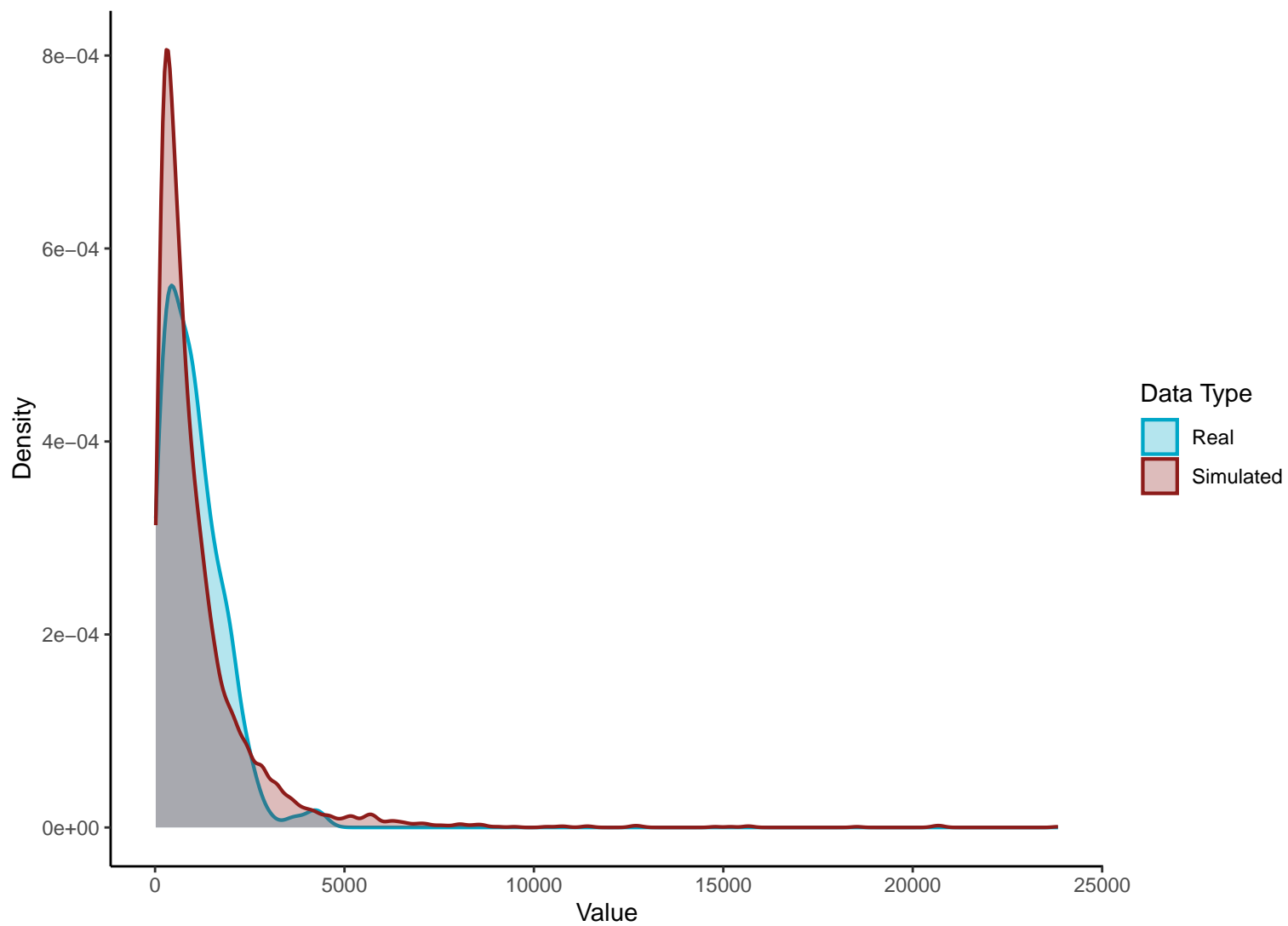
Sutterella



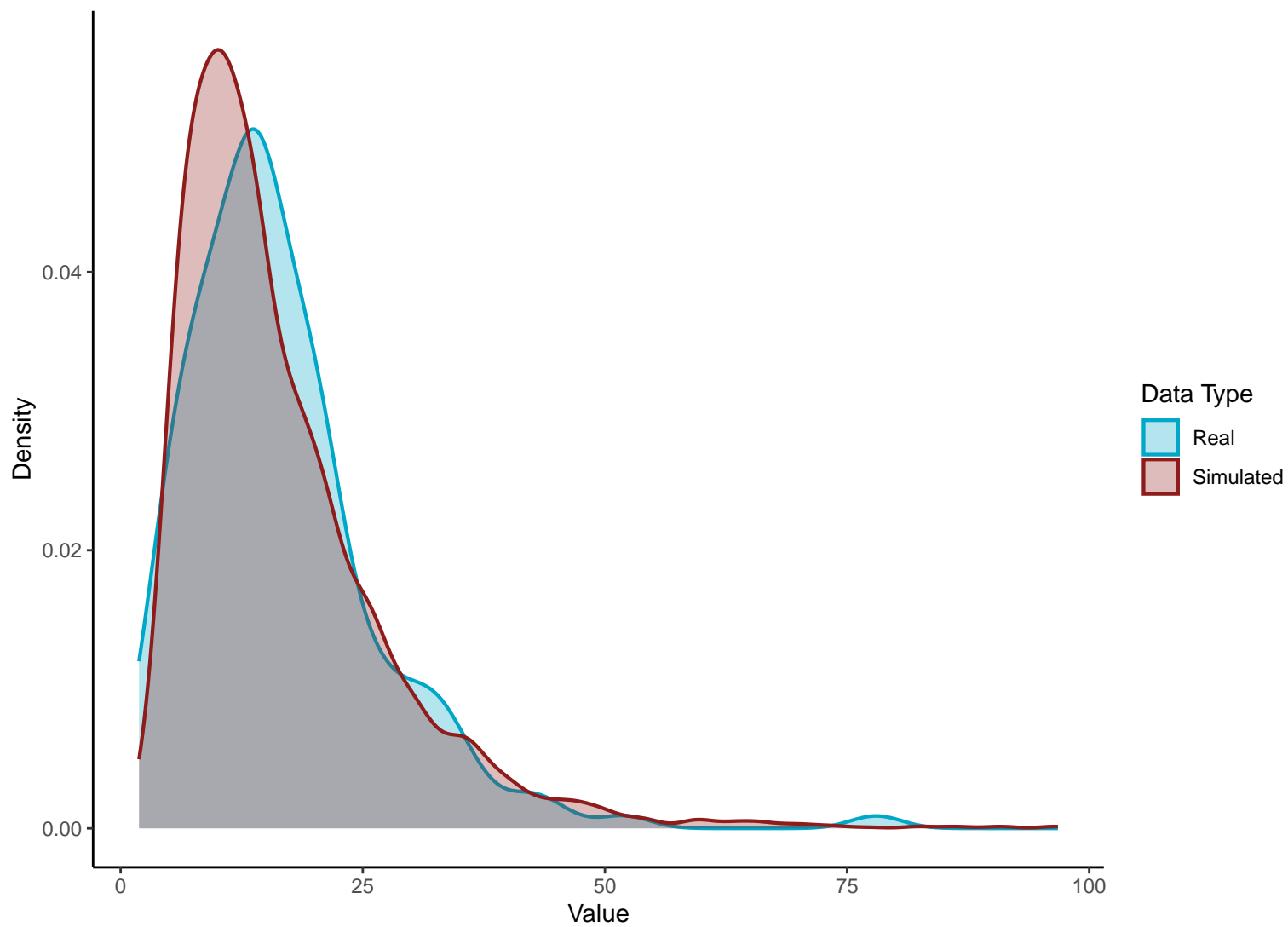
Christensenellaceae.R.7.group



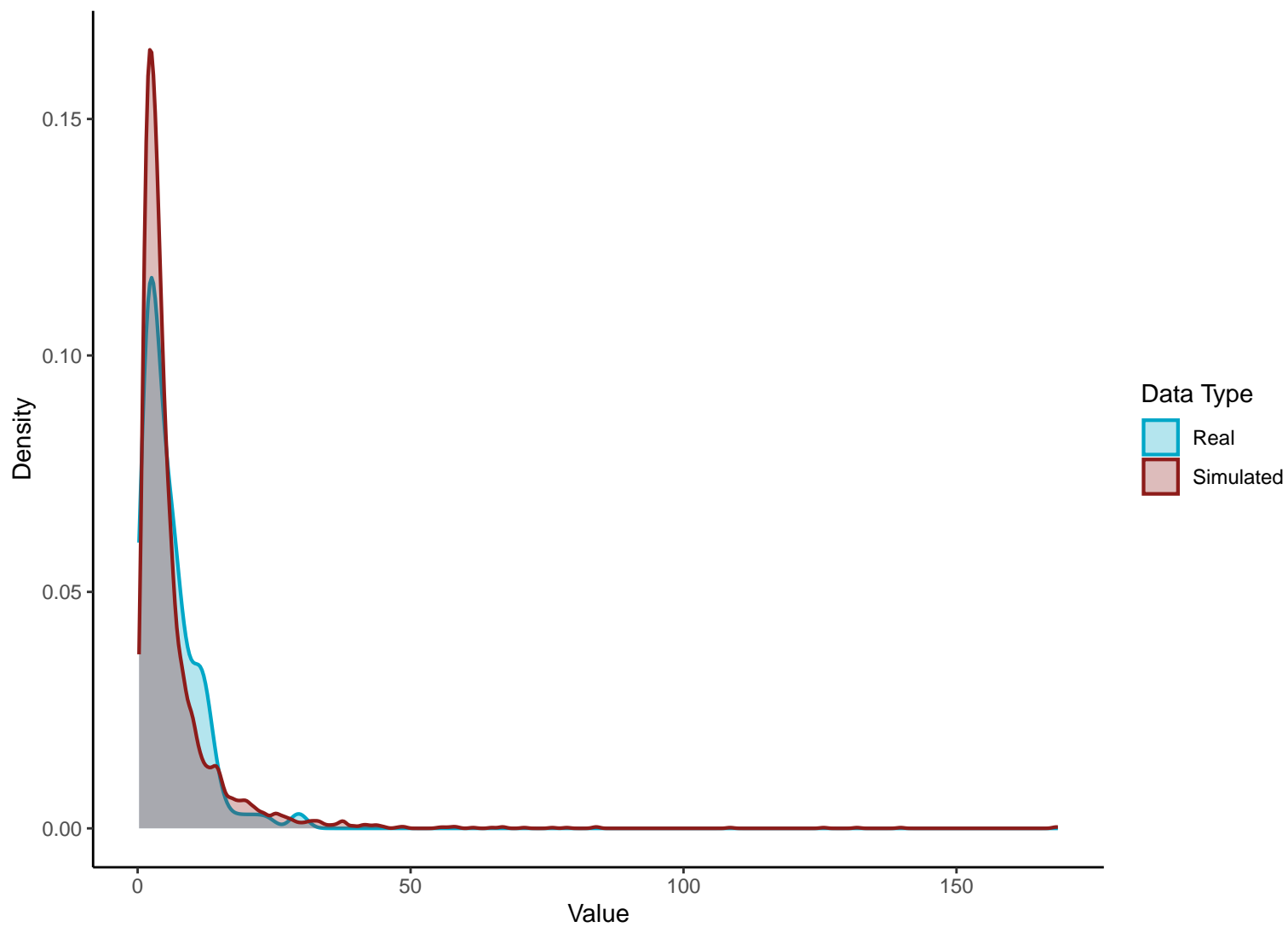
UCG.005



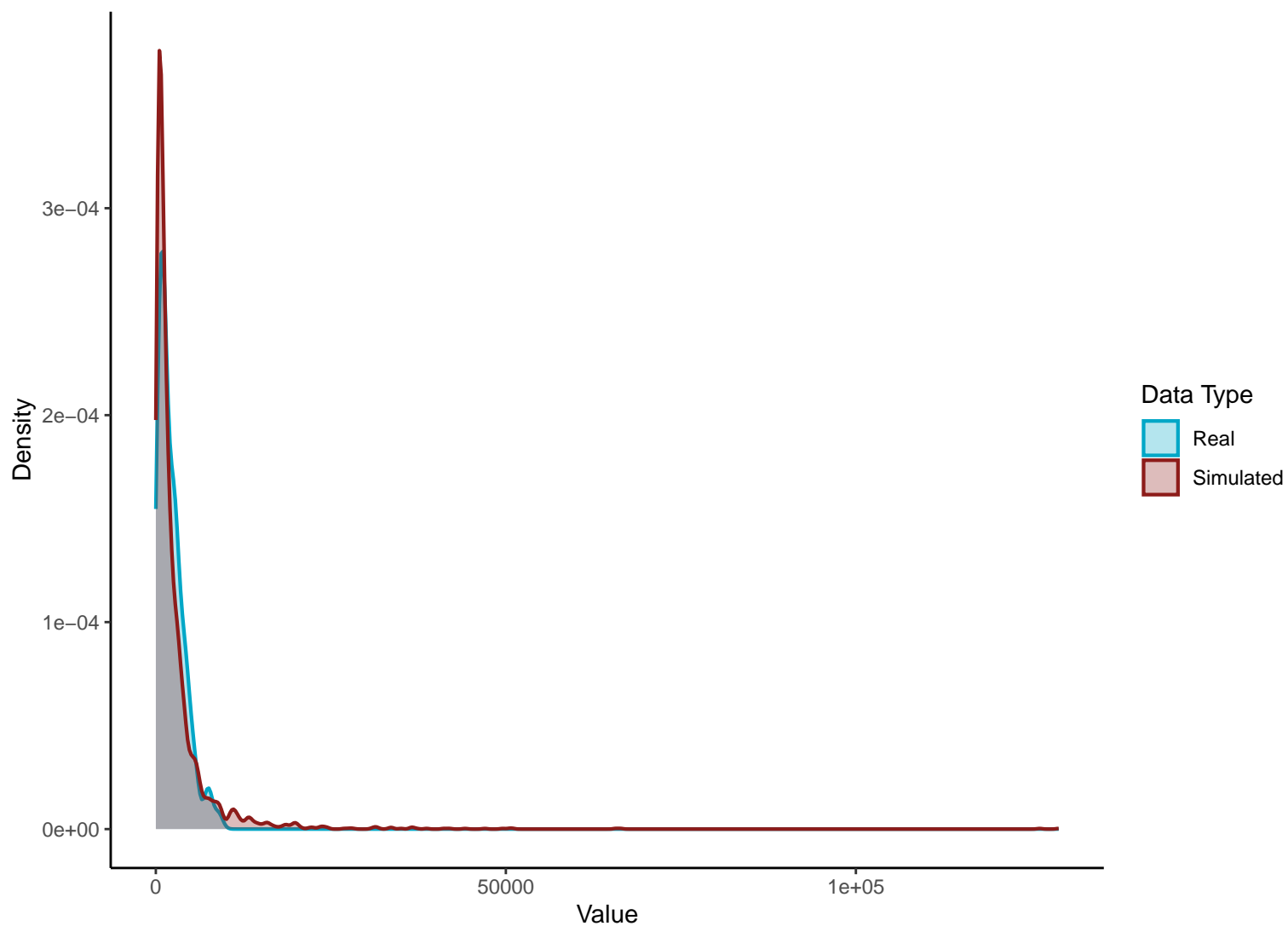
Slackia



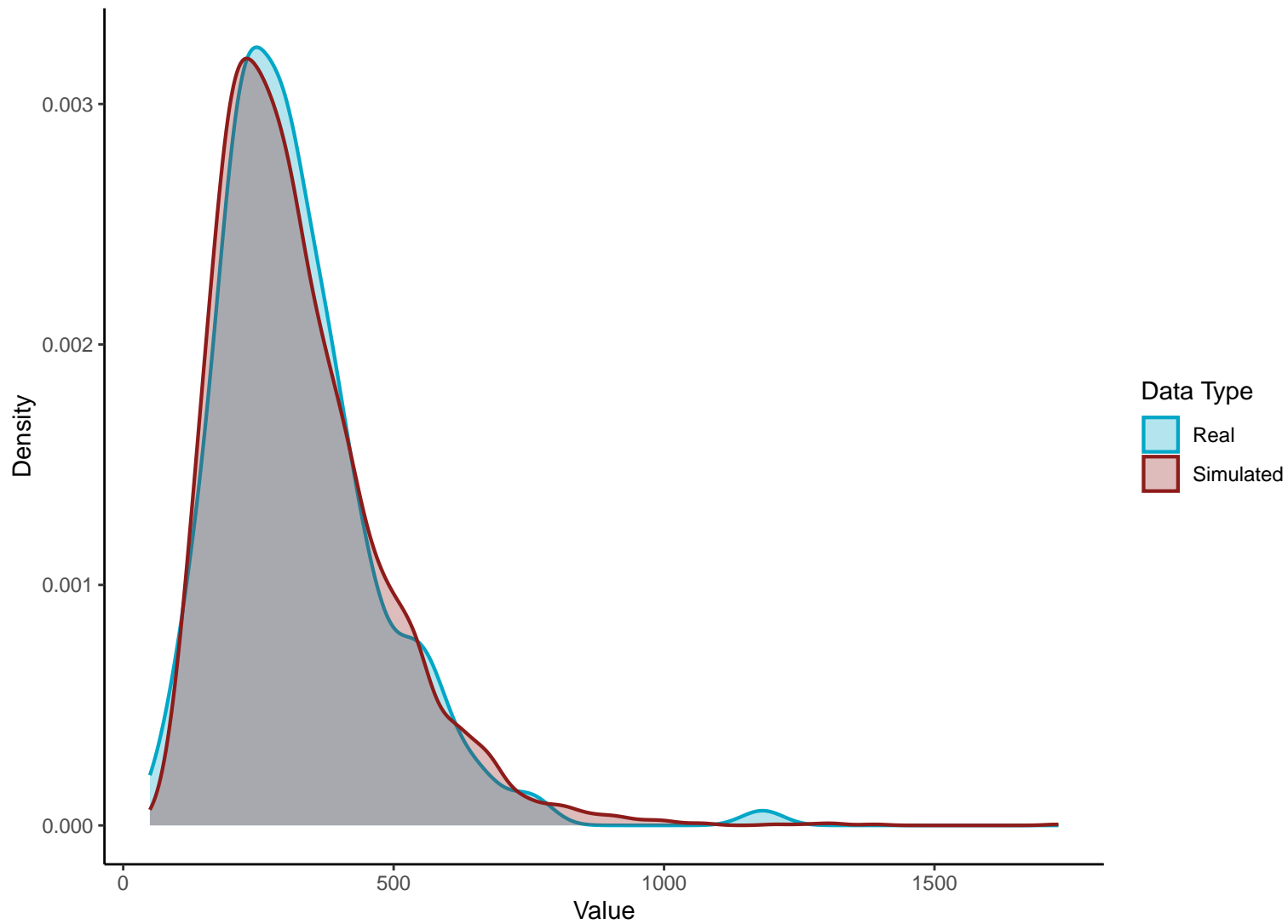
UCG.007



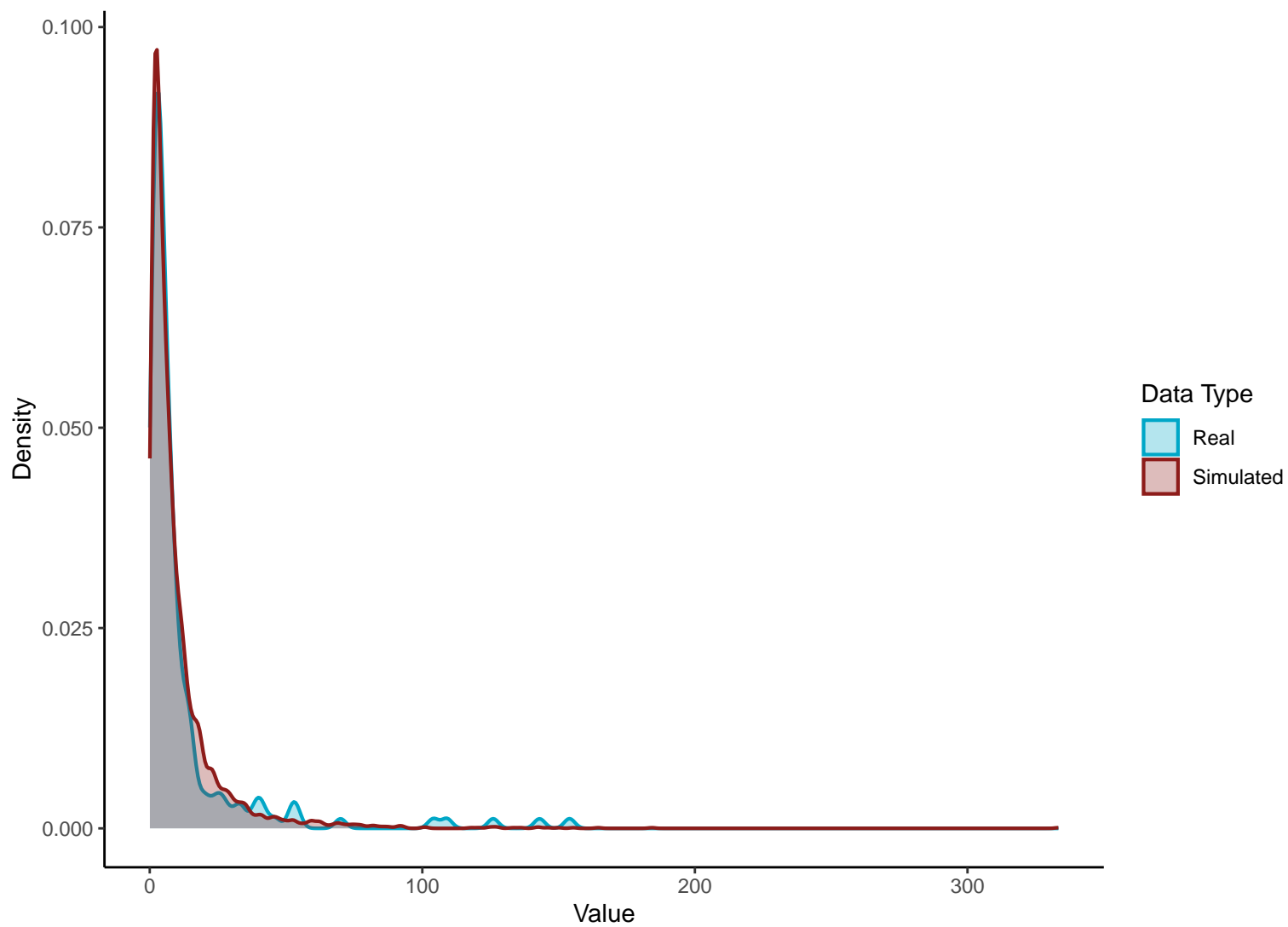
Terrisporobacter



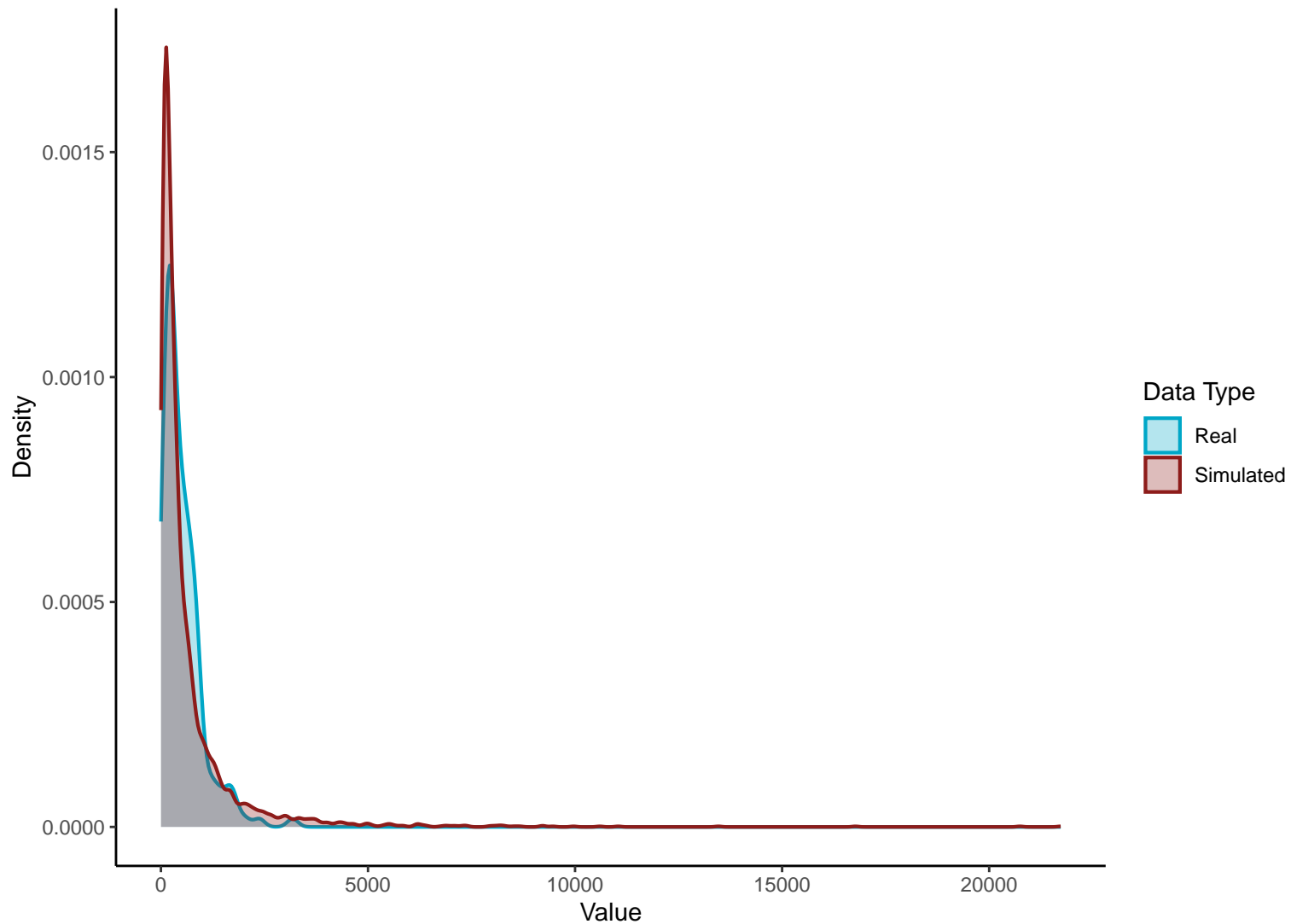
X.Eubacterium..hallii.group



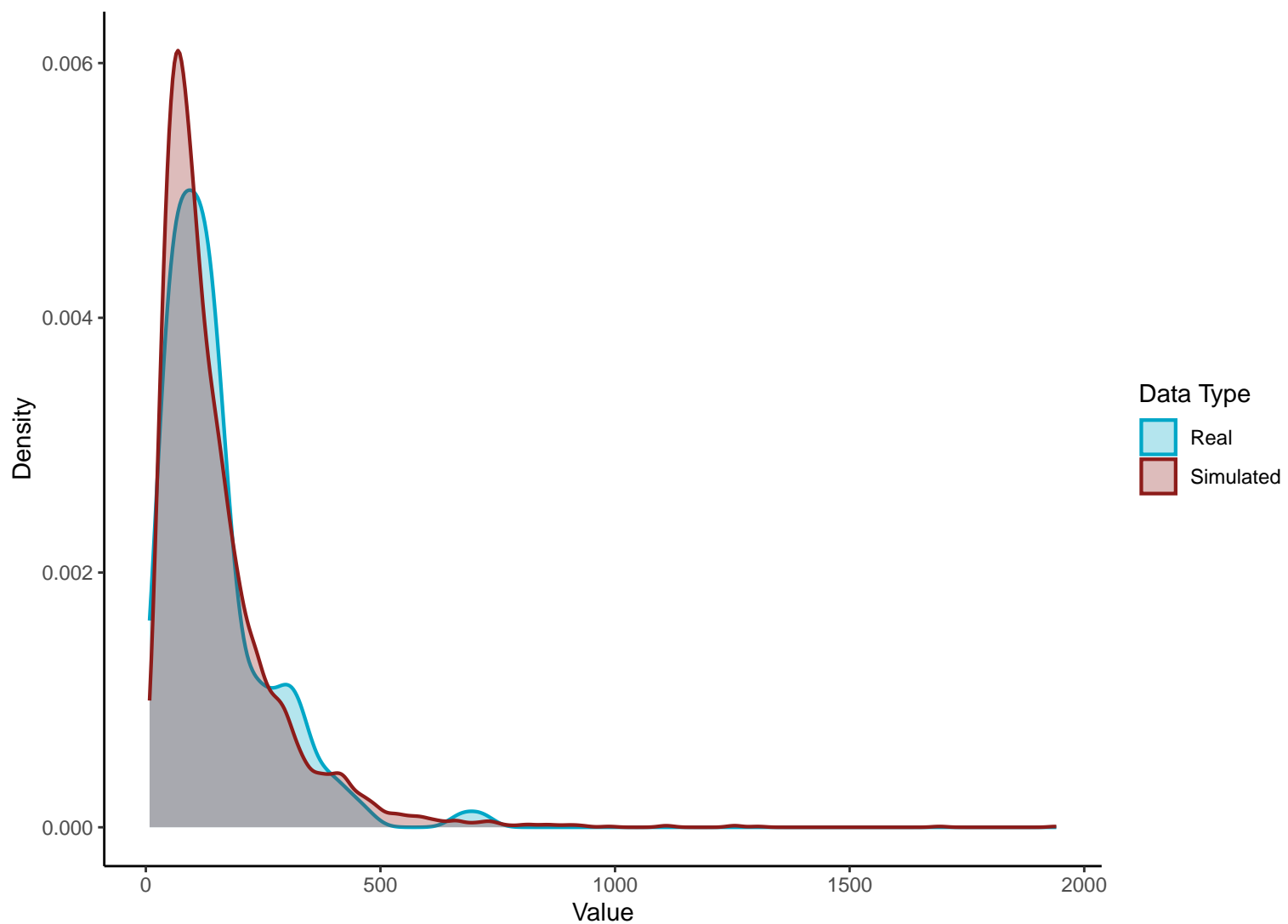
UCG.004



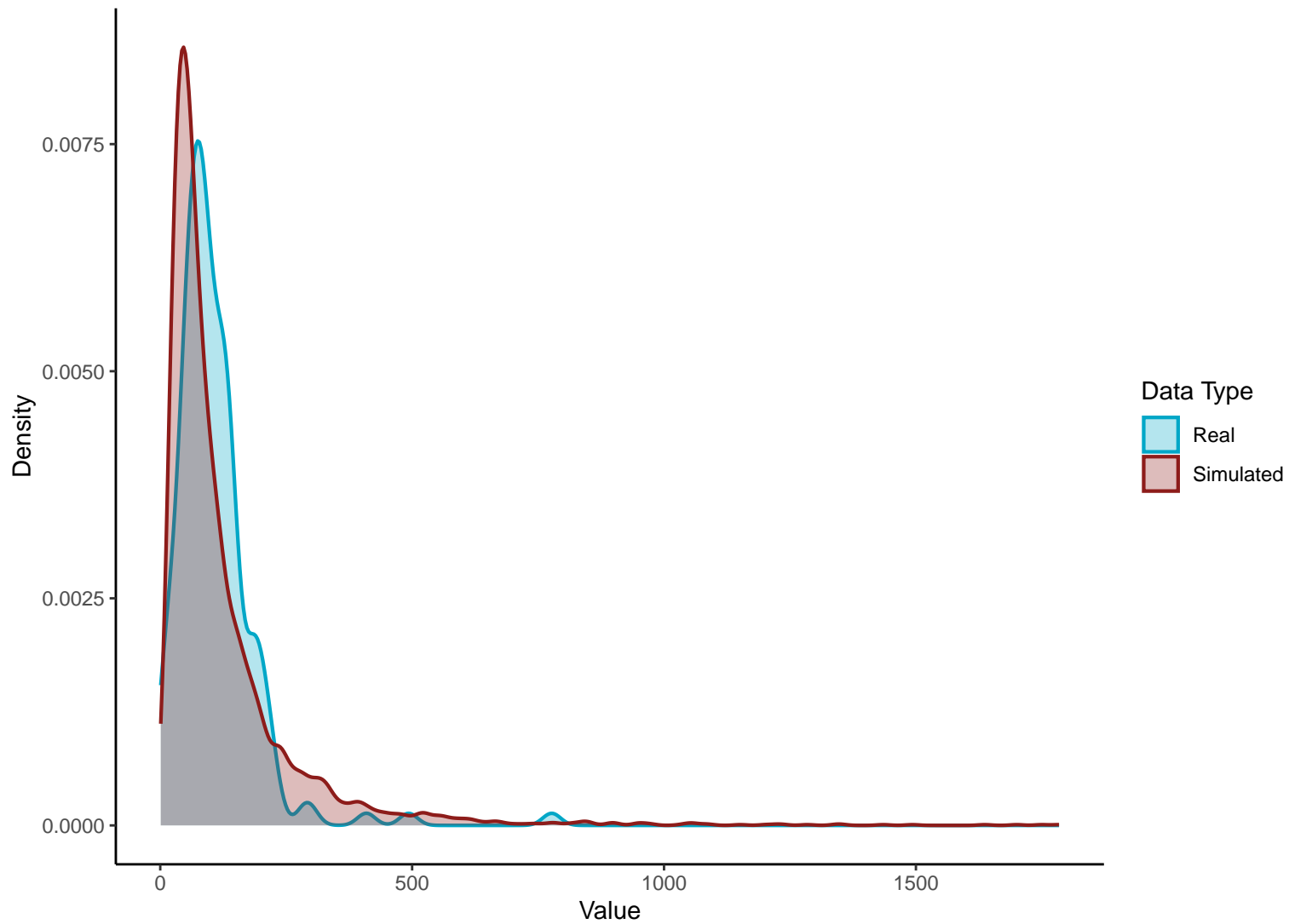
NK4A214.group



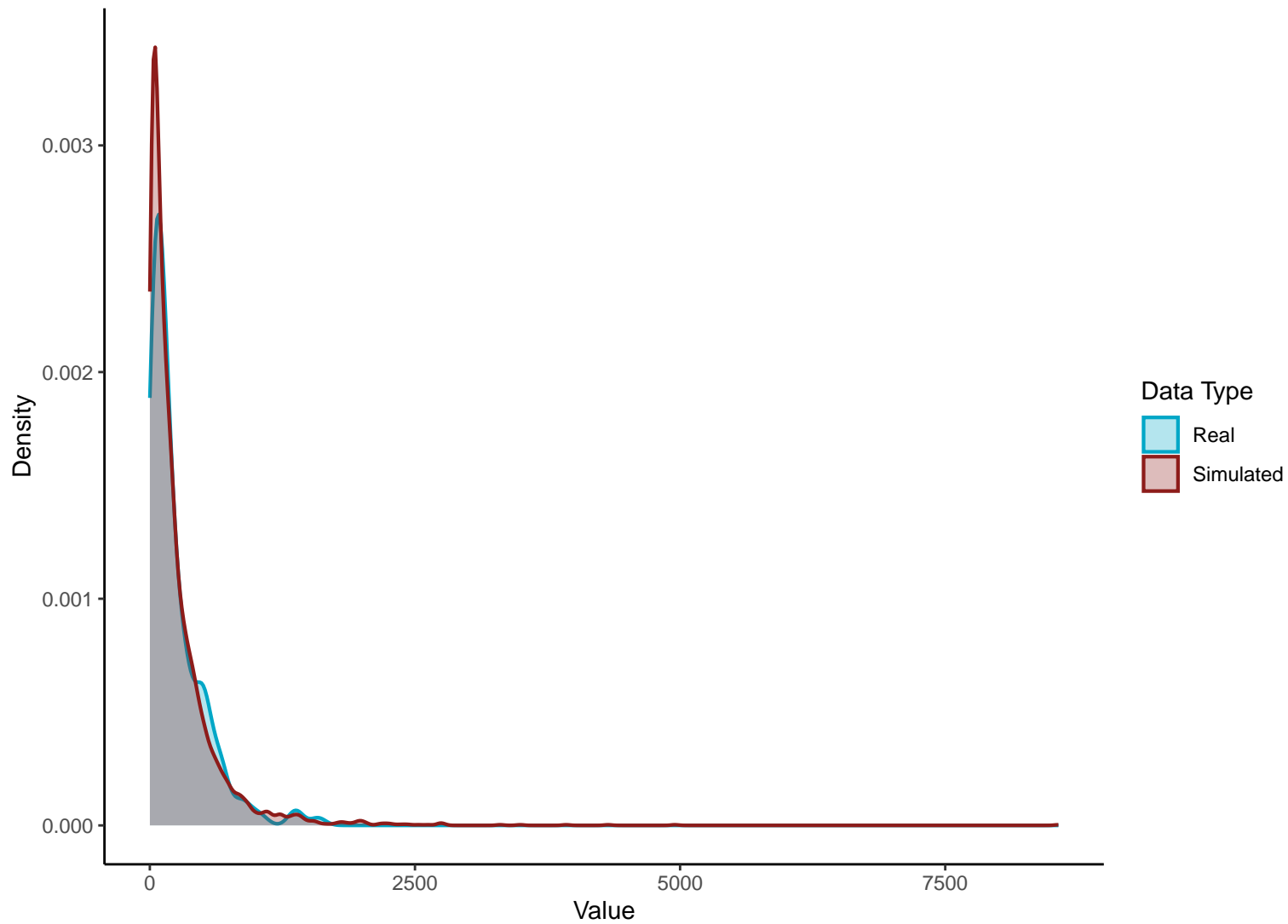
Lachnospiraceae.NK4A136.group



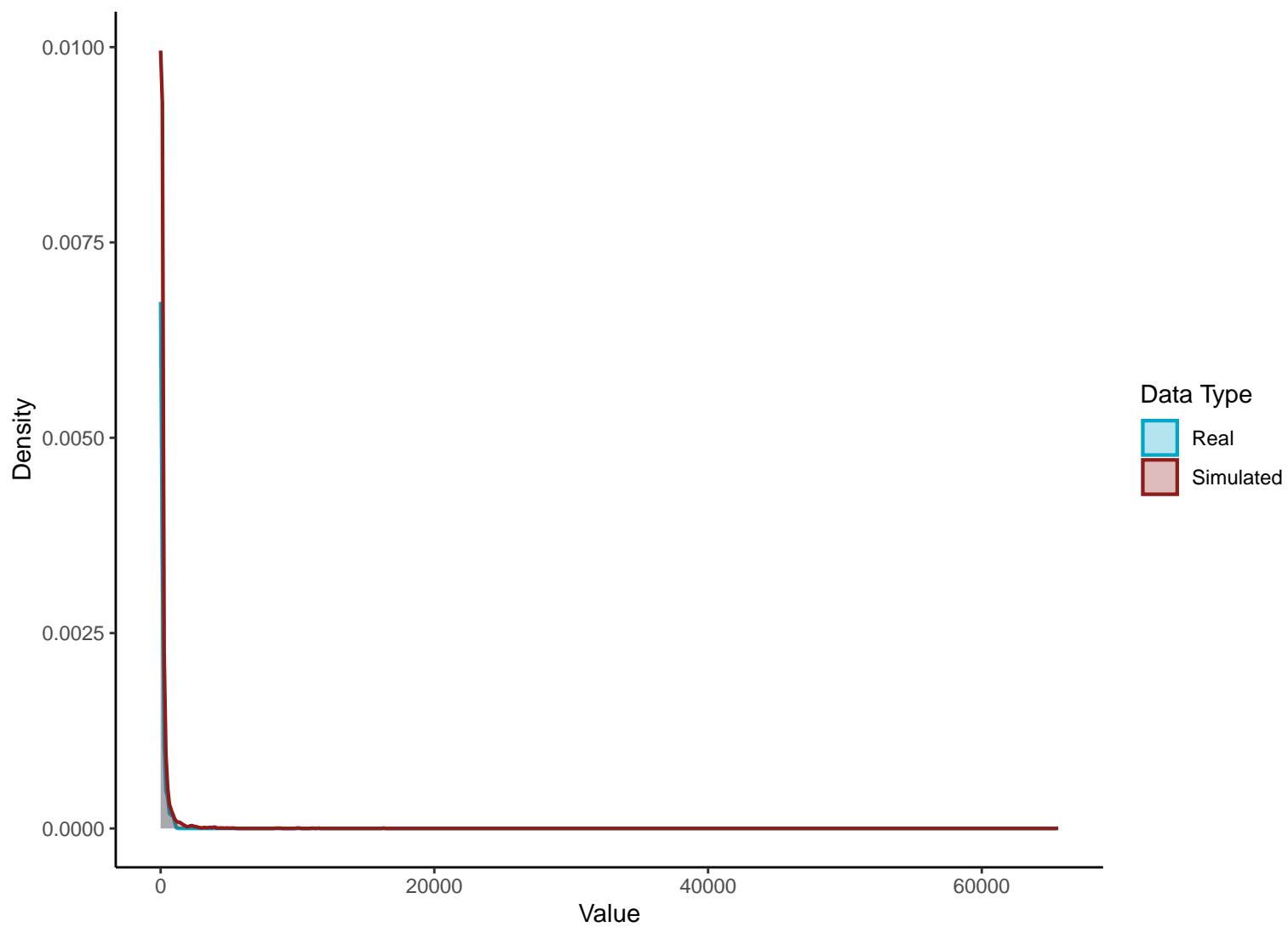
Monoglobus



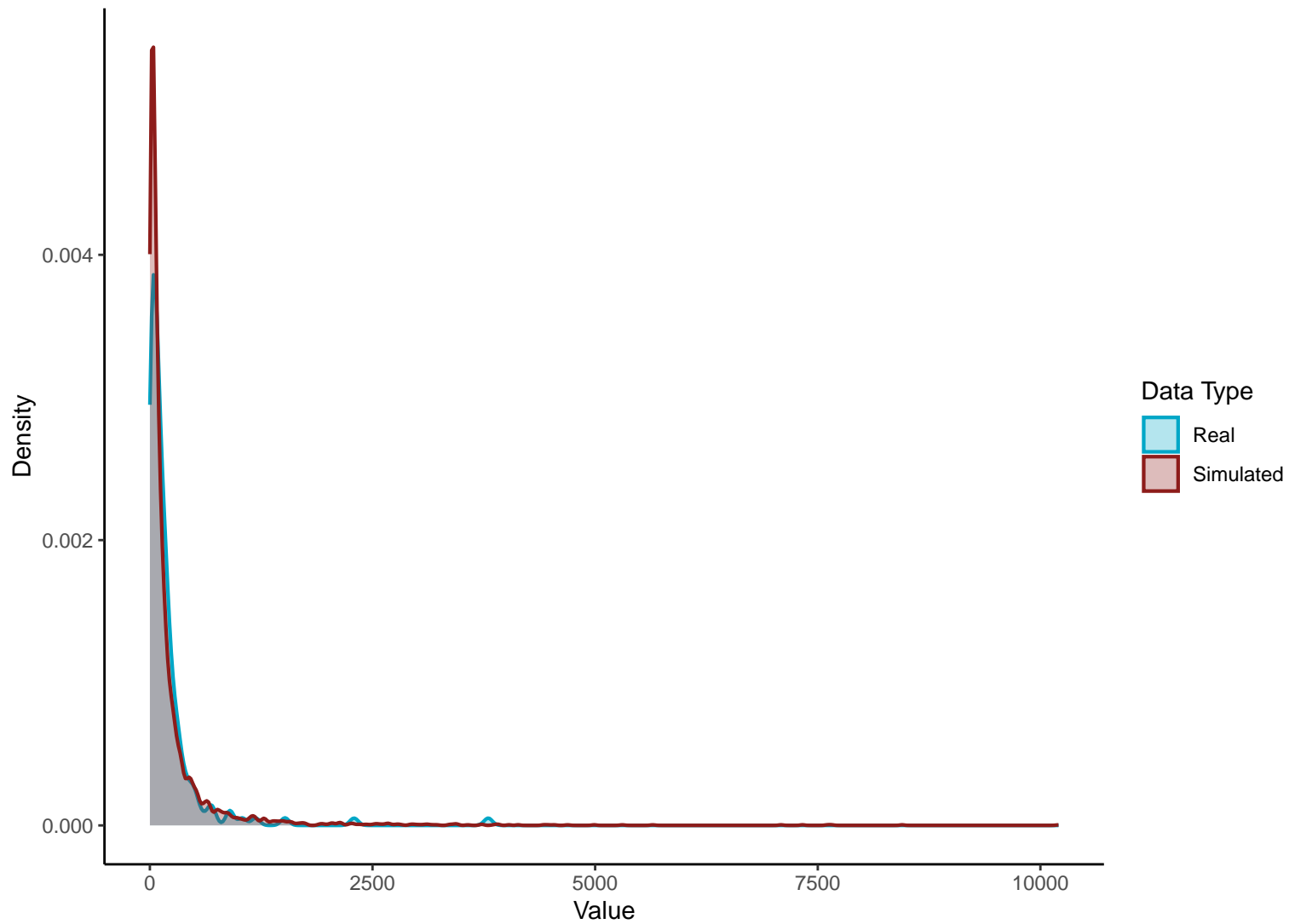
Prevotella



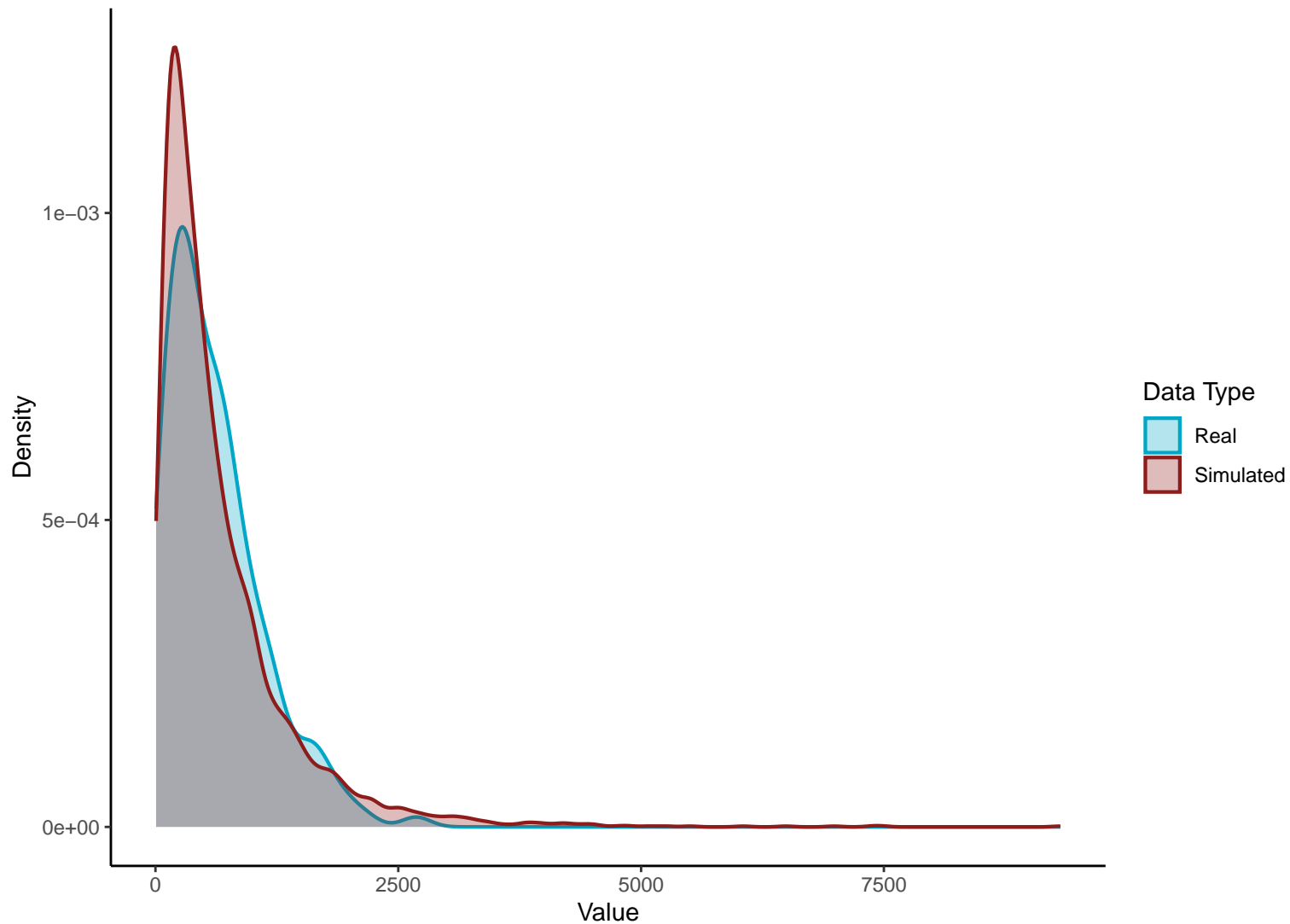
Treponema



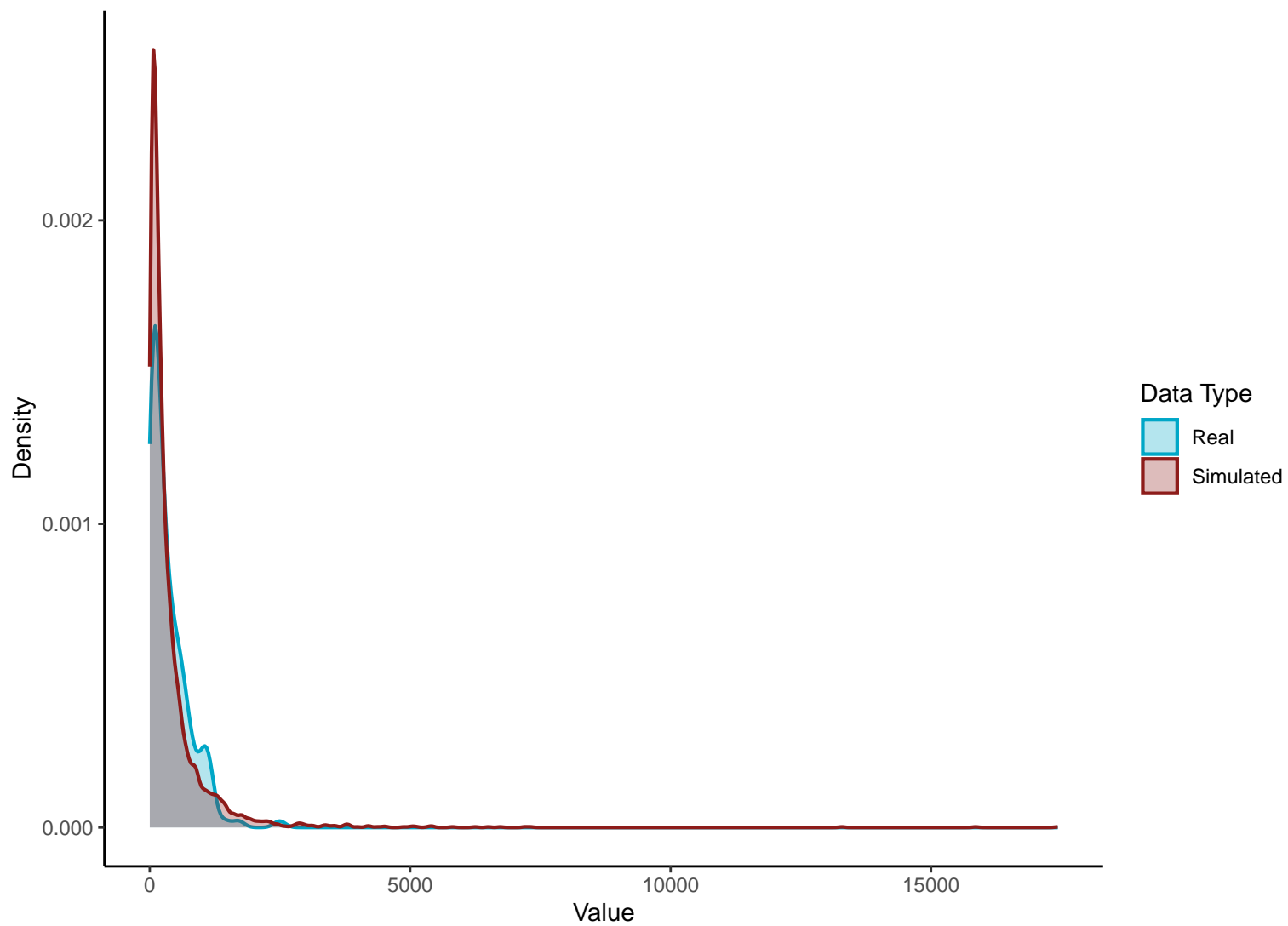
Rikenellaceae.RC9.gut.group



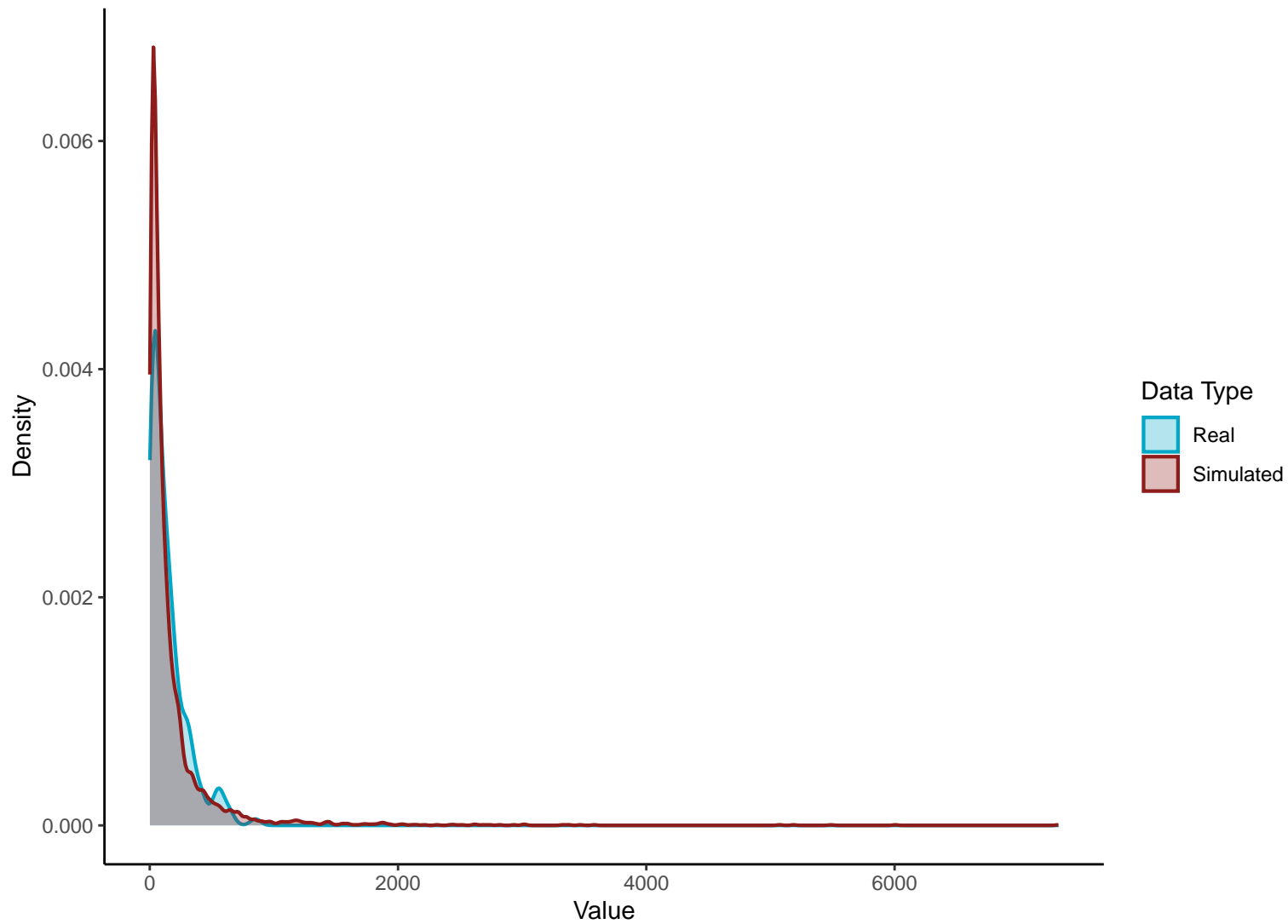
Faecalibacterium



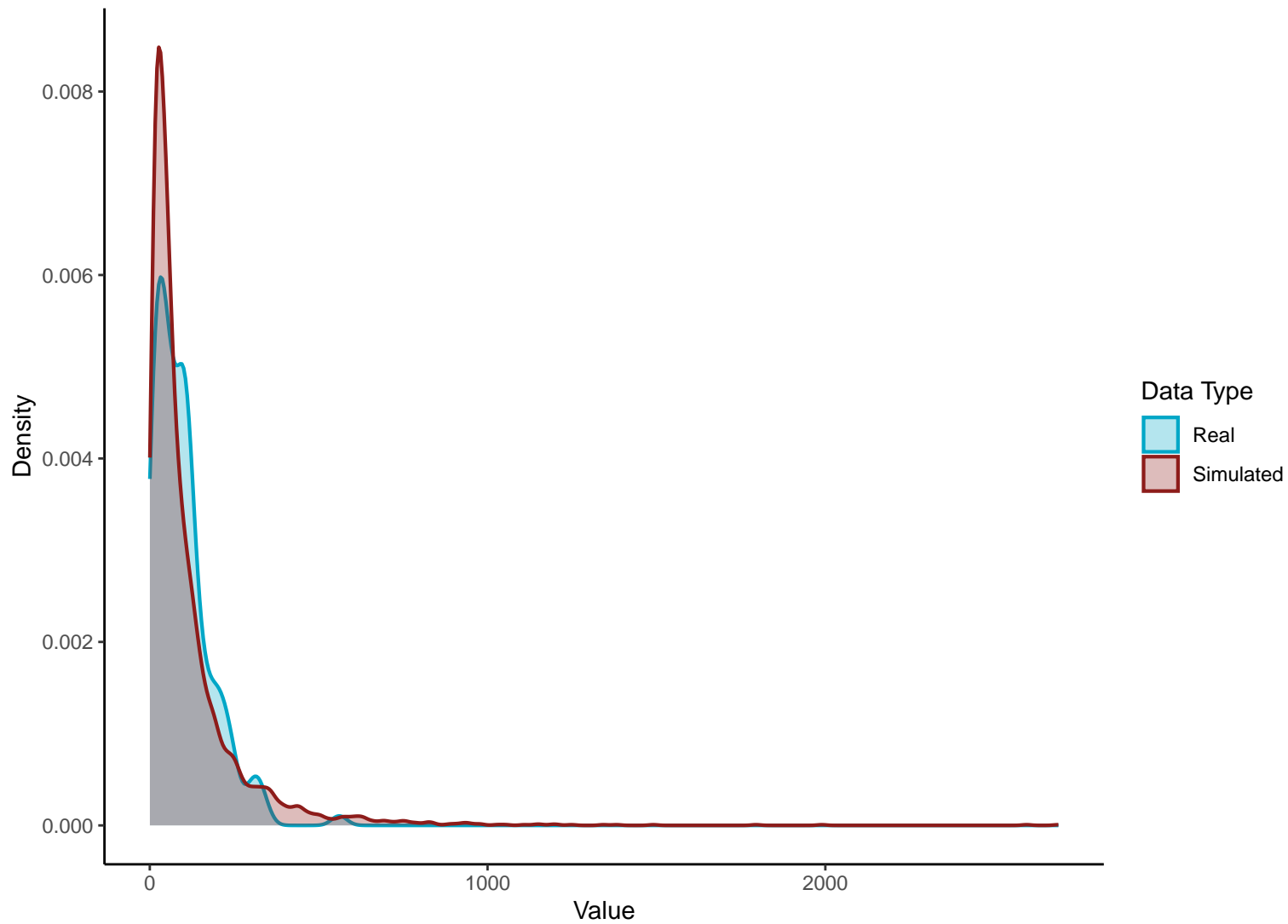
Anaerovibrio



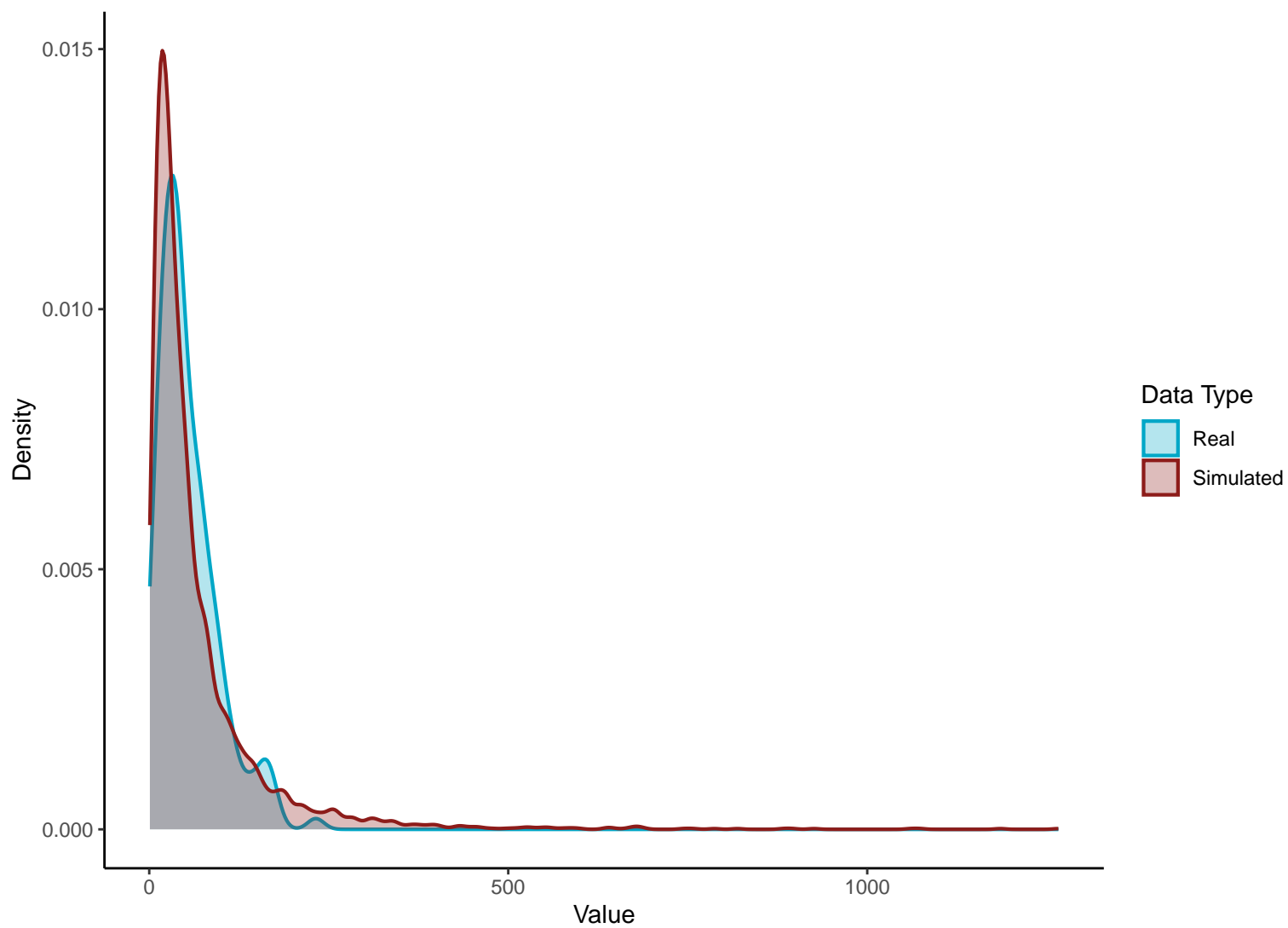
X.Eubacterium..xylanophilum.group



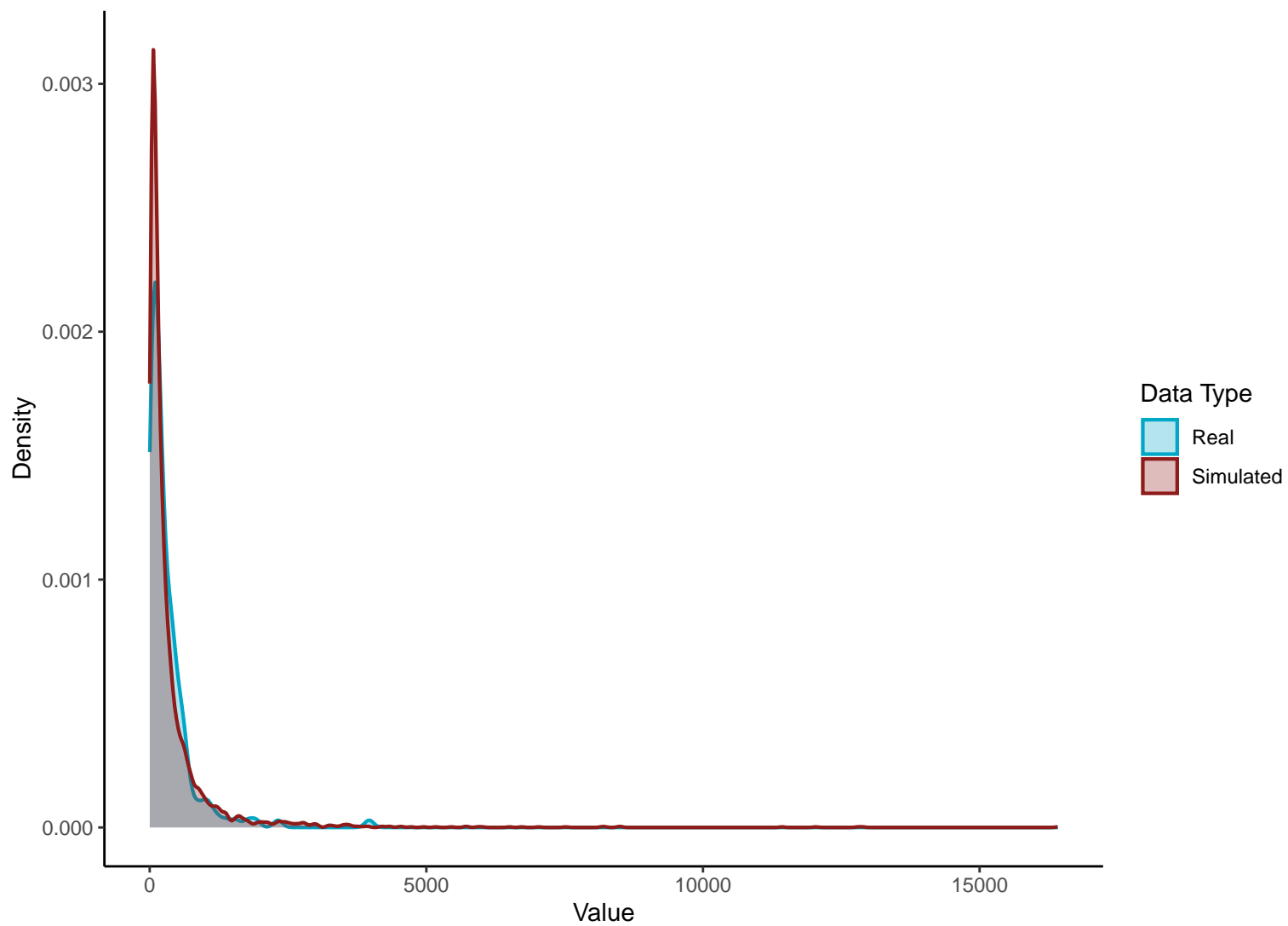
X.Ruminococcus..torques.group



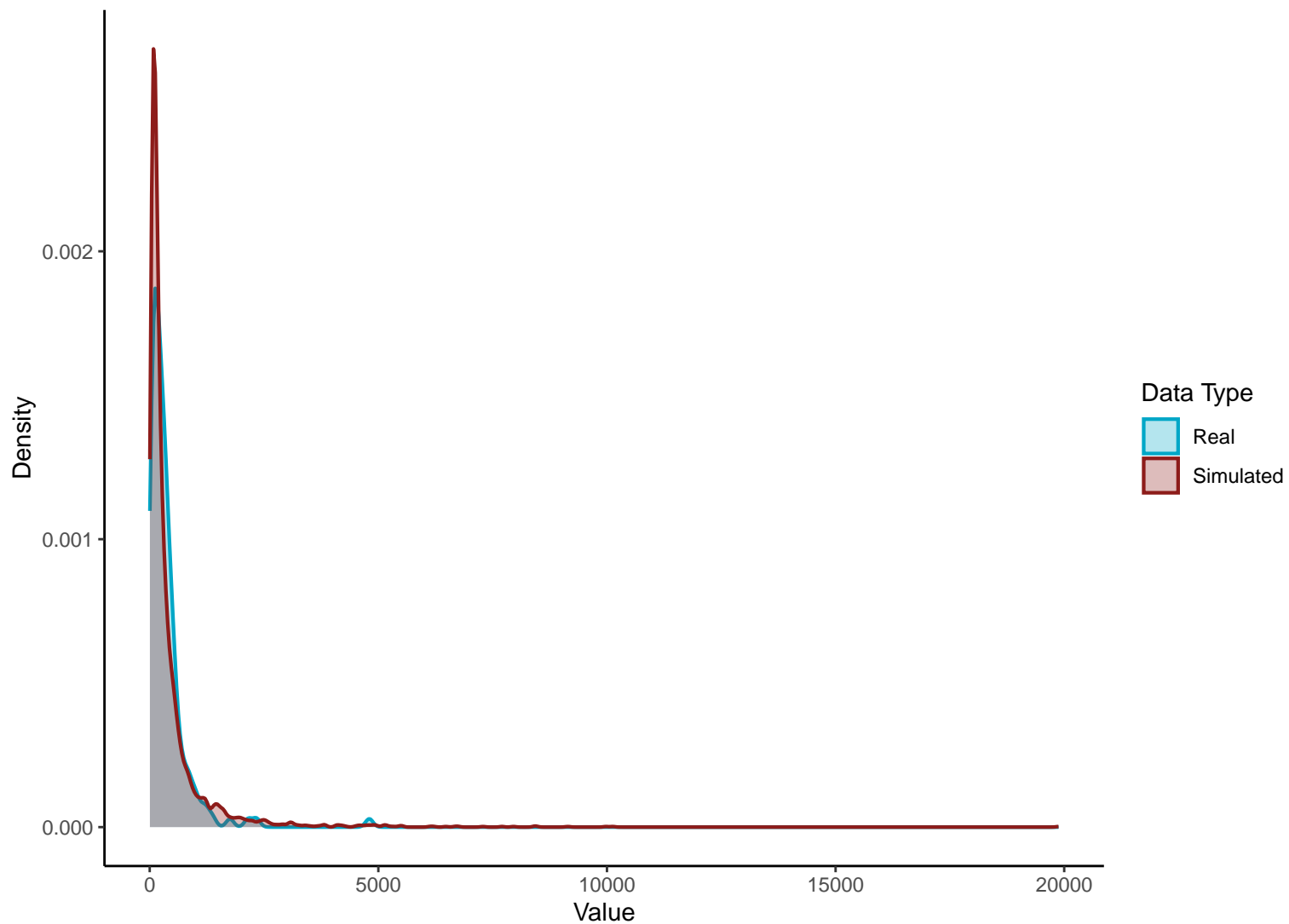
X.Eubacterium..siraeum.group



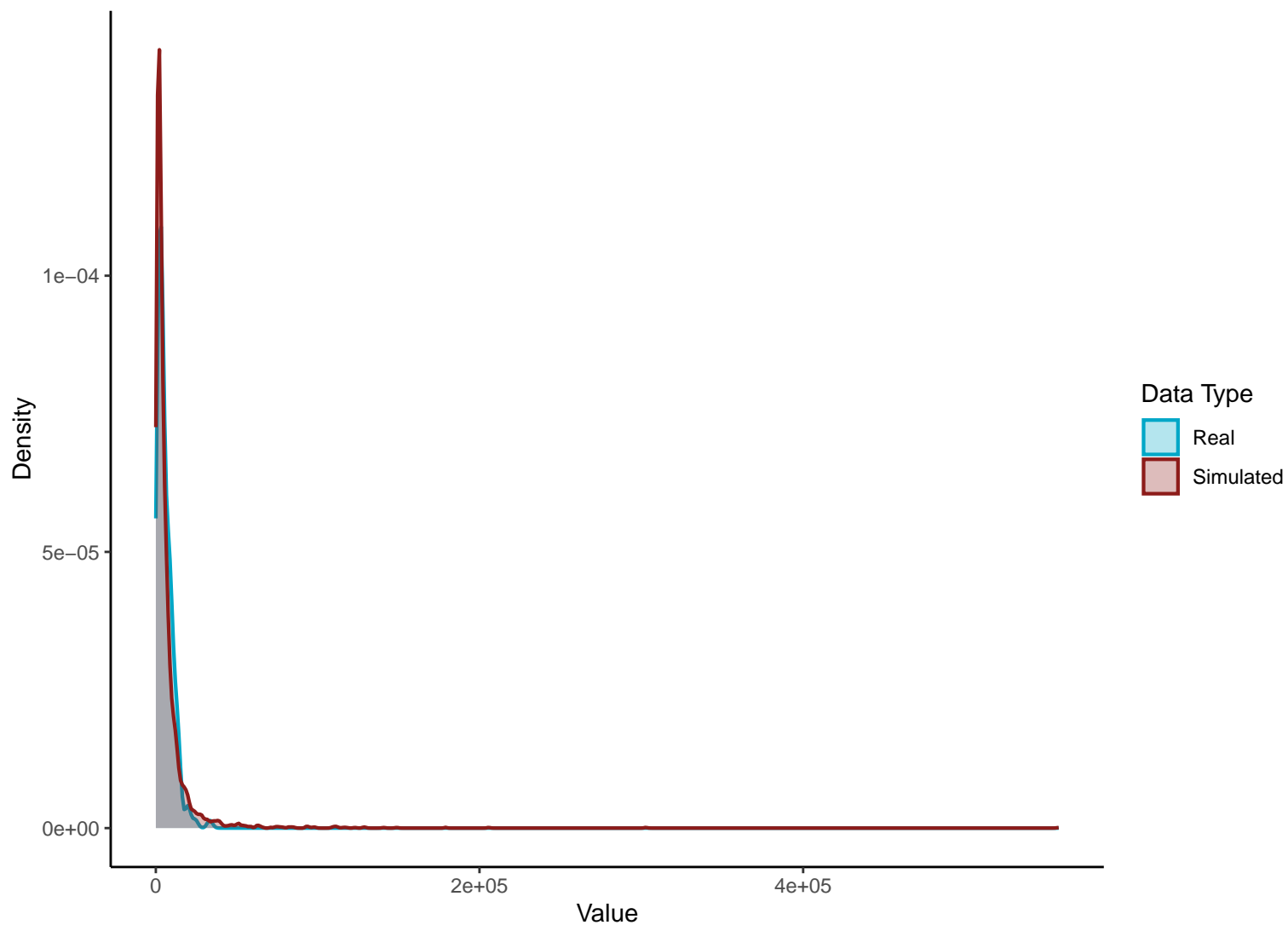
Alloprevotella



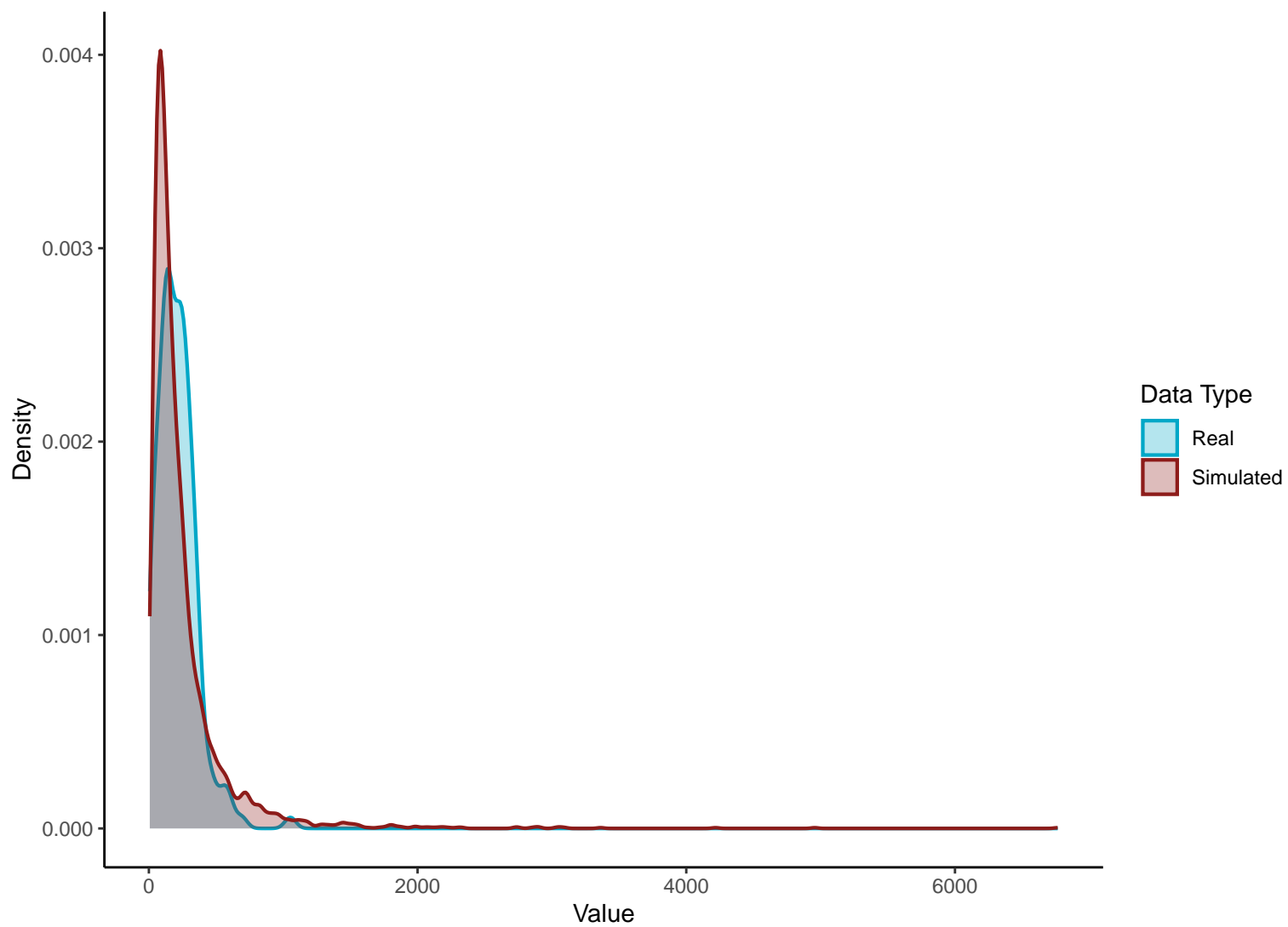
Catenibacterium



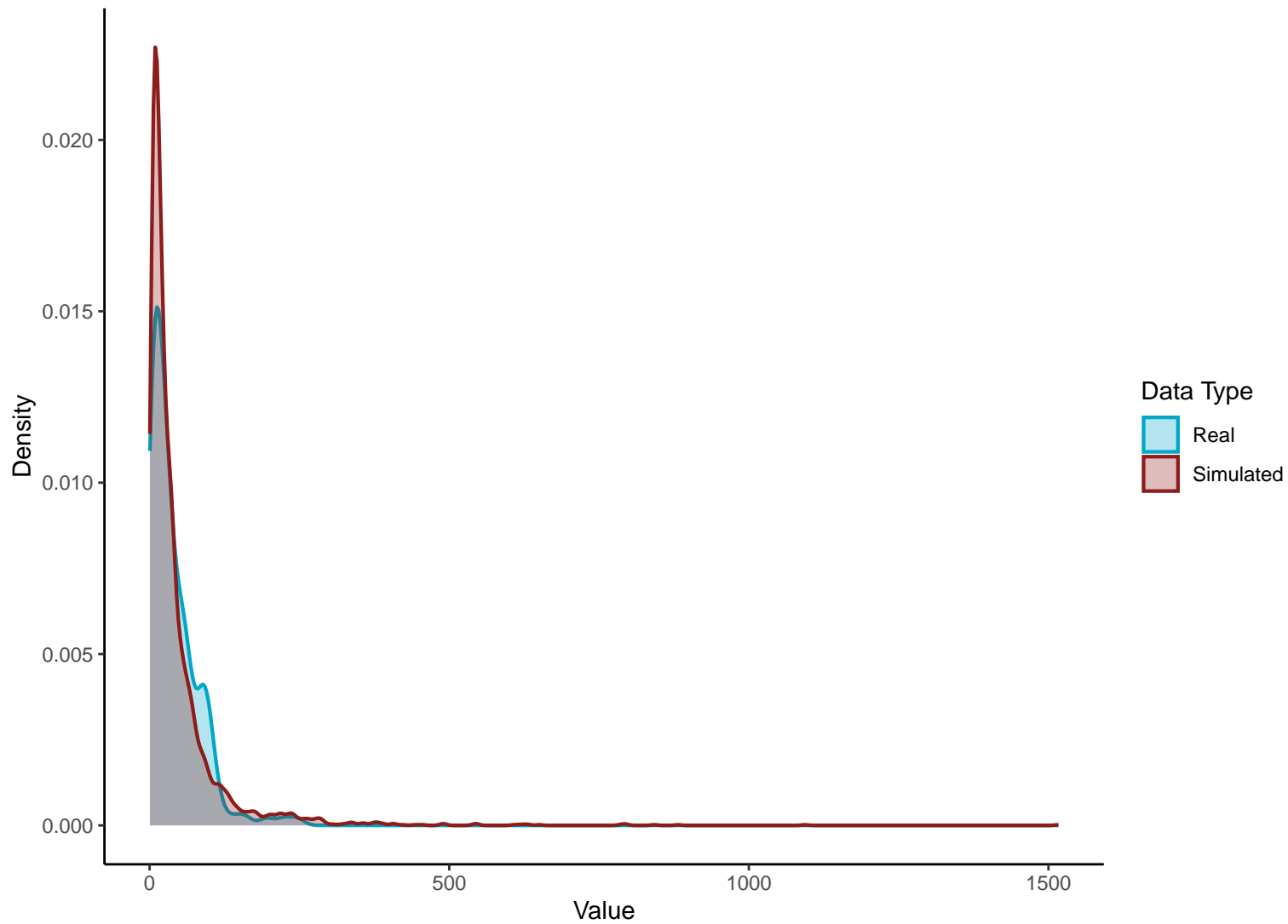
Clostridium.sensu.stricto.1



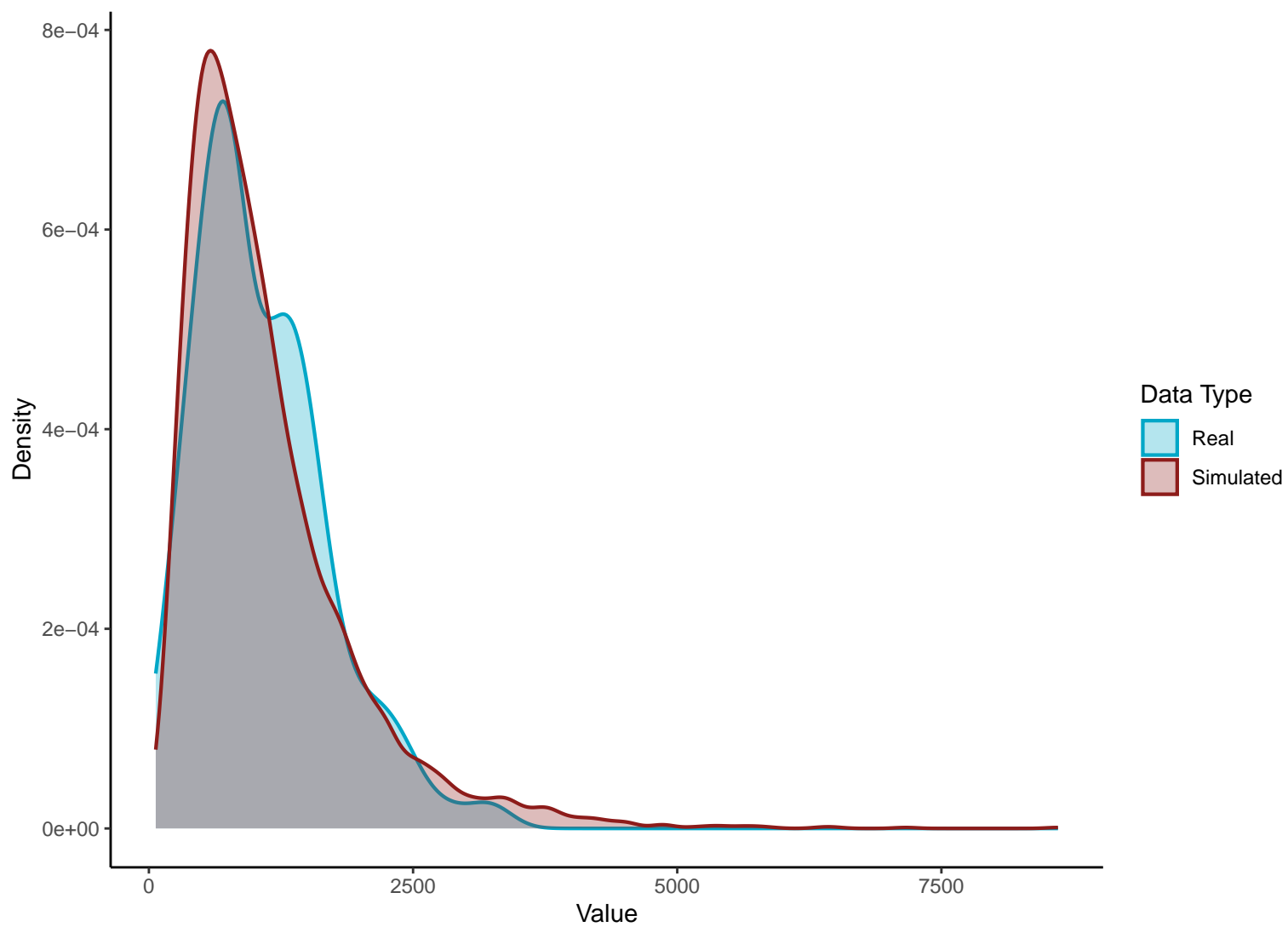
Butyricicoccus



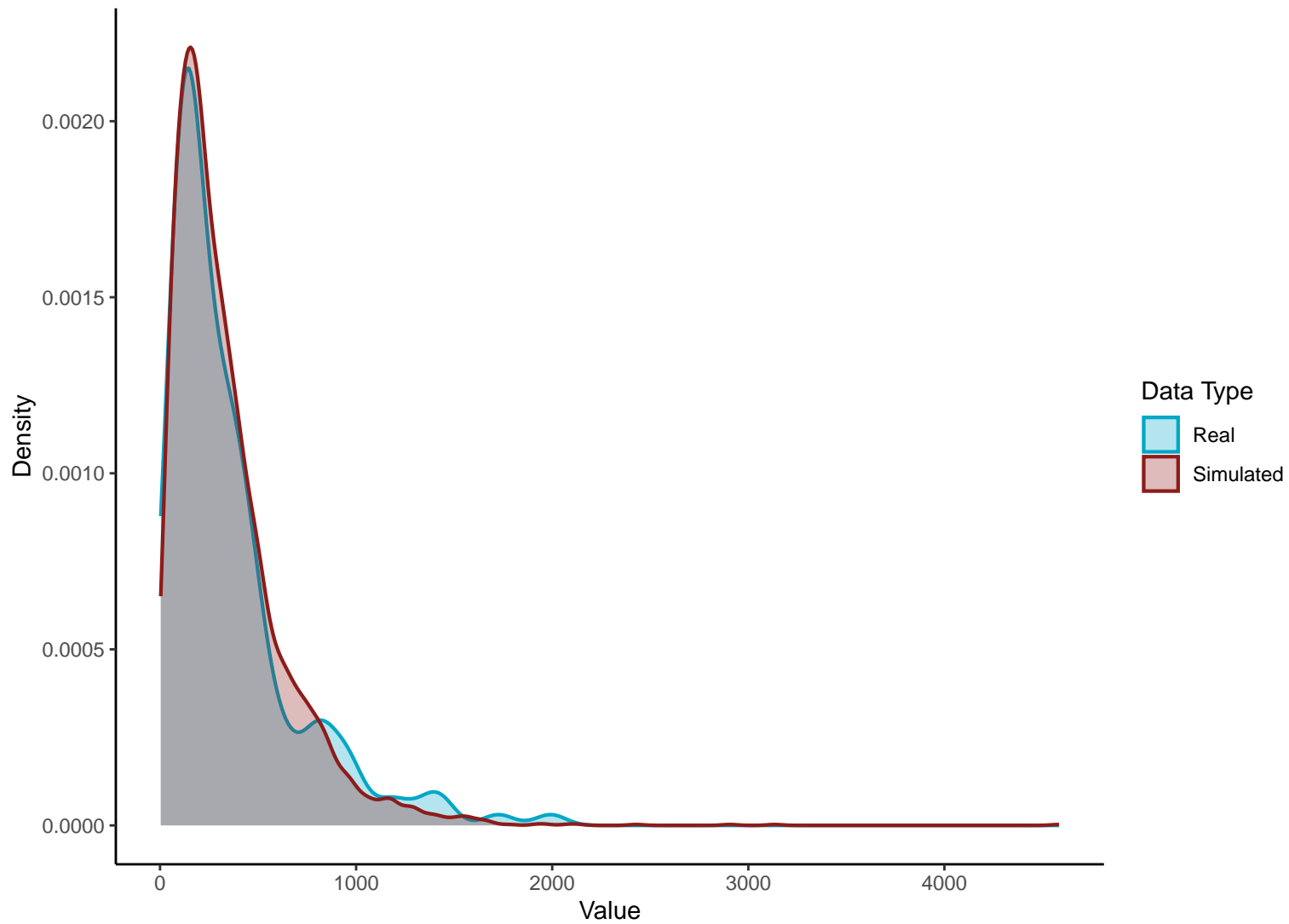
Intestinimonas



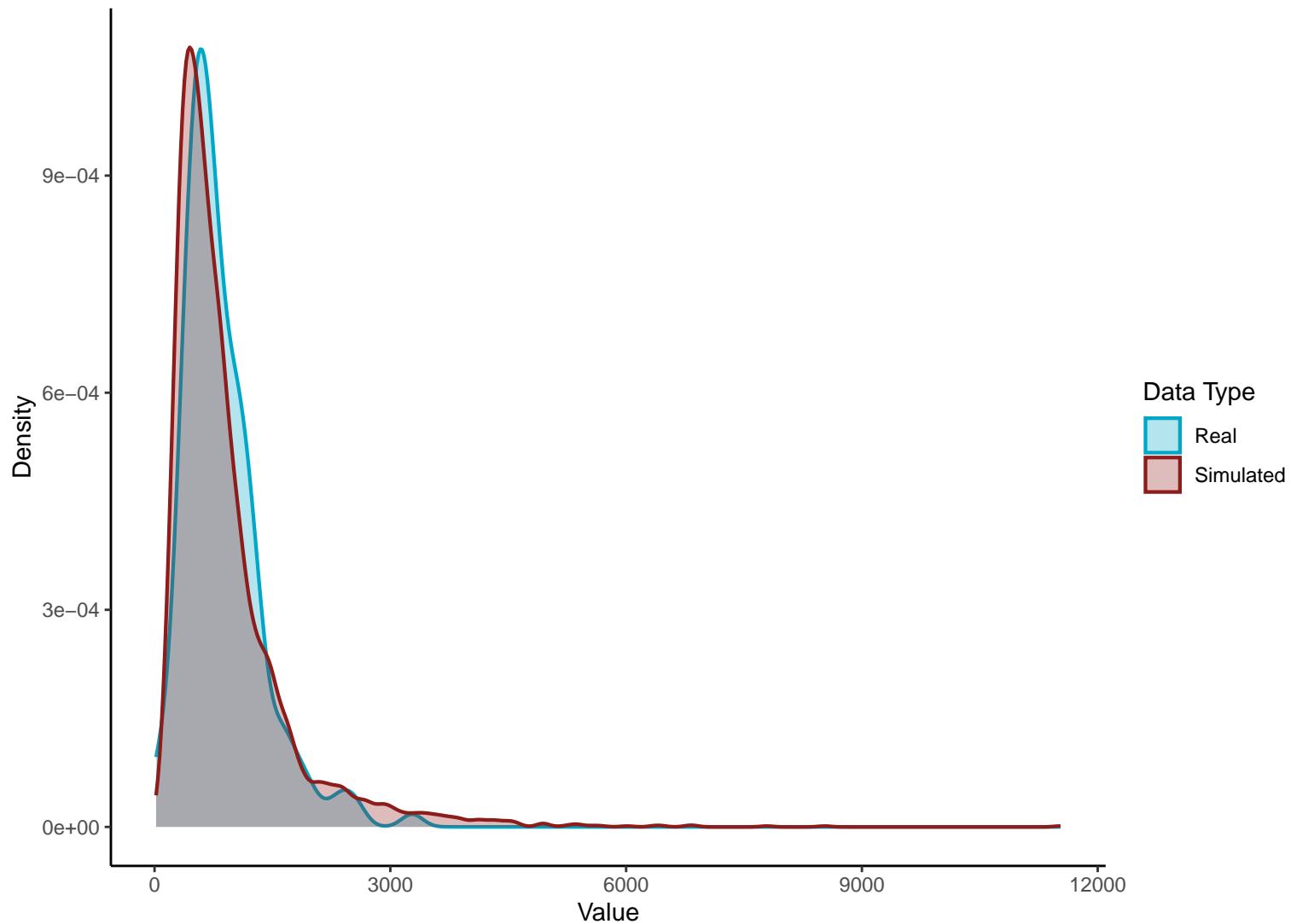
Subdoligranulum



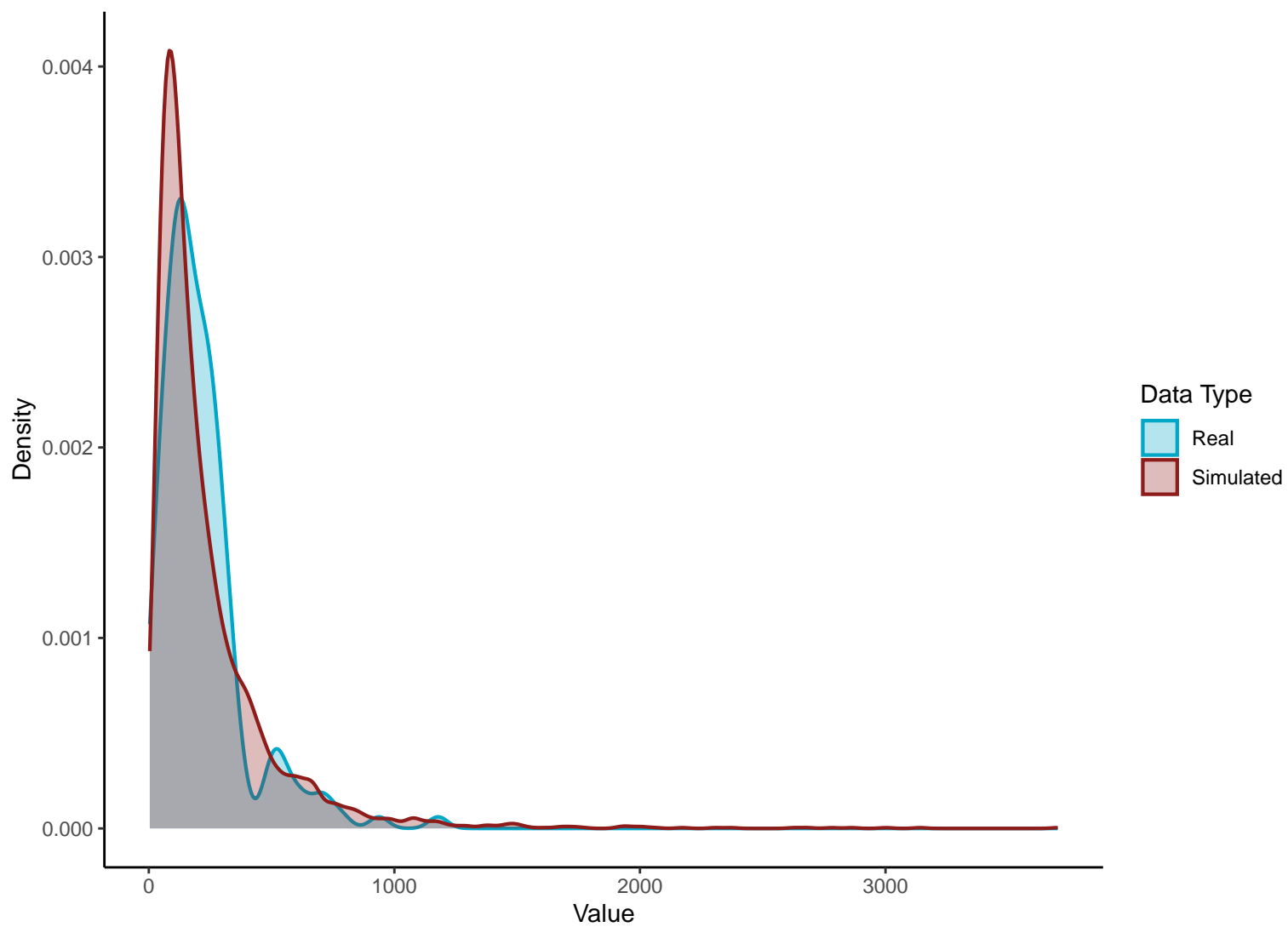
Roseburia



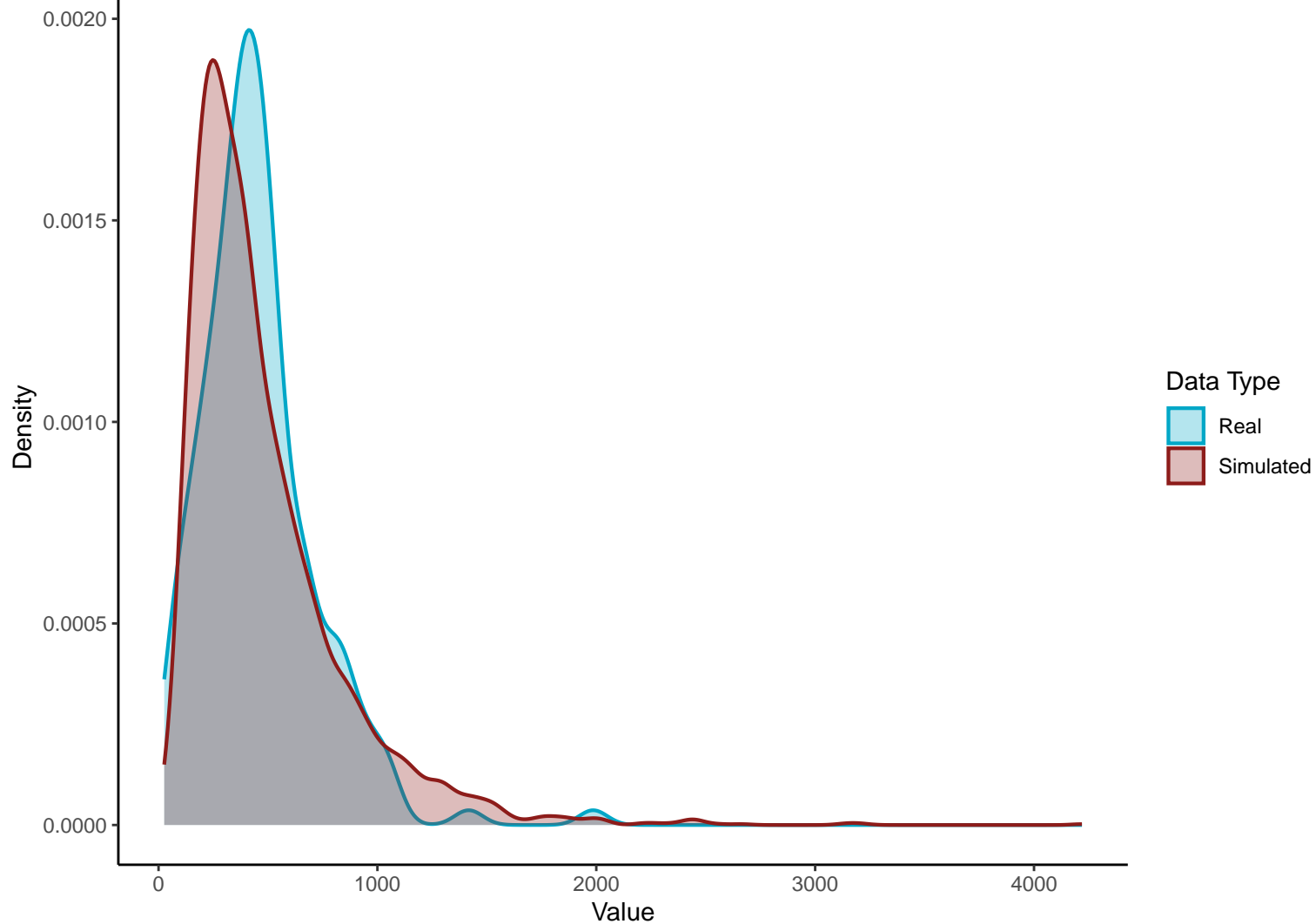
Ruminococcus



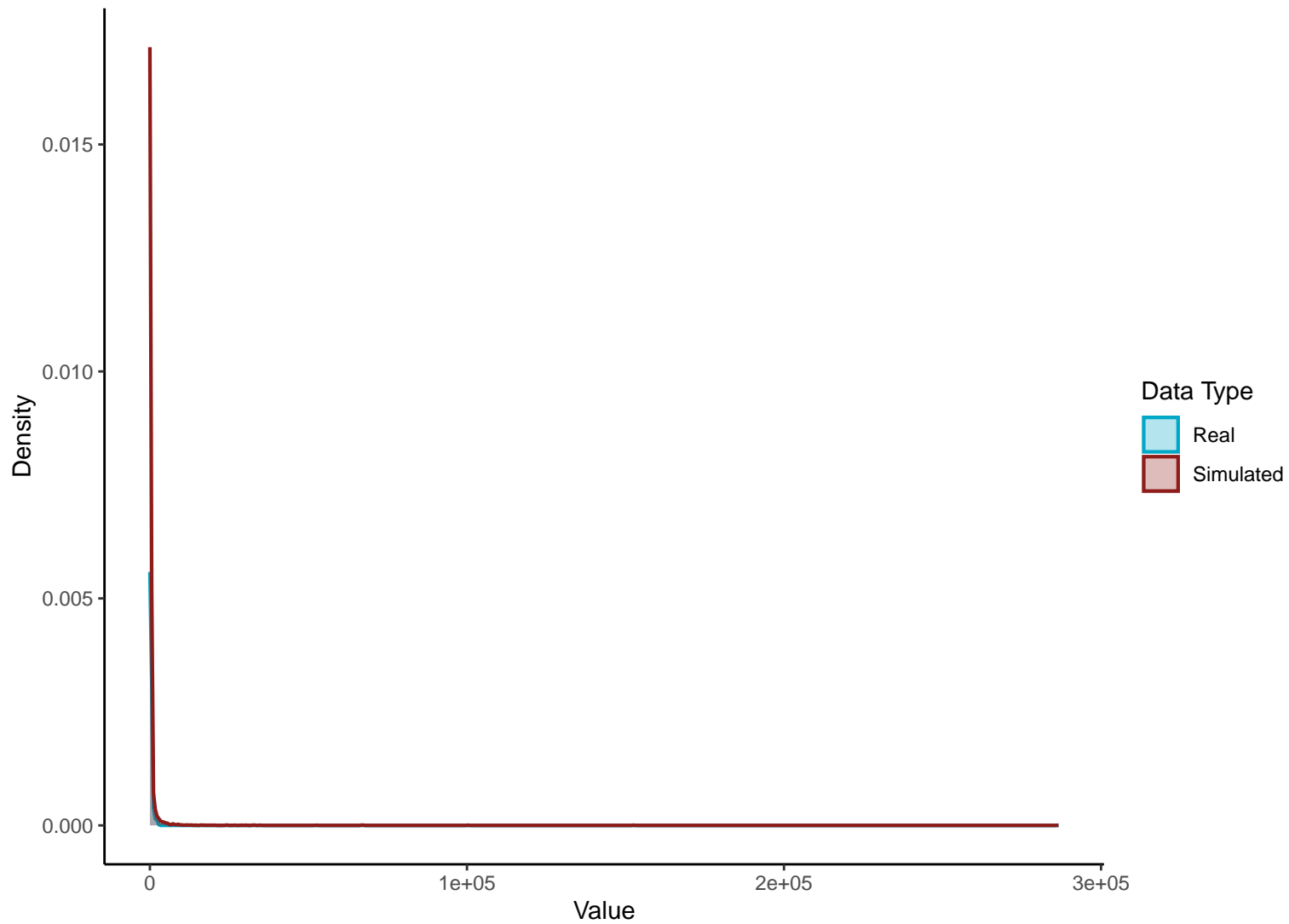
Family.XIII.AD3011.group



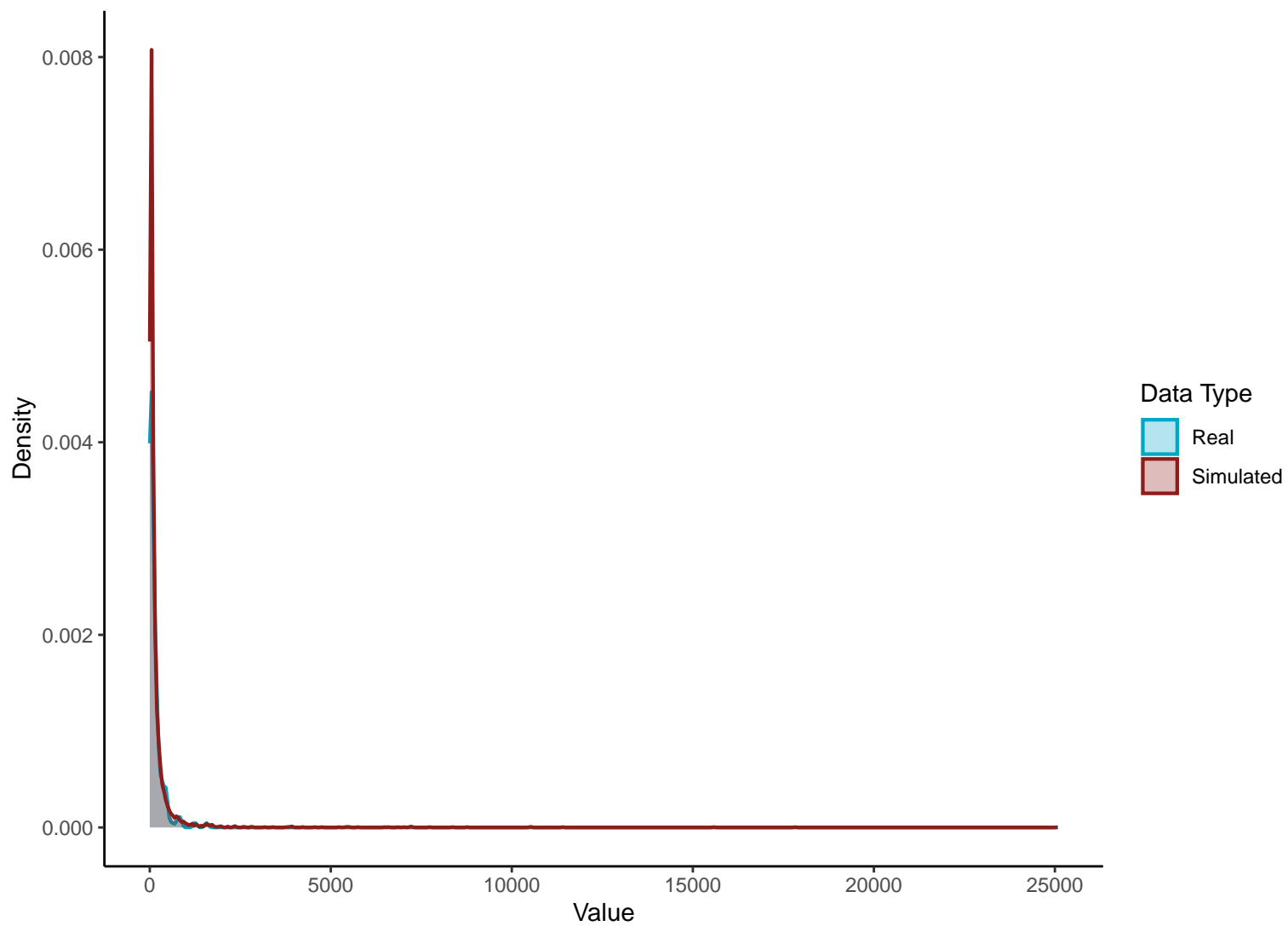
Solobacterium



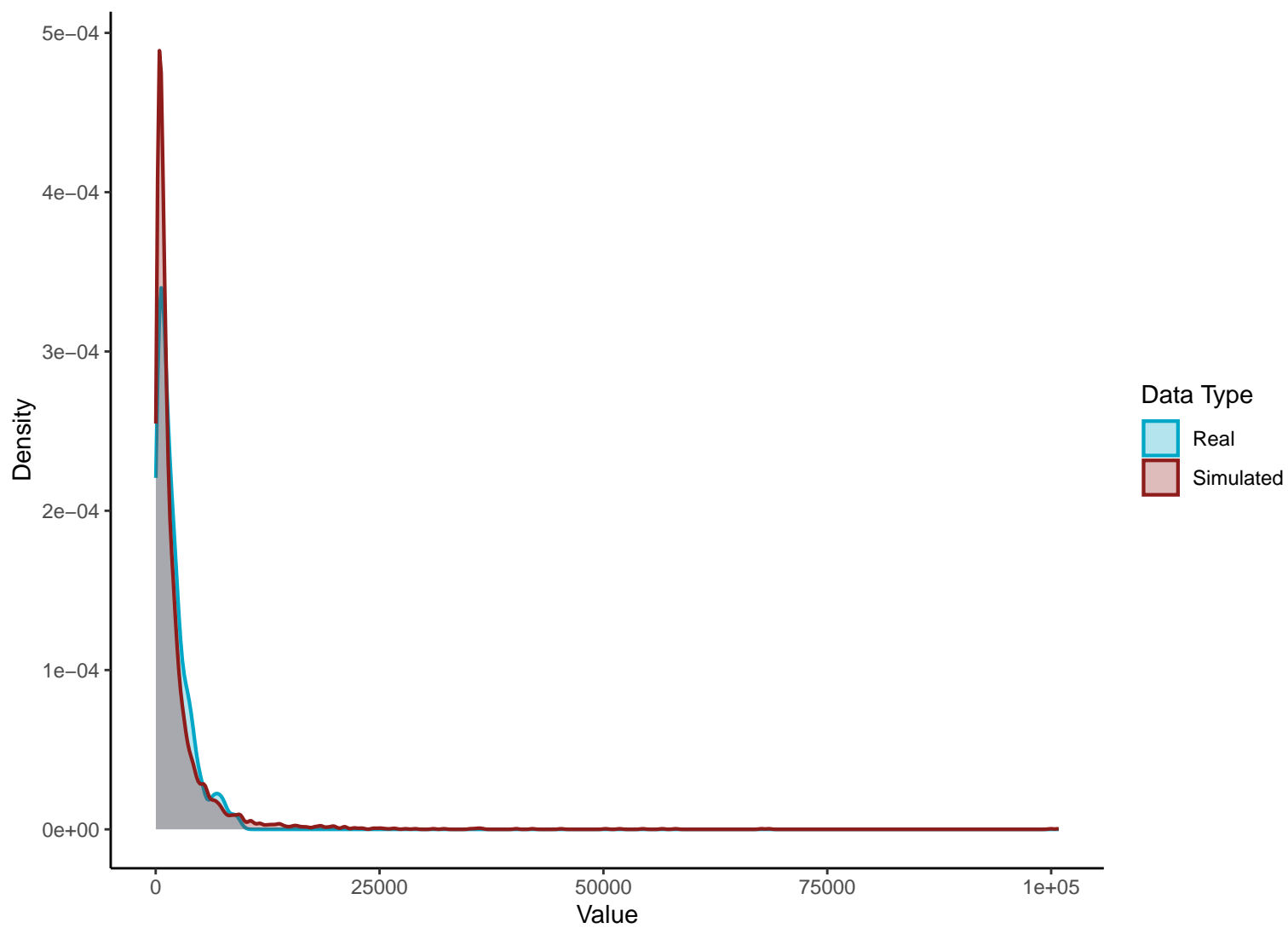
Lachnospiraceae.XPB1014.group



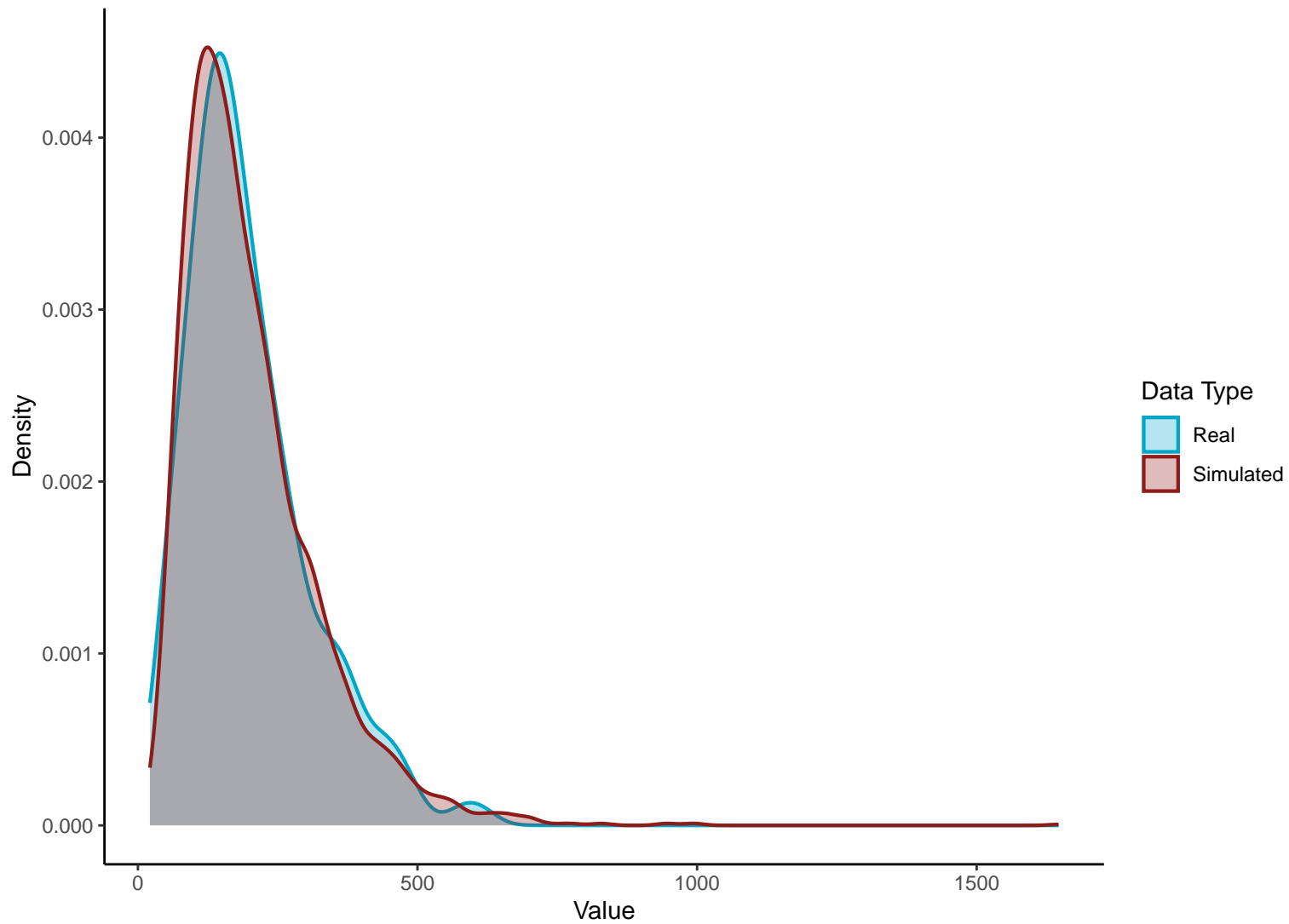
Prevotella_7



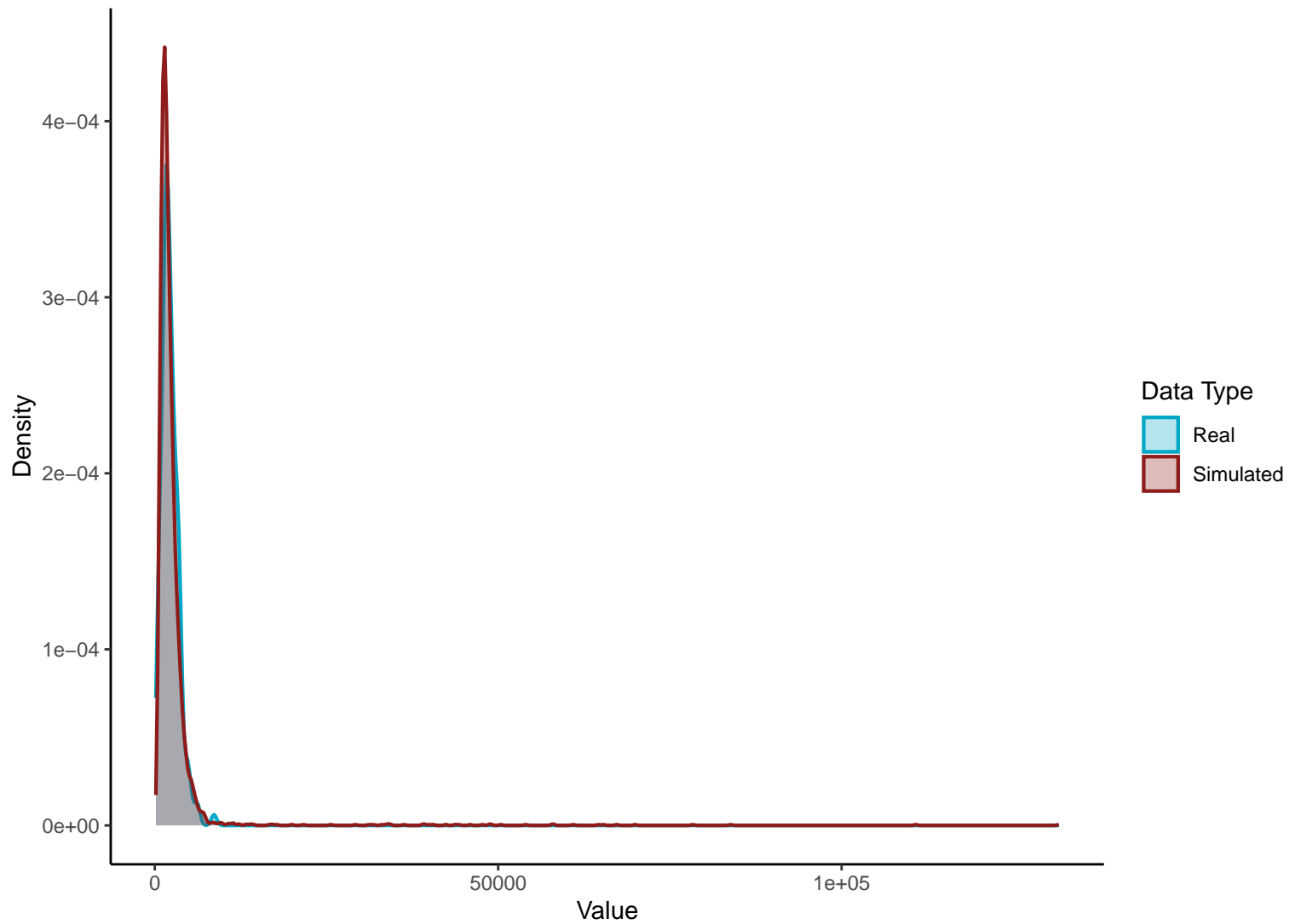
Prevotella_9



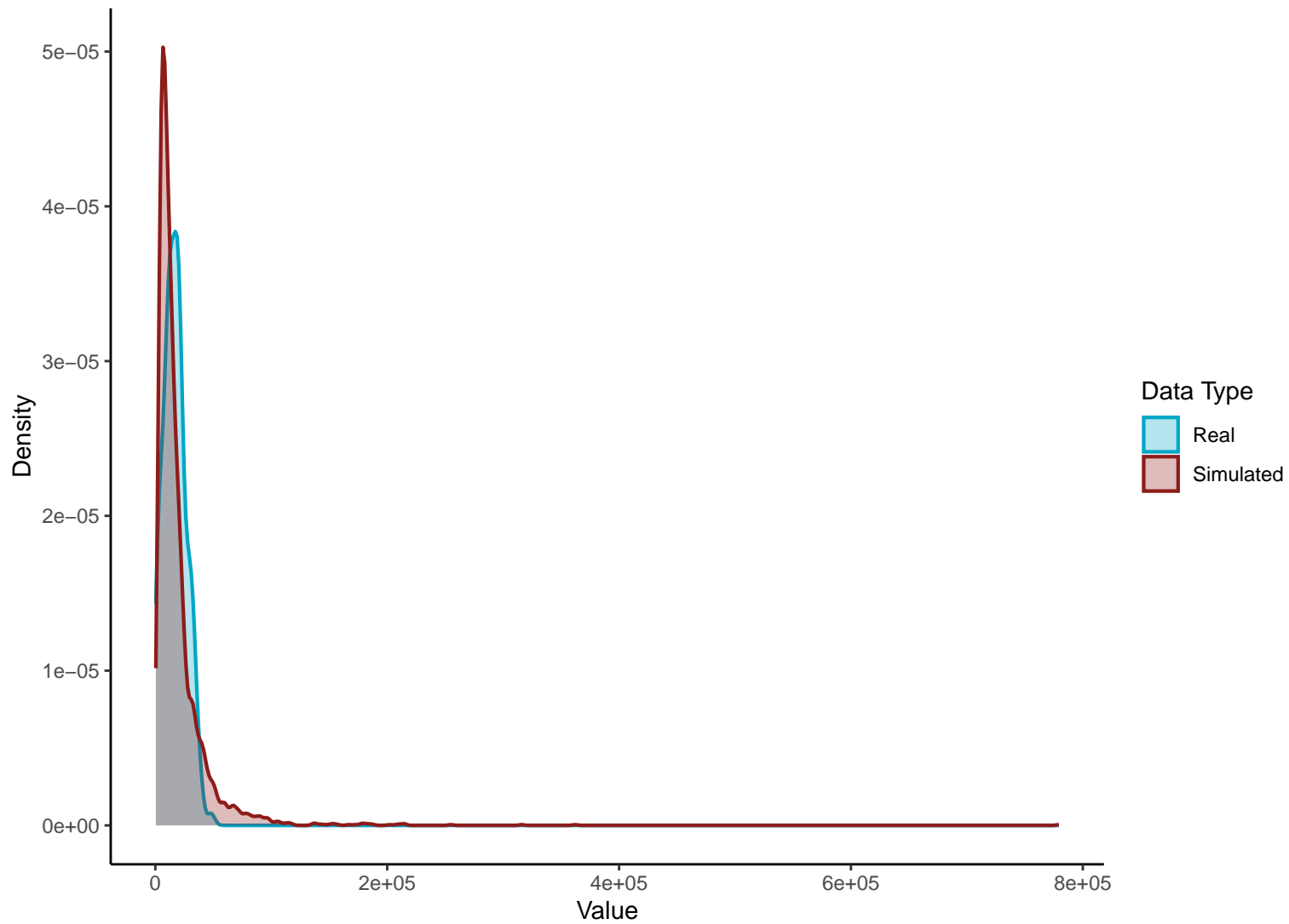
Lachnospiraceae.ND3007.group



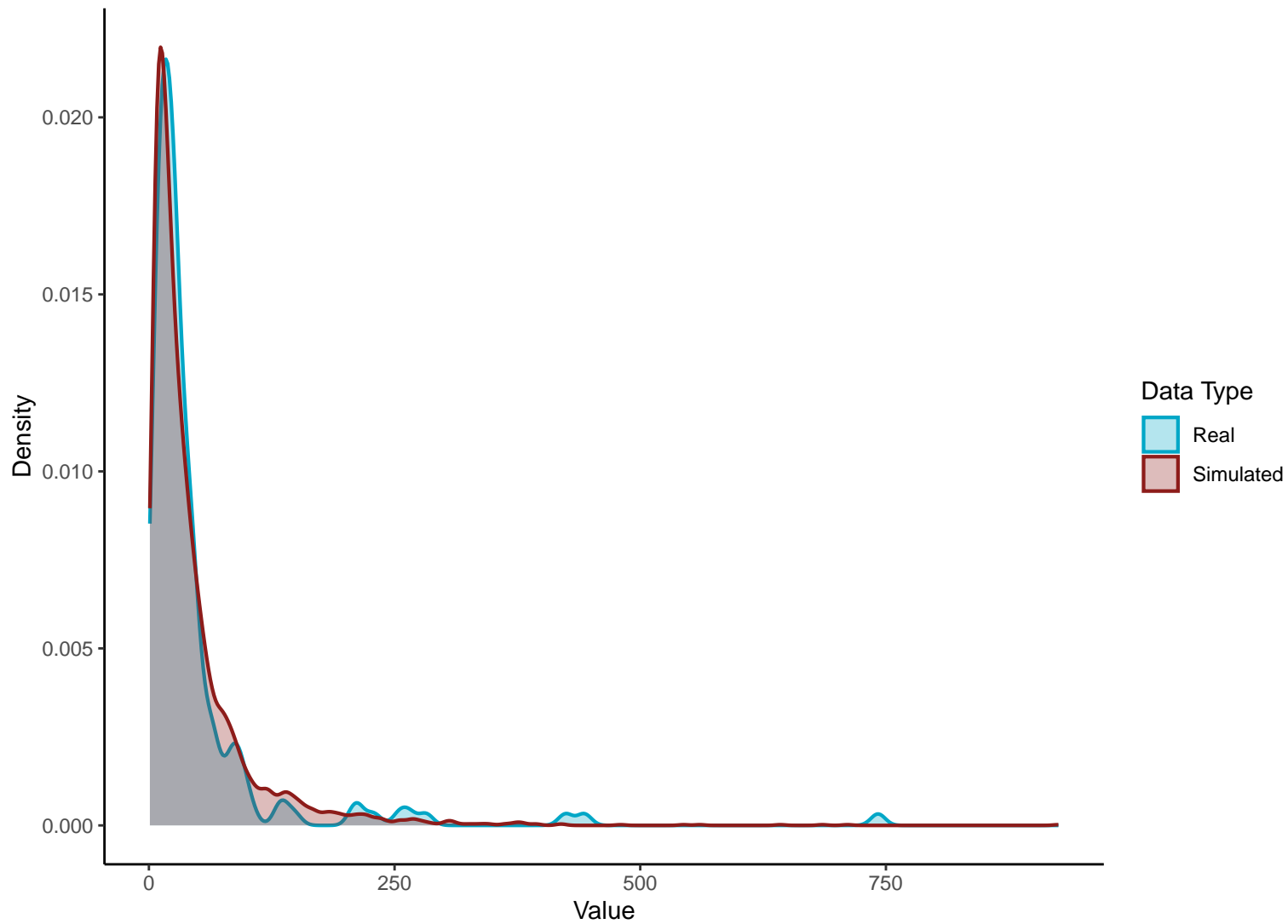
Coprococcus



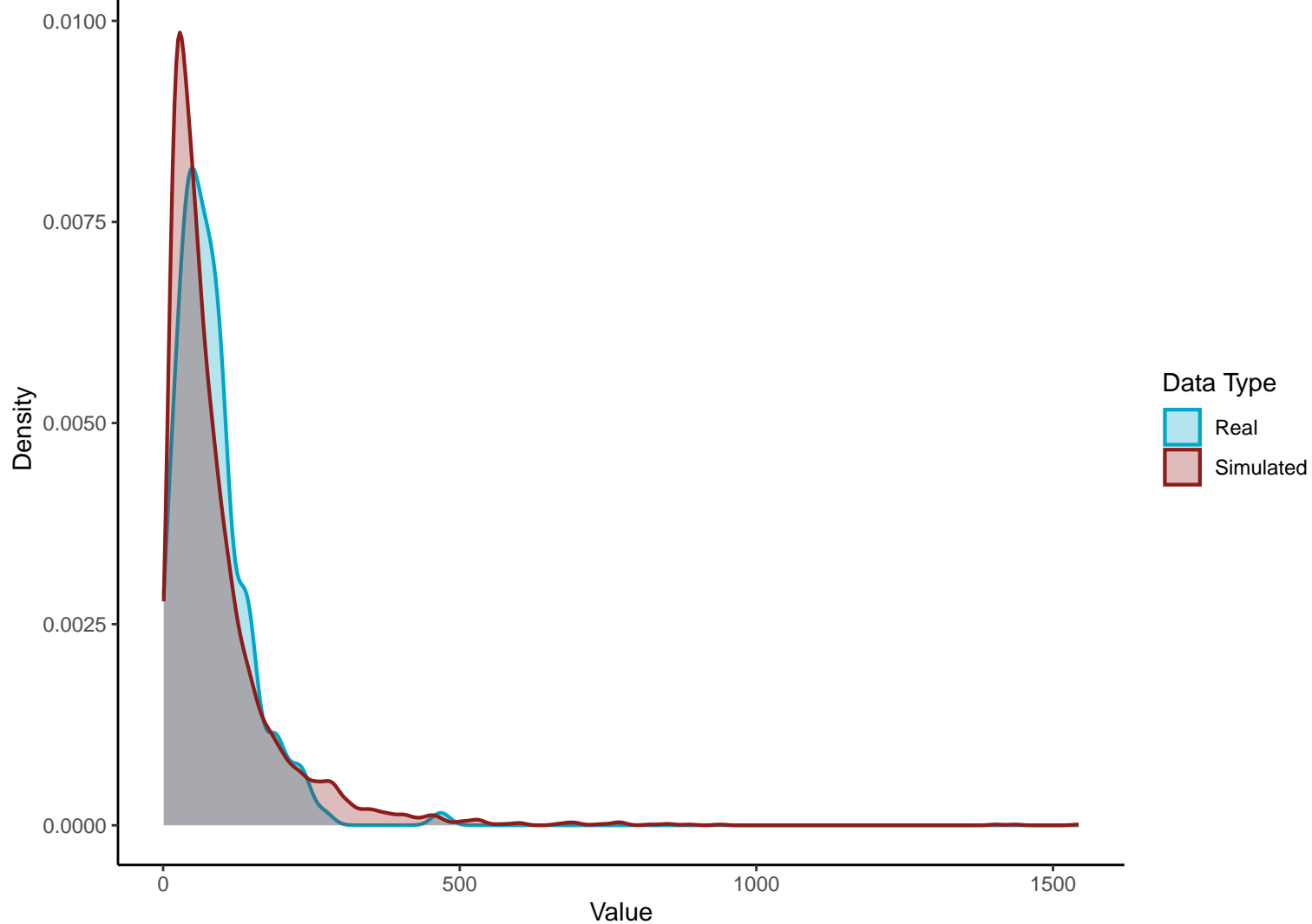
Lactobacillus



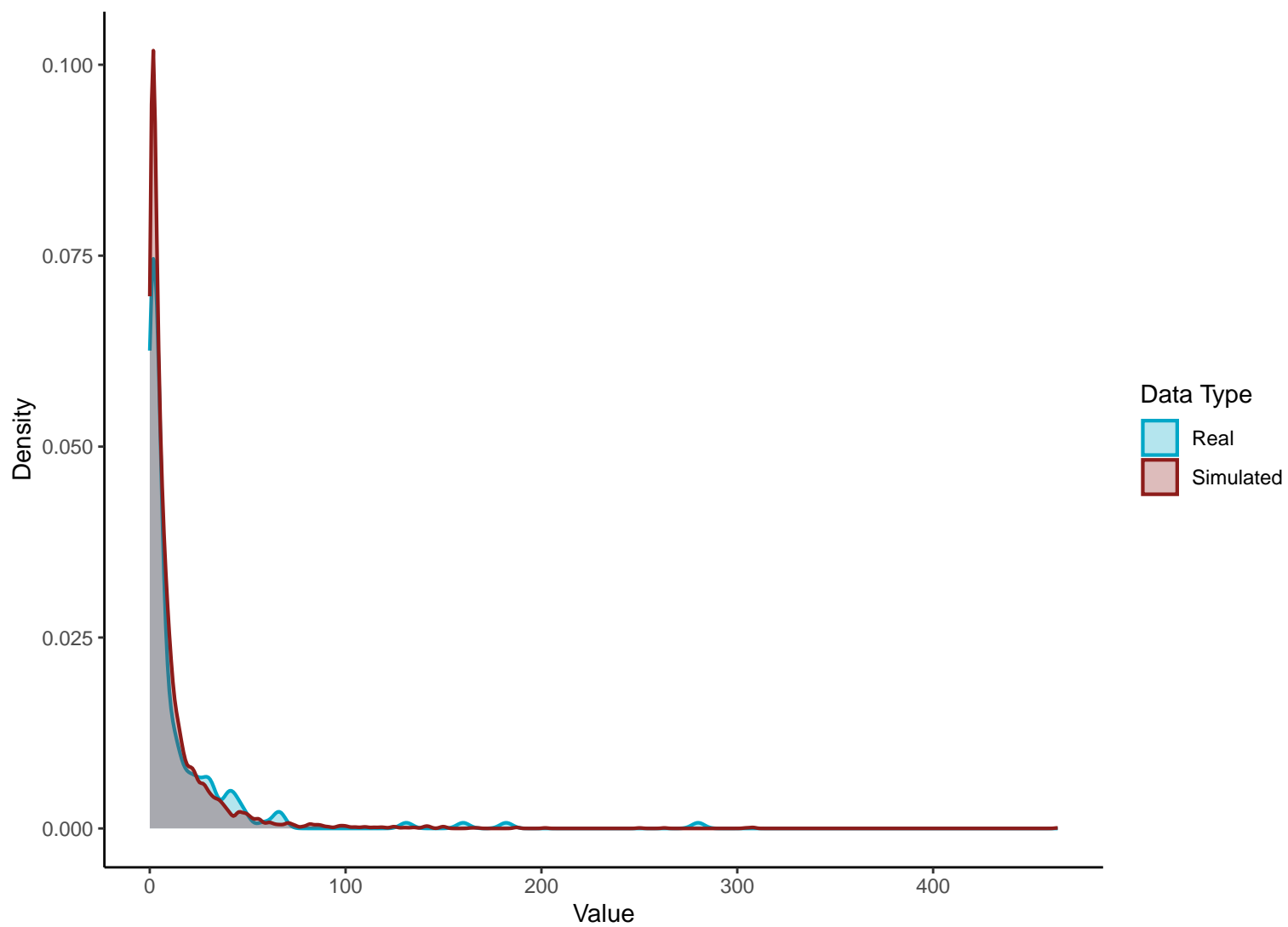
UCG.009



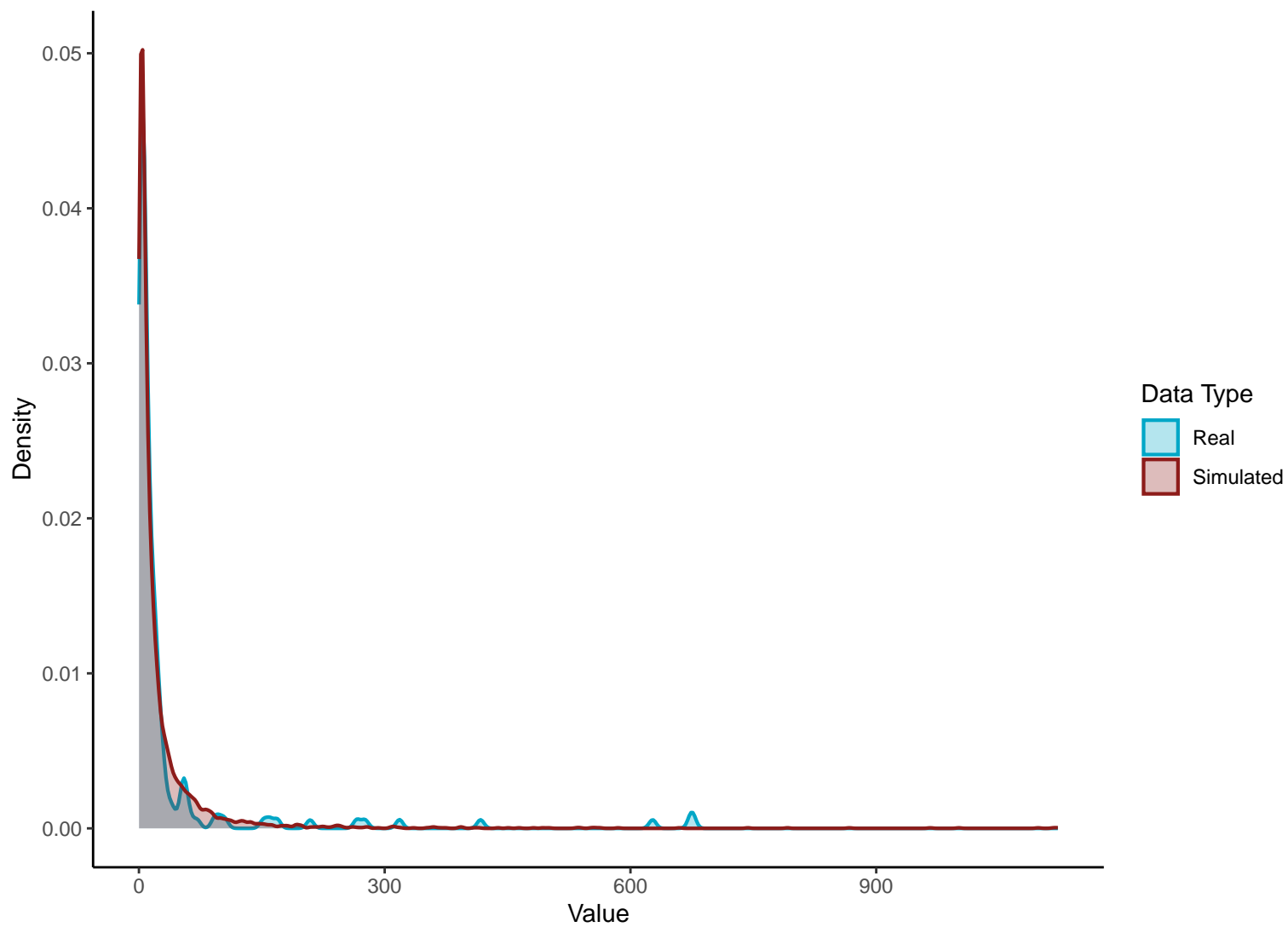
Colidextribacter



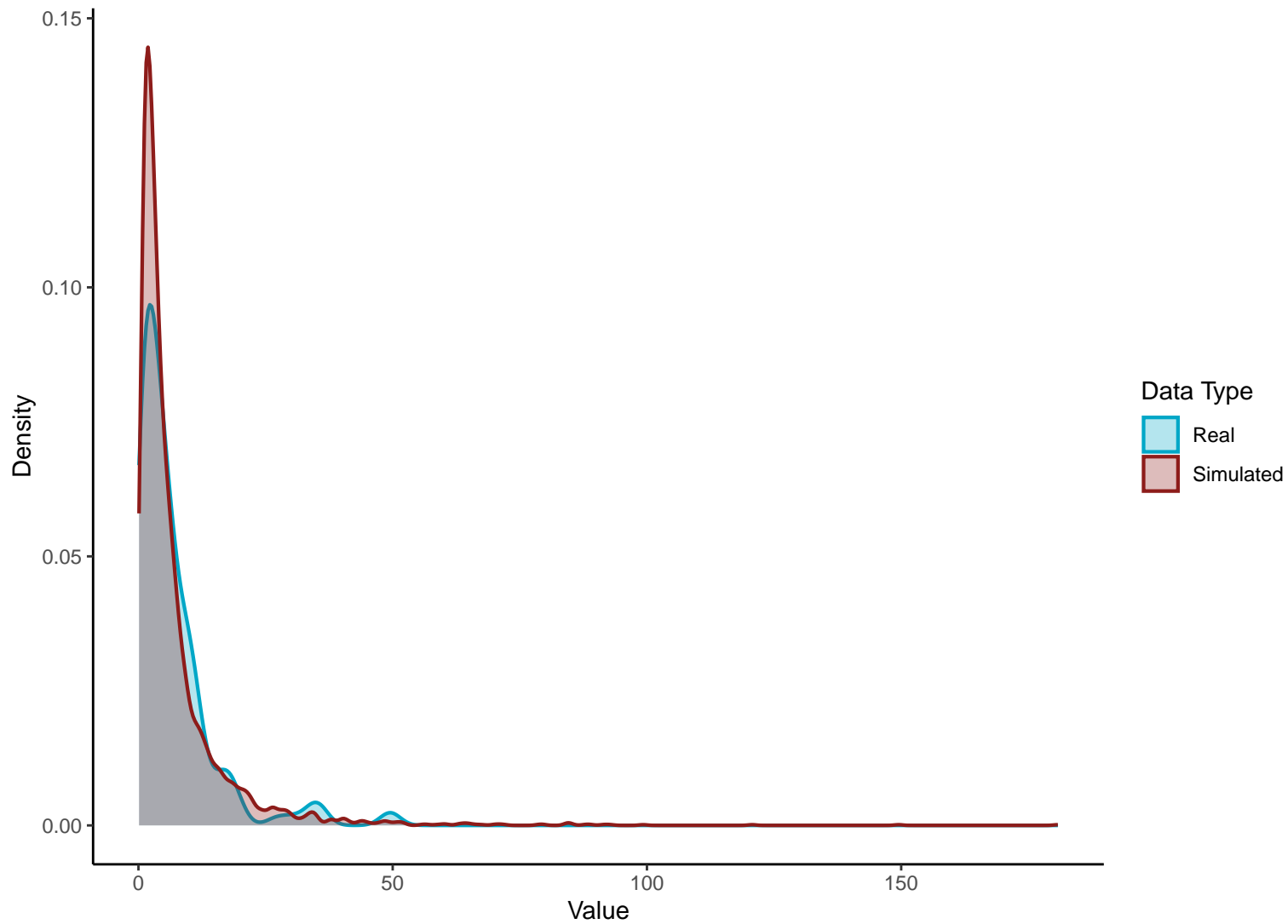
Acidaminococcus



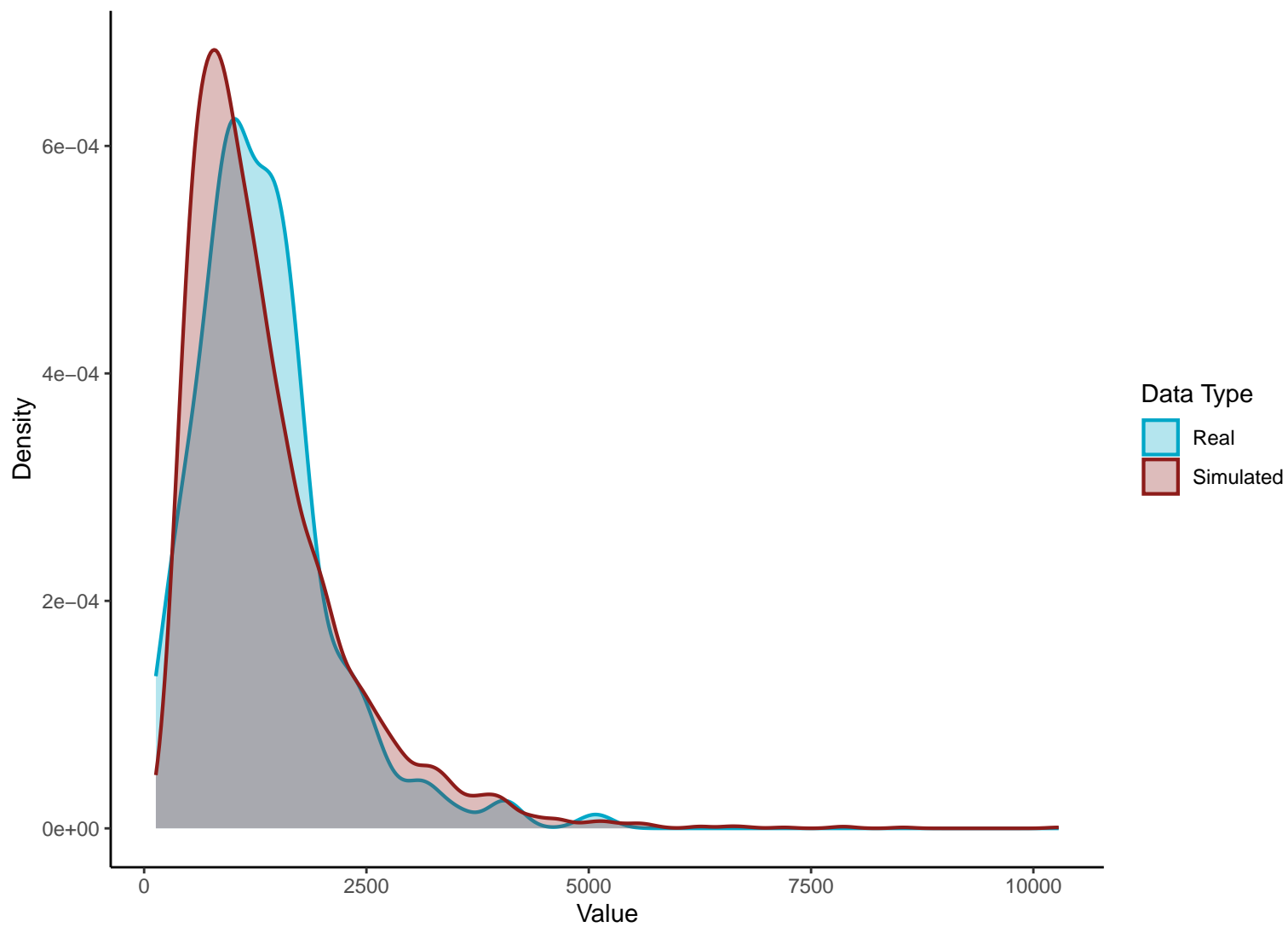
Parabacteroides



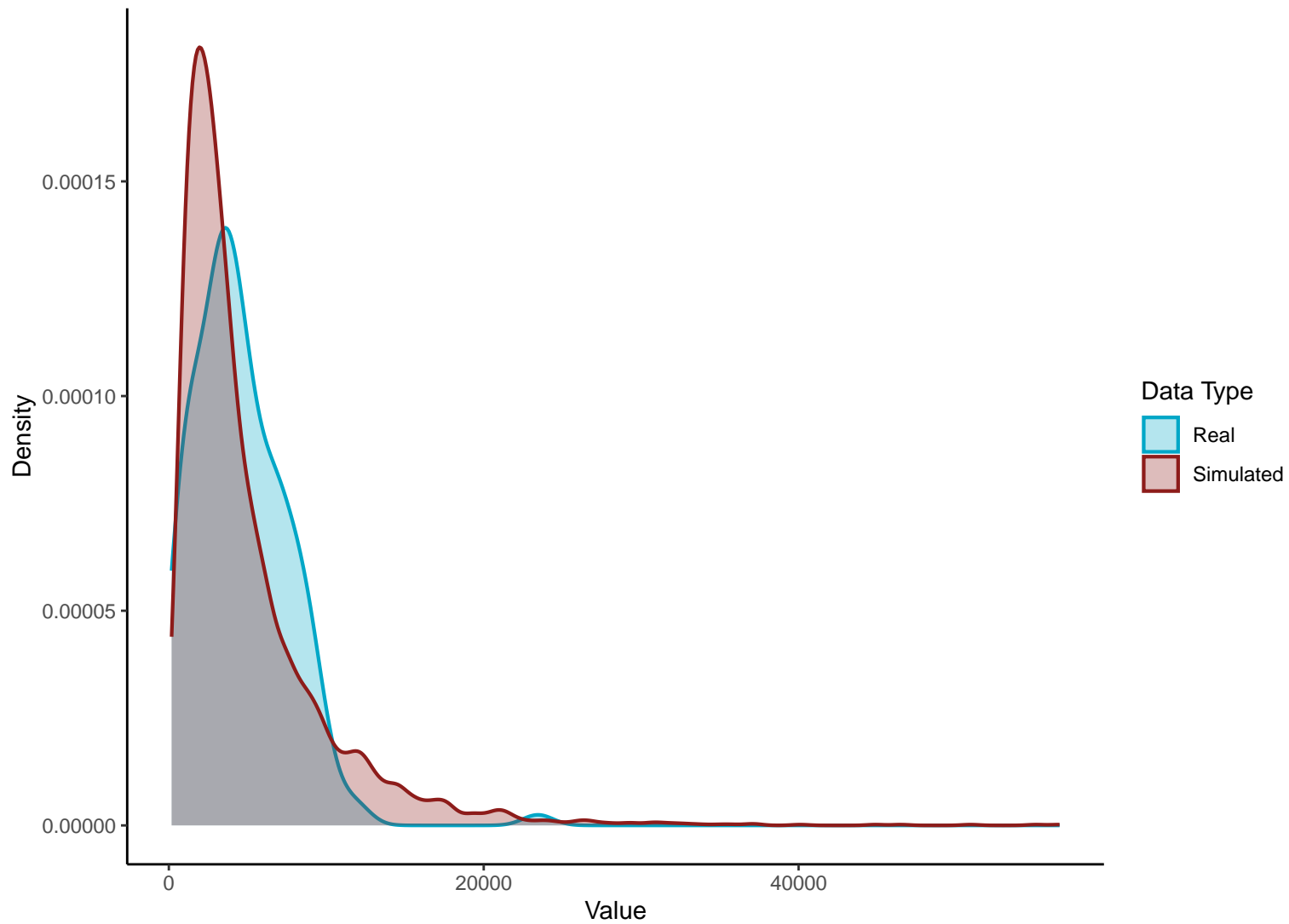
Allisonella



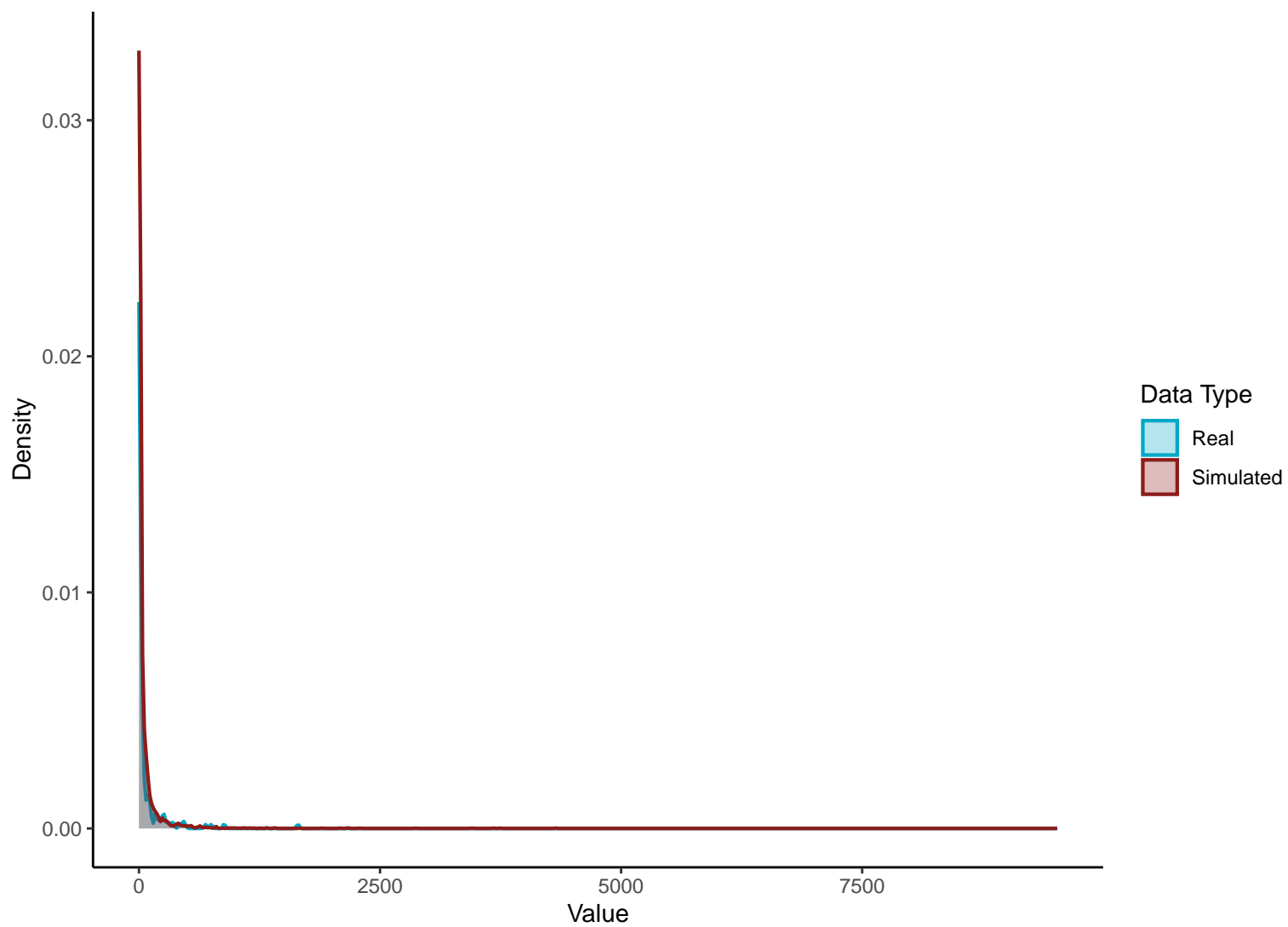
Blautia



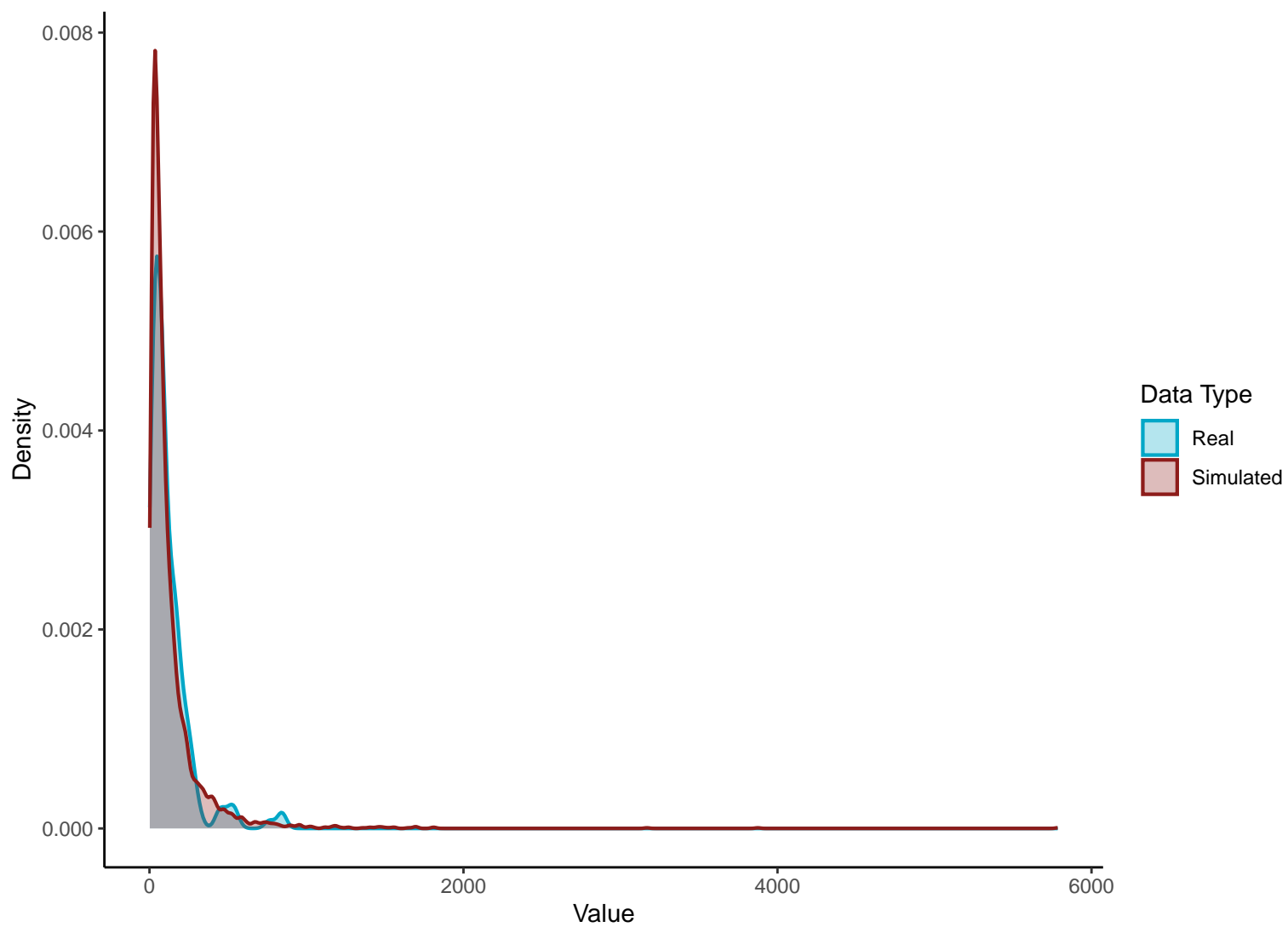
HT002



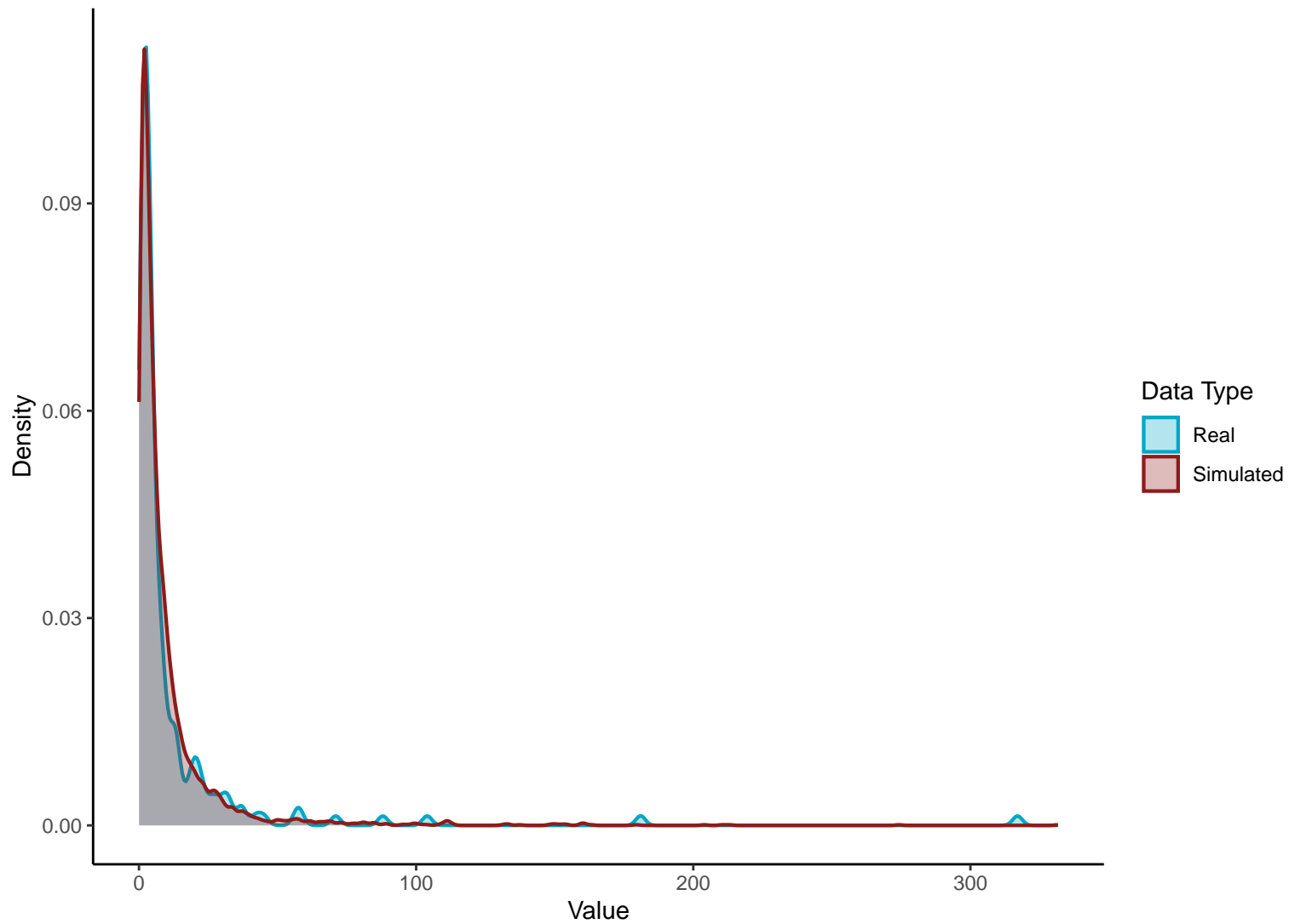
Frisingicoccus



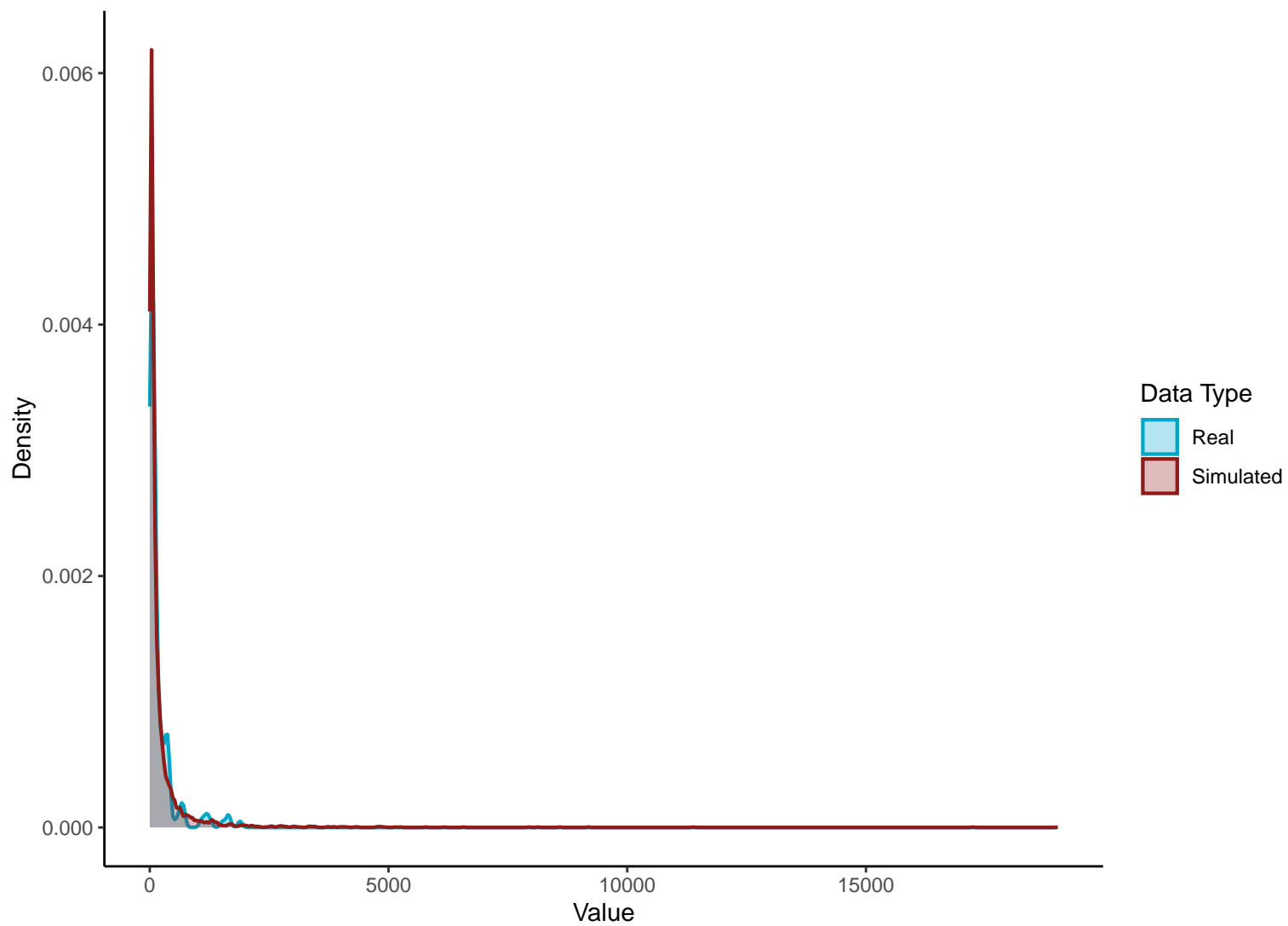
Ligilactobacillus



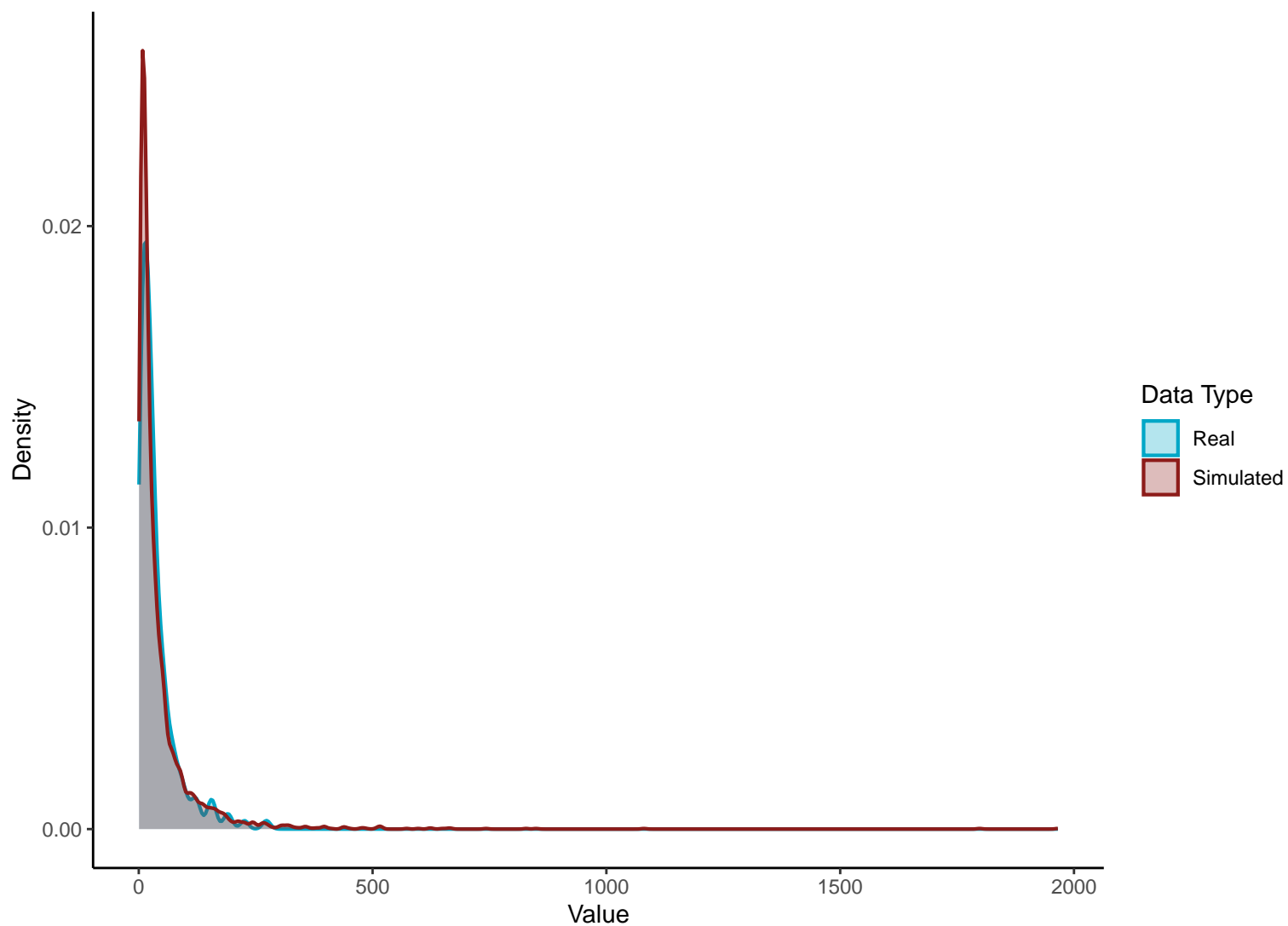
Sphaerochaeta



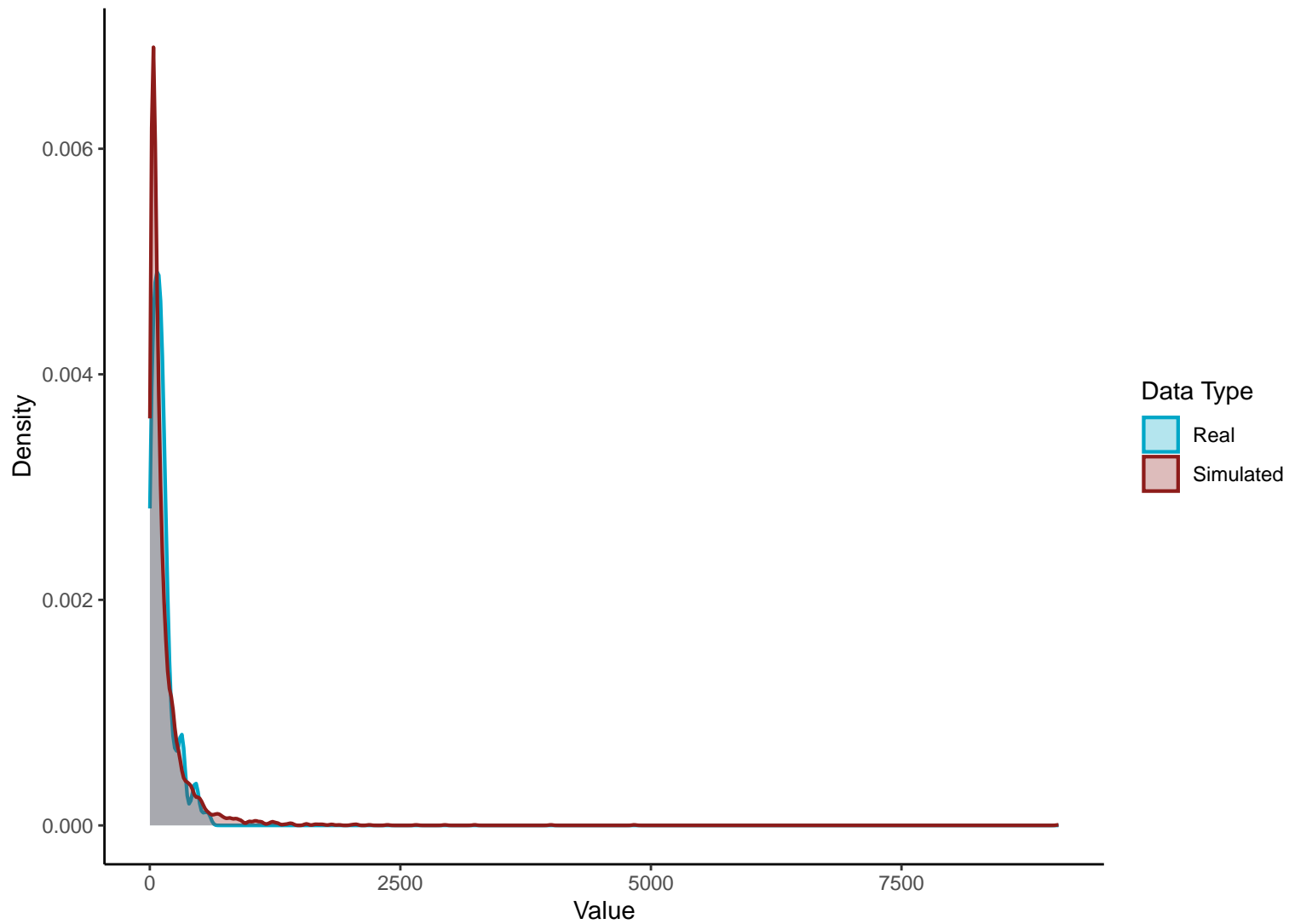
Romboutsia



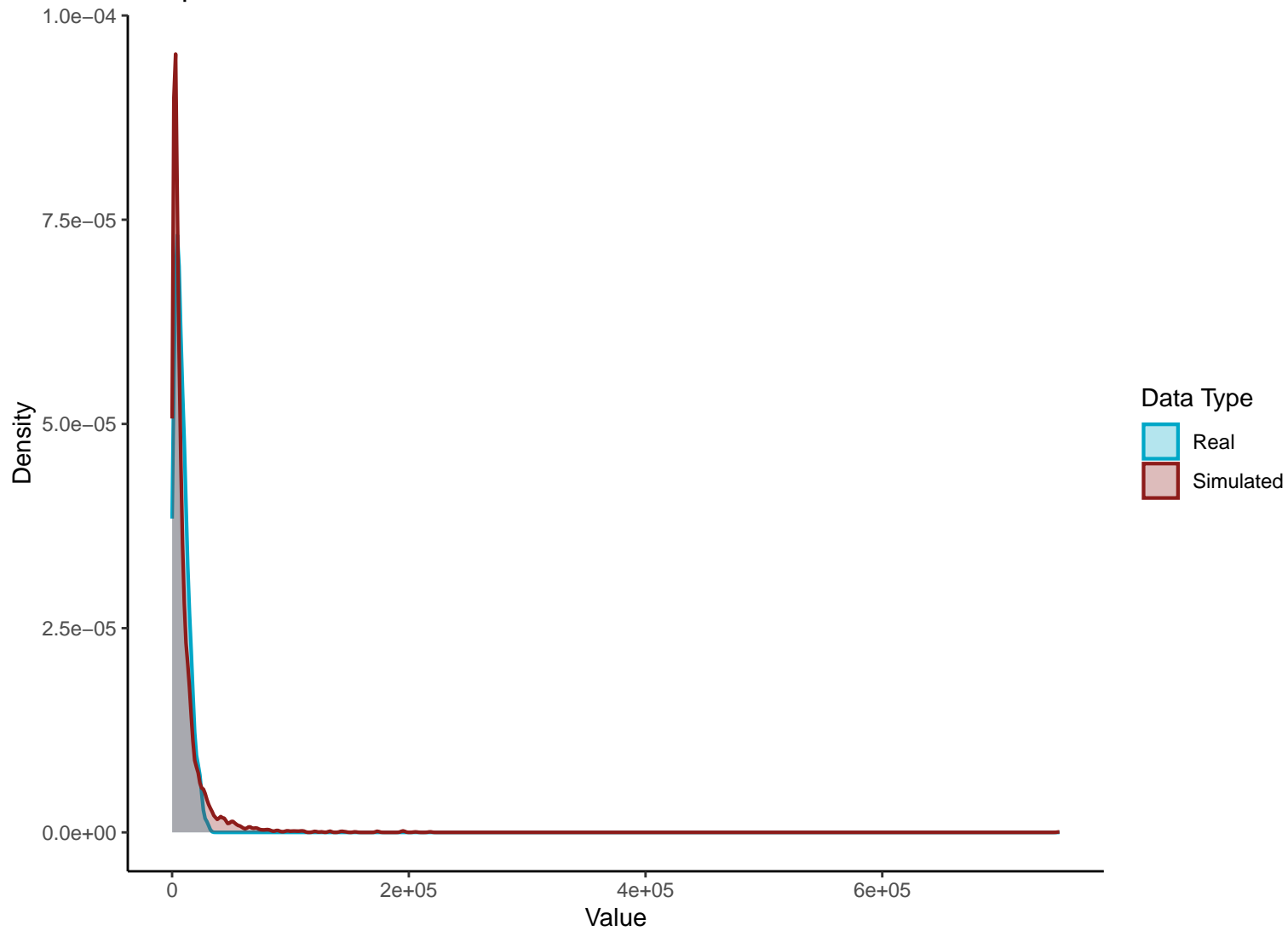
Lachnospiraceae.UGC.001



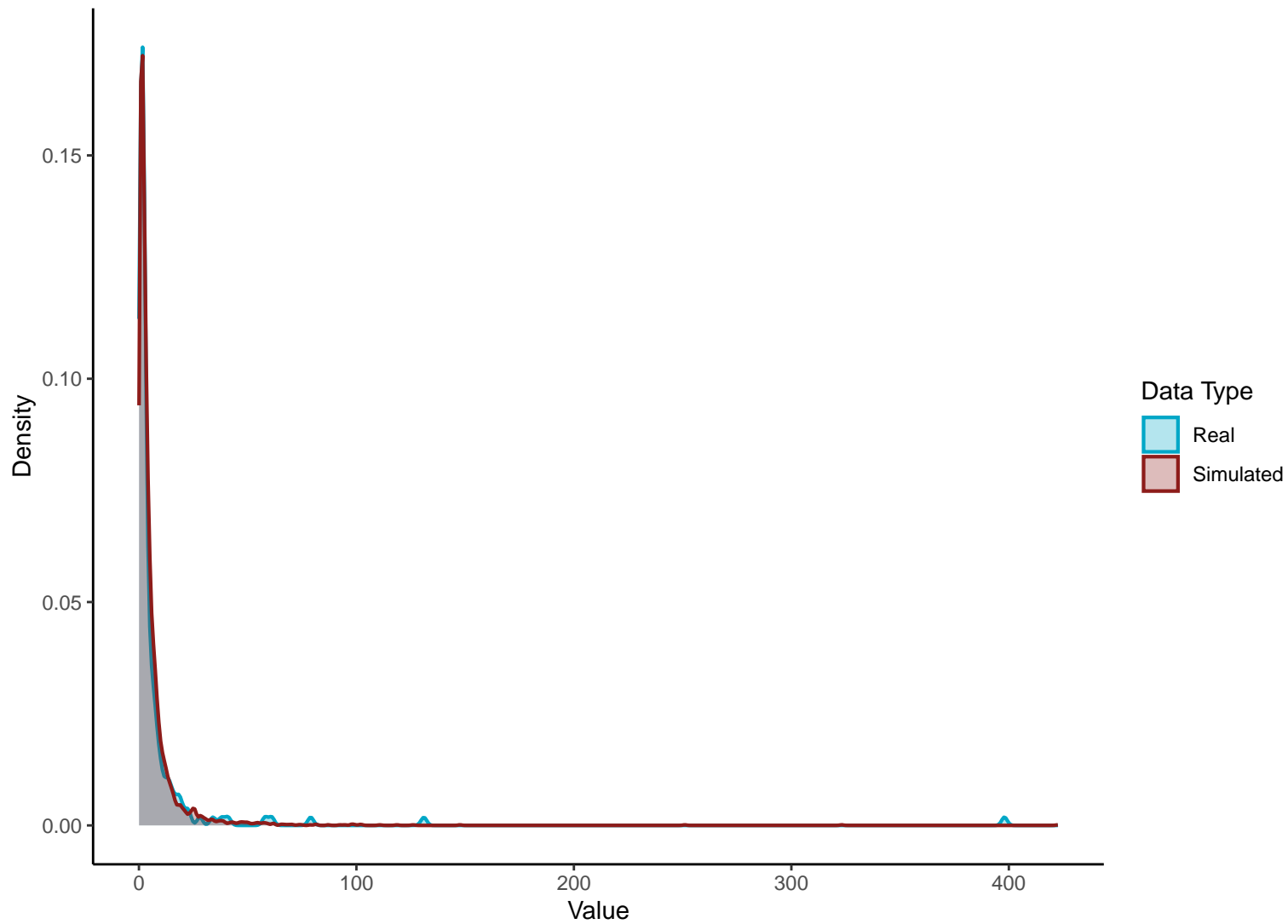
Oscillibacter



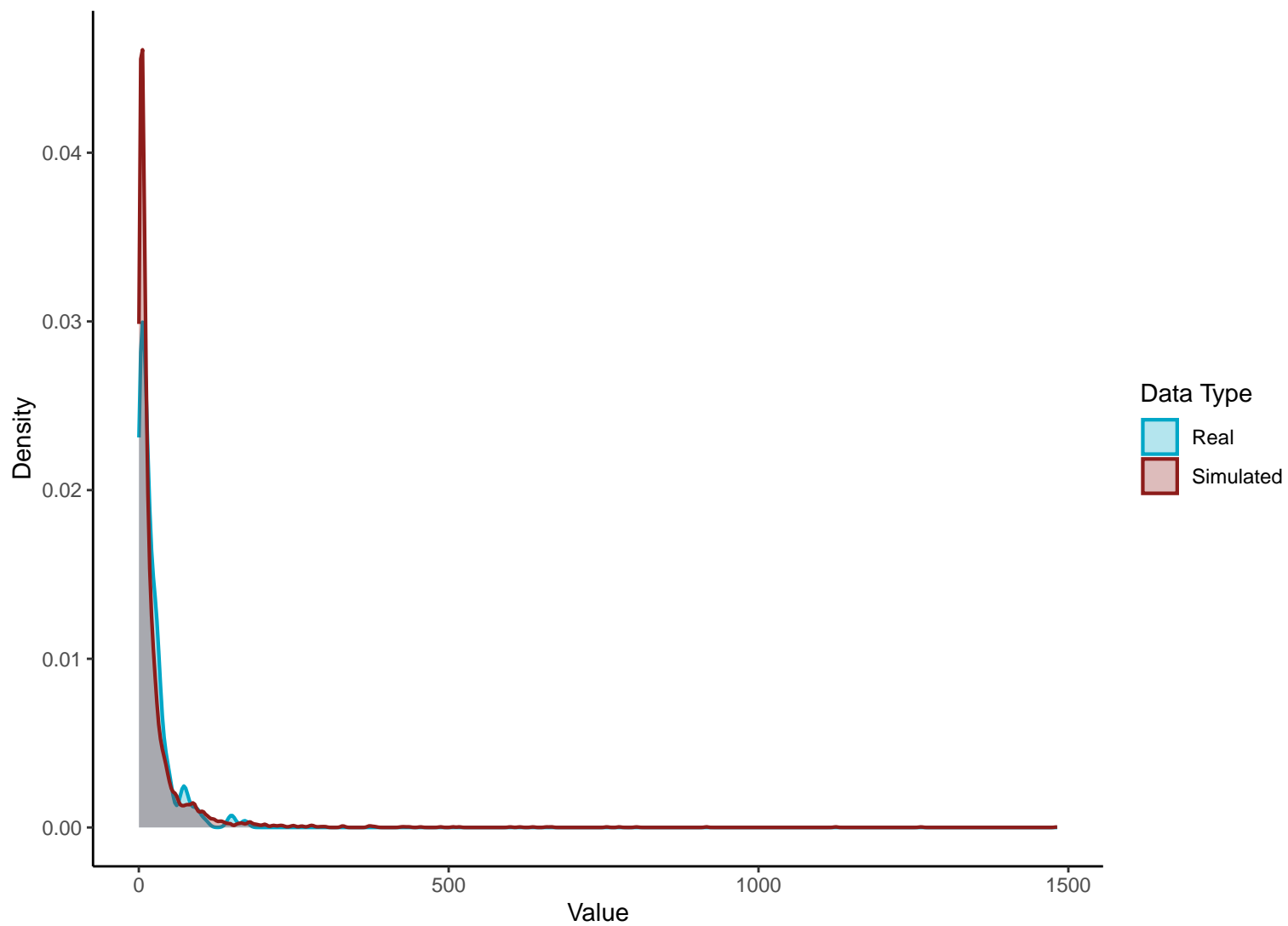
Streptococcus



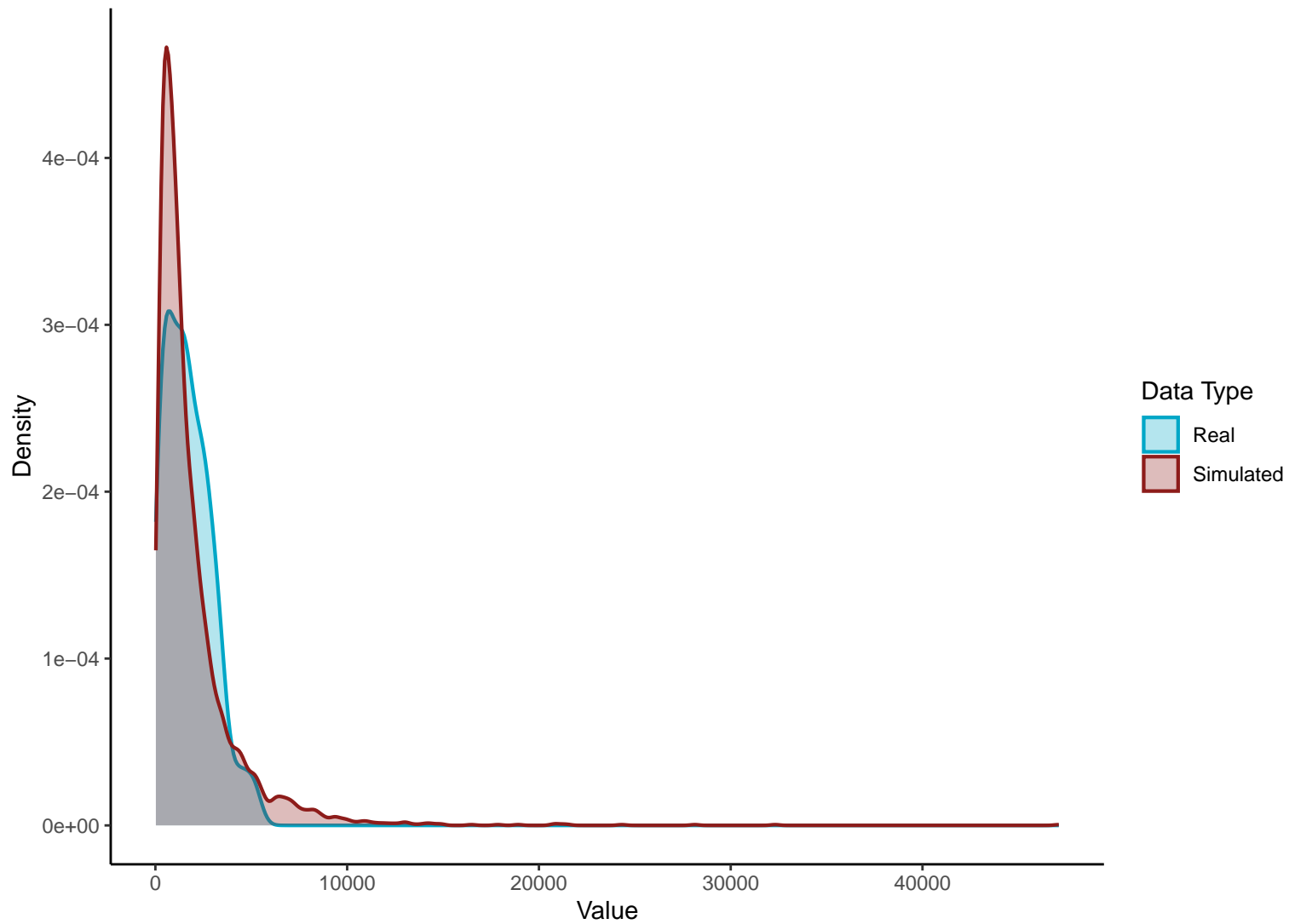
Cellulosilyticum



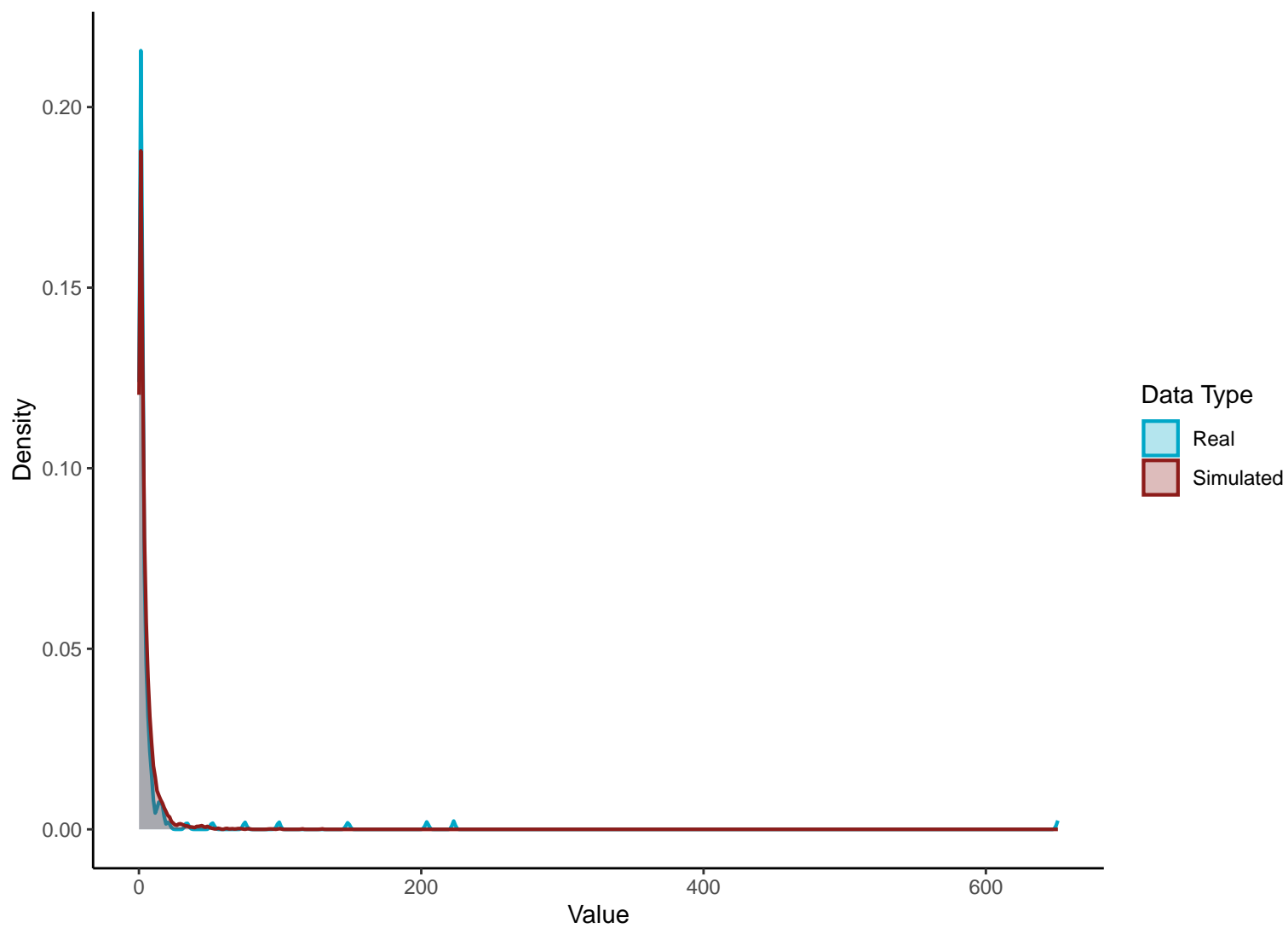
Mitsuokella



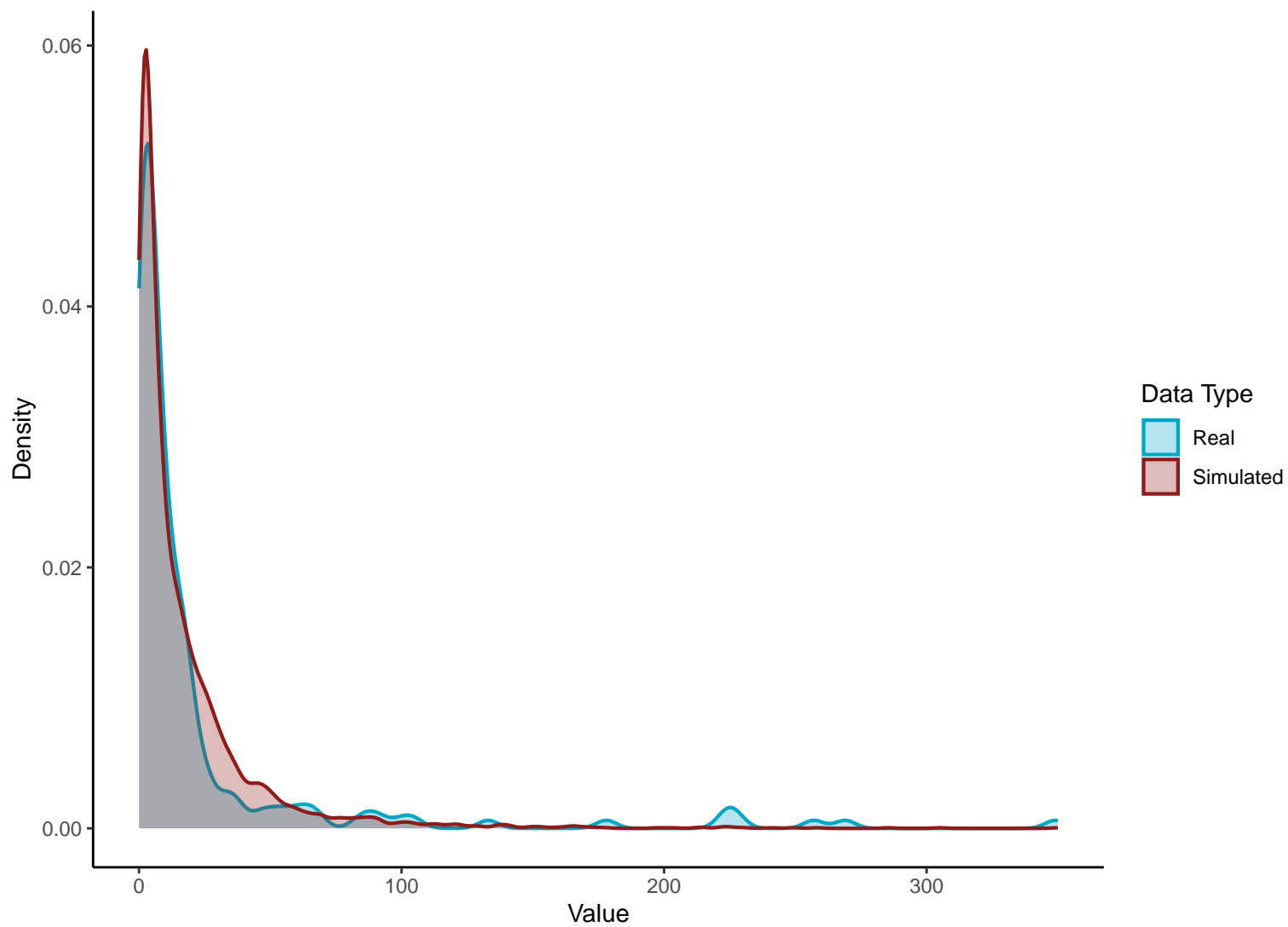
Agathobacter



Bacteroides



p.1088.a5.gut.group



Anaeroplasma

Density

0.15

0.10

0.05

0.00

0

250

500

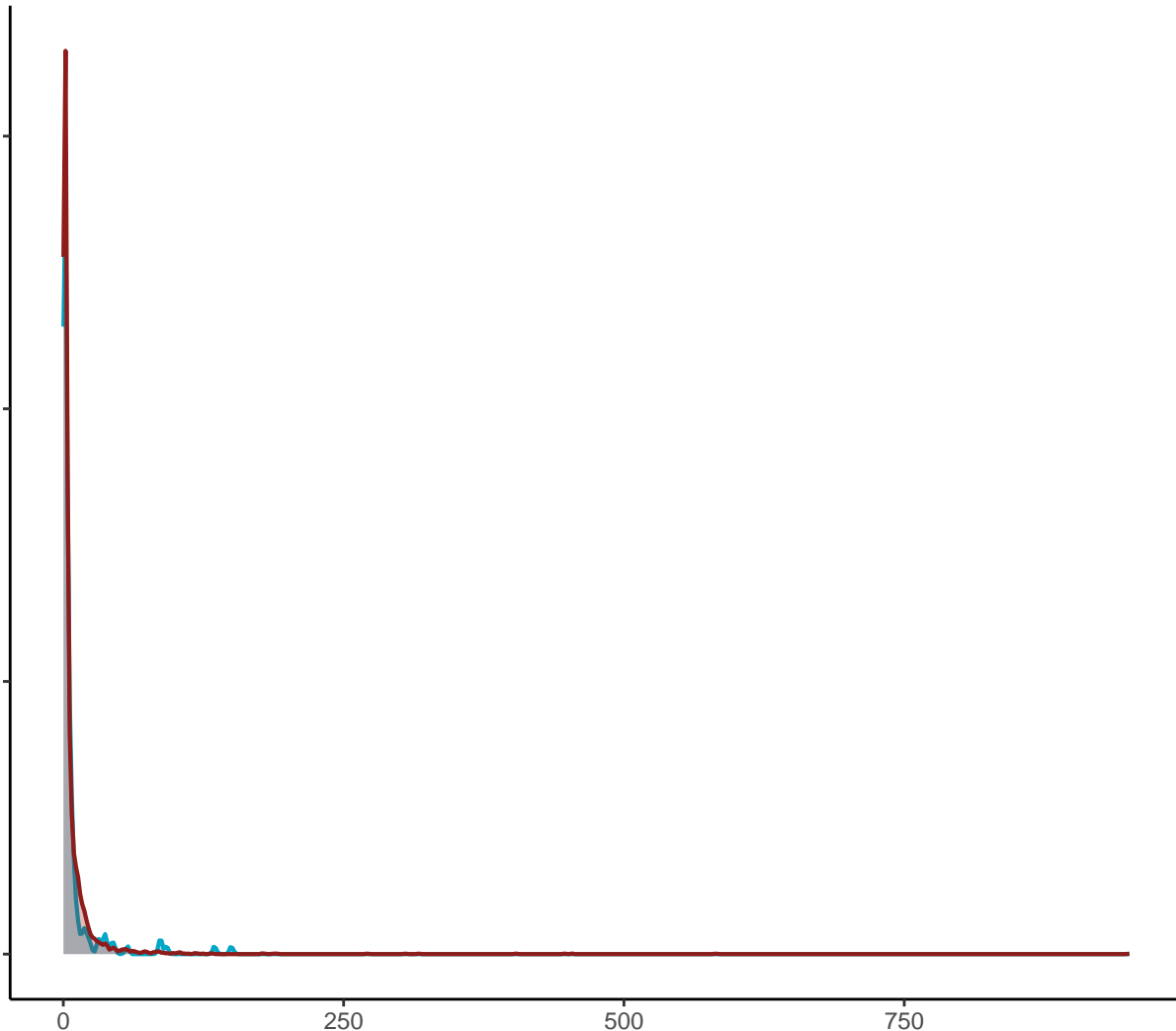
750

Value

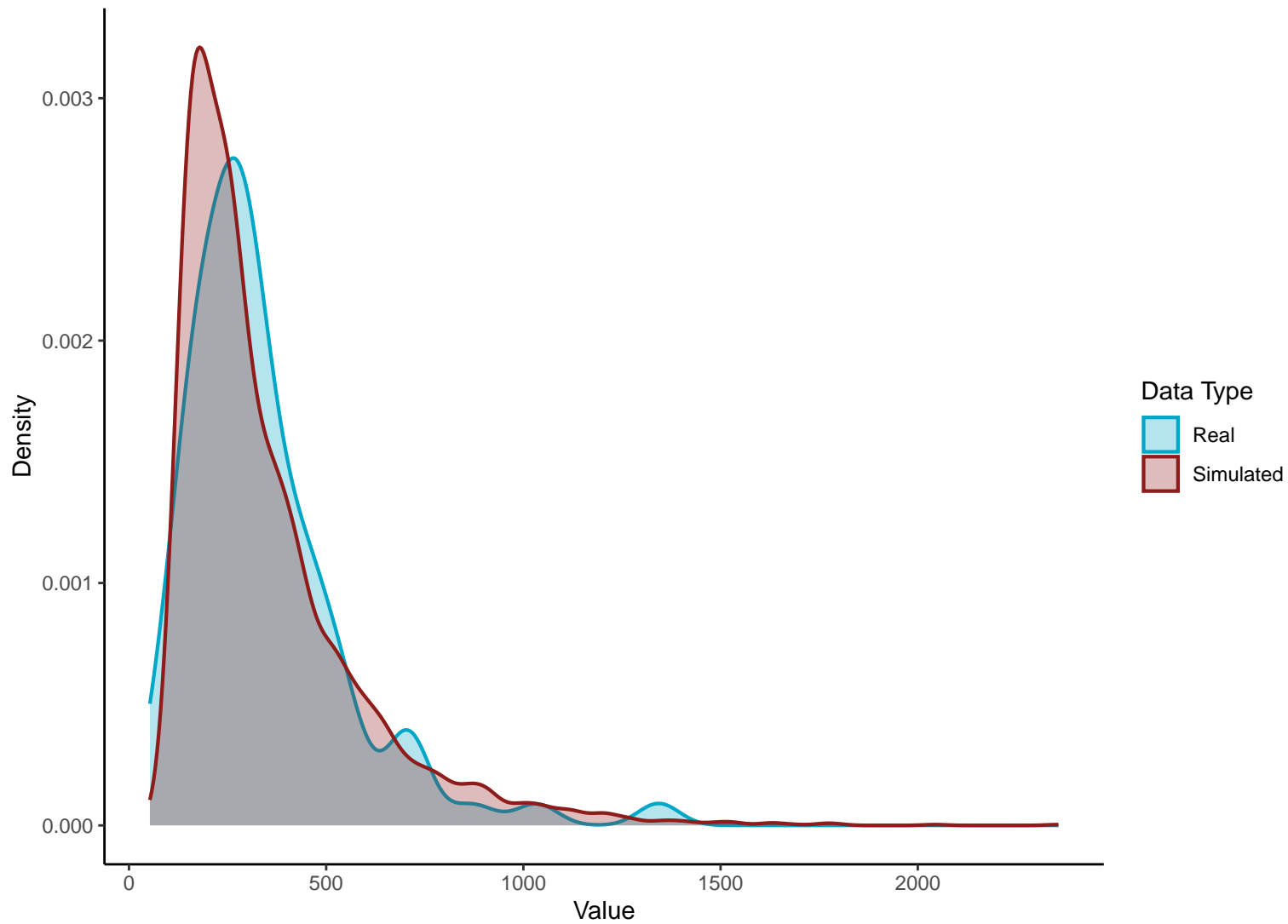
Data Type

Real

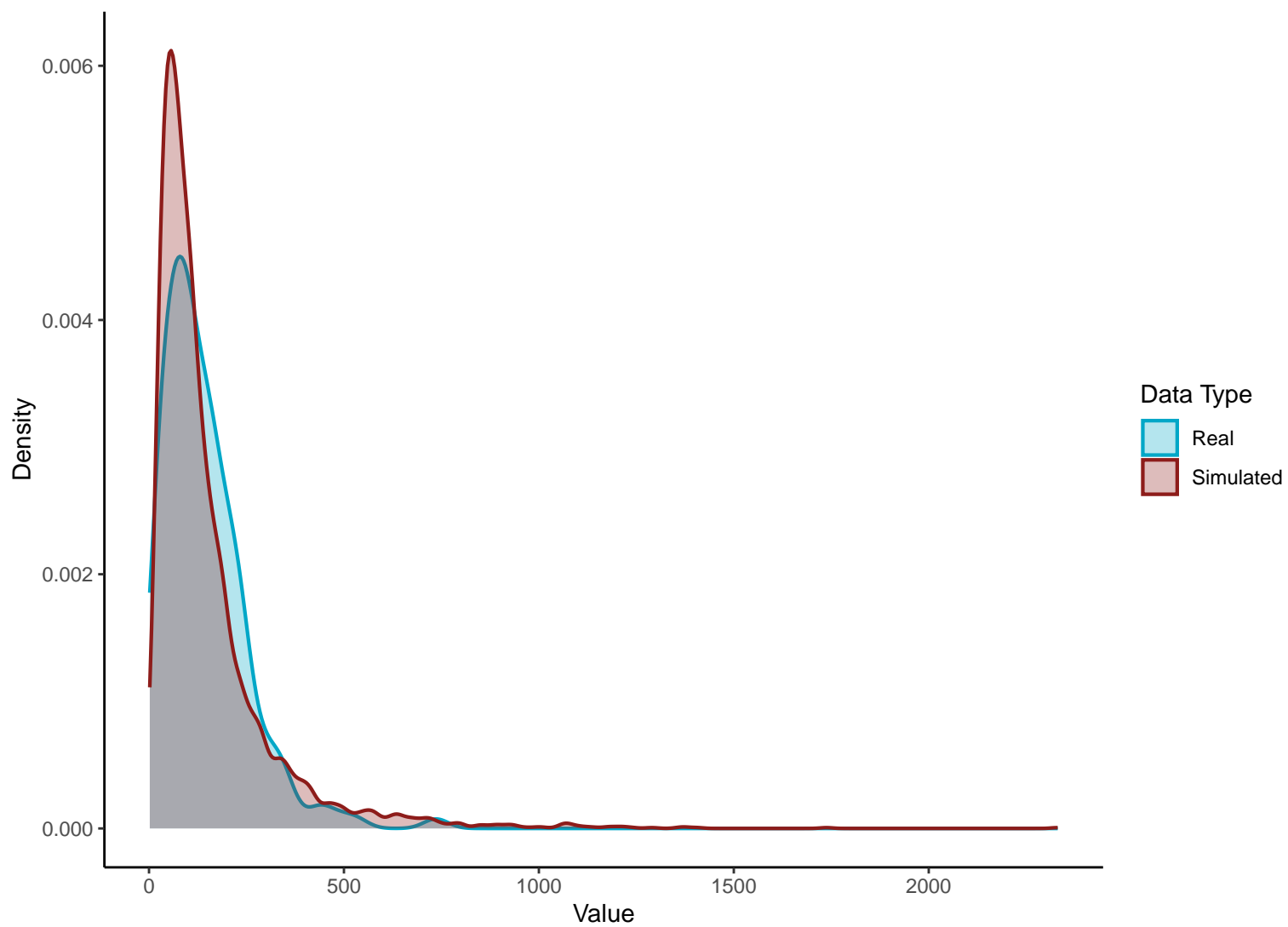
Simulated



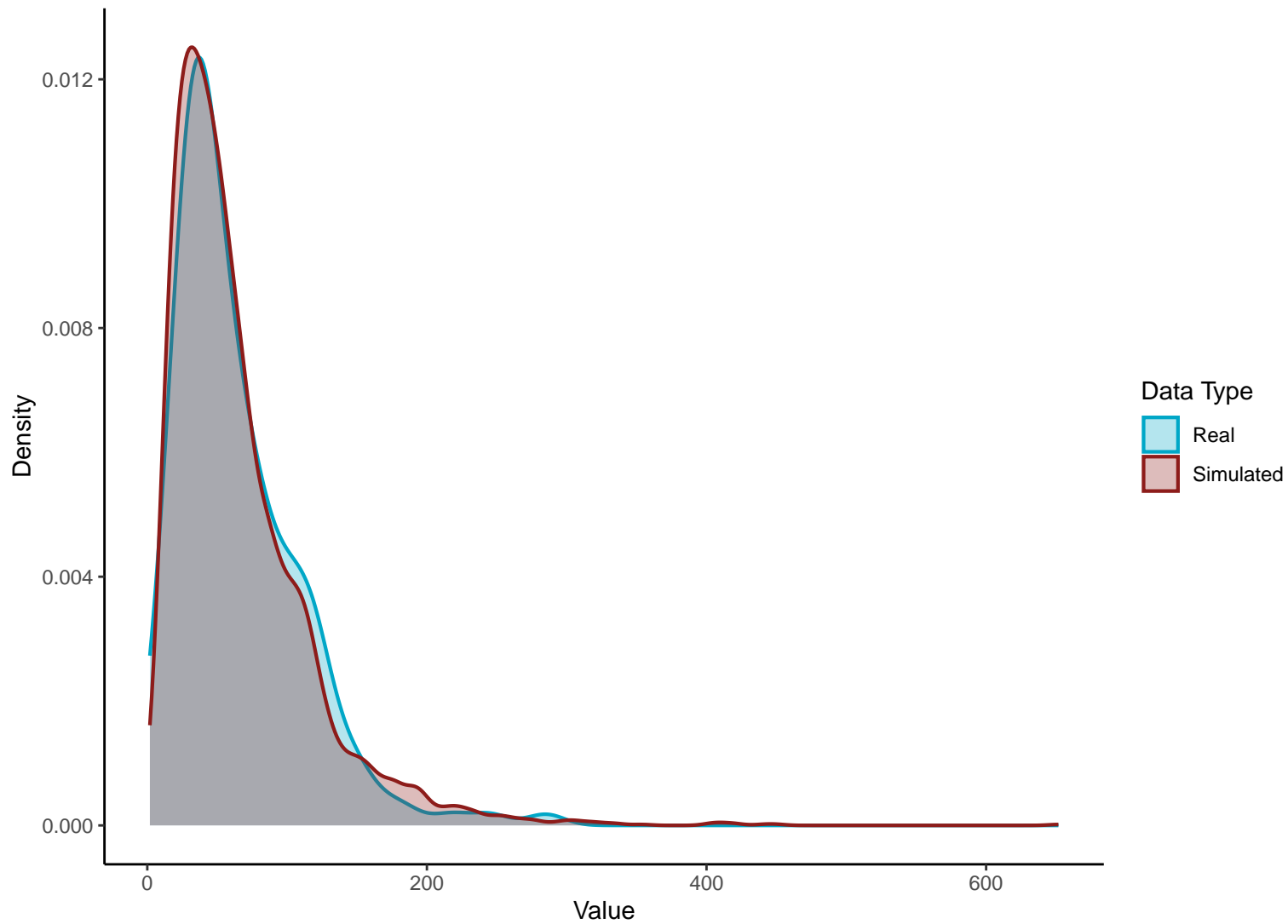
Marvinbryantia



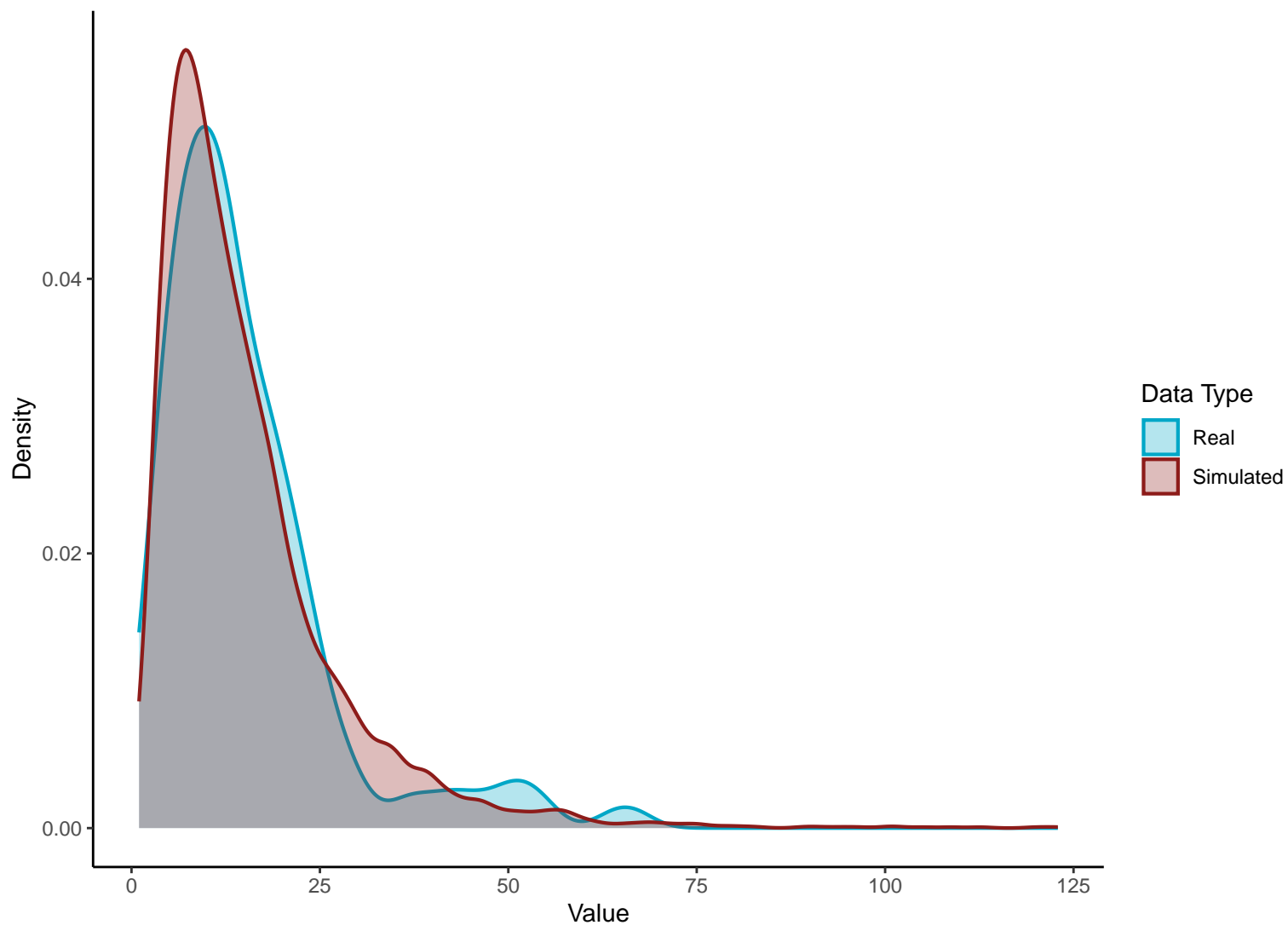
Mogibacterium



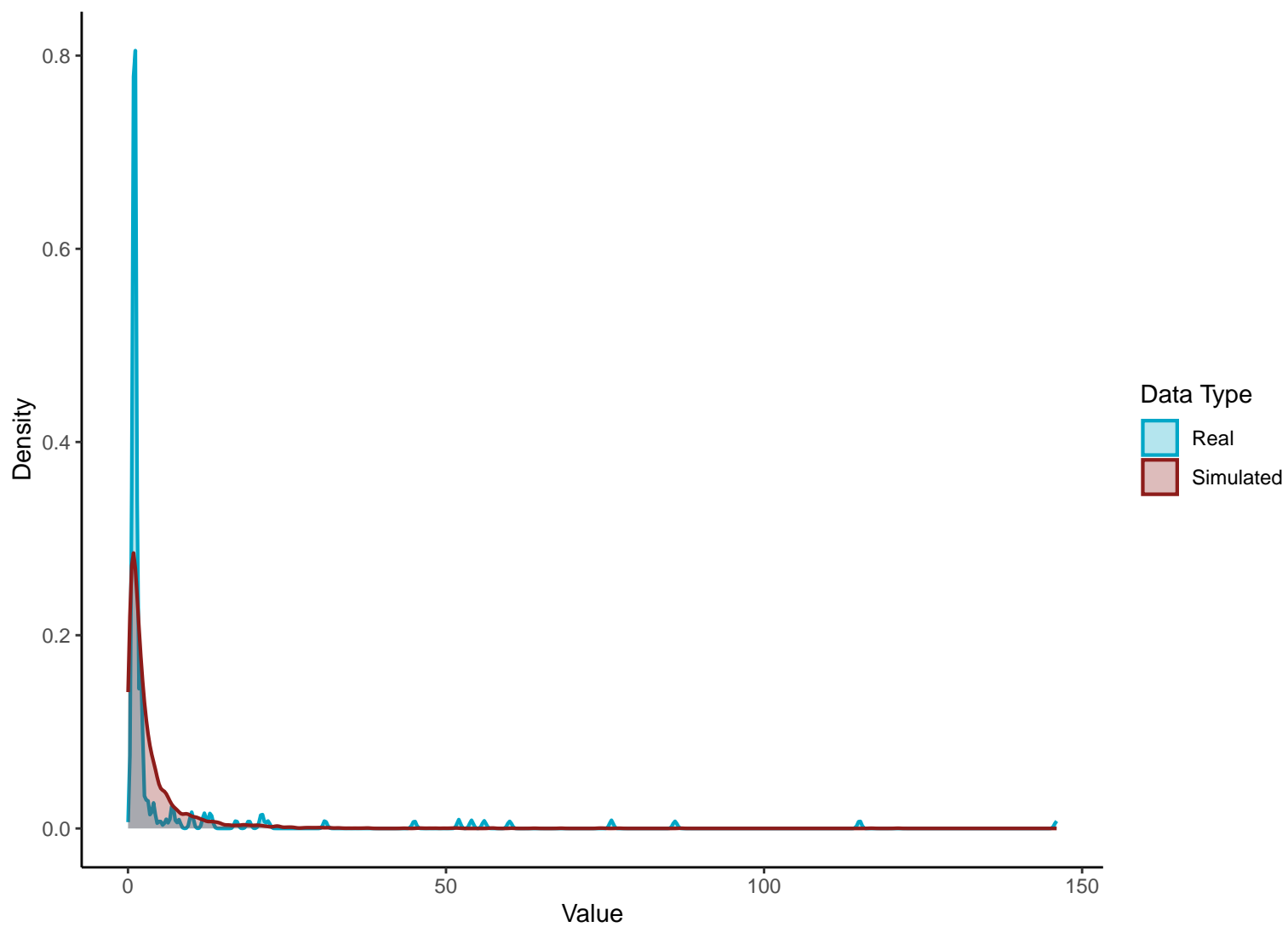
Family.XIII.UCG.001



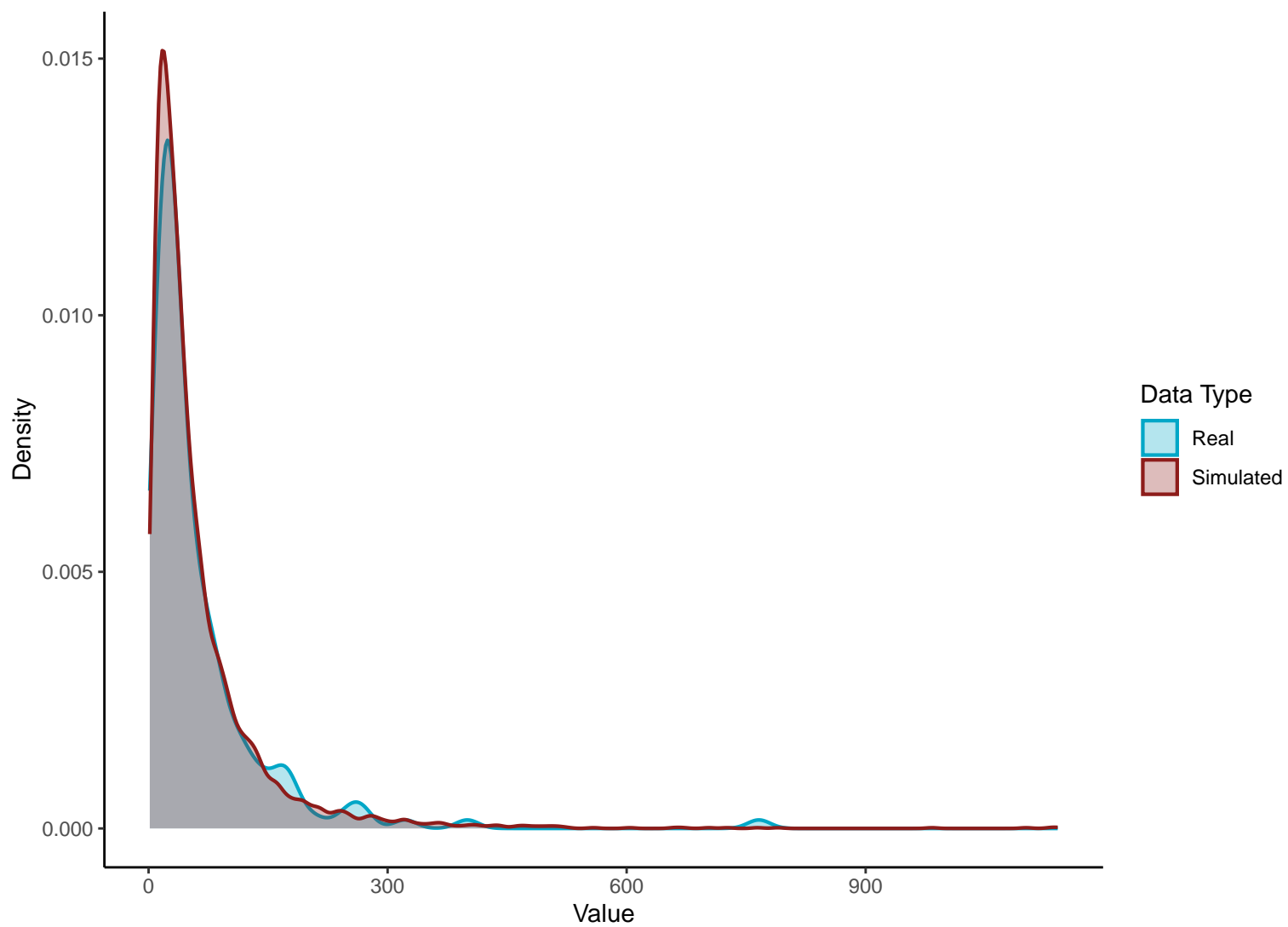
Lachnospiraceae.UCG.010



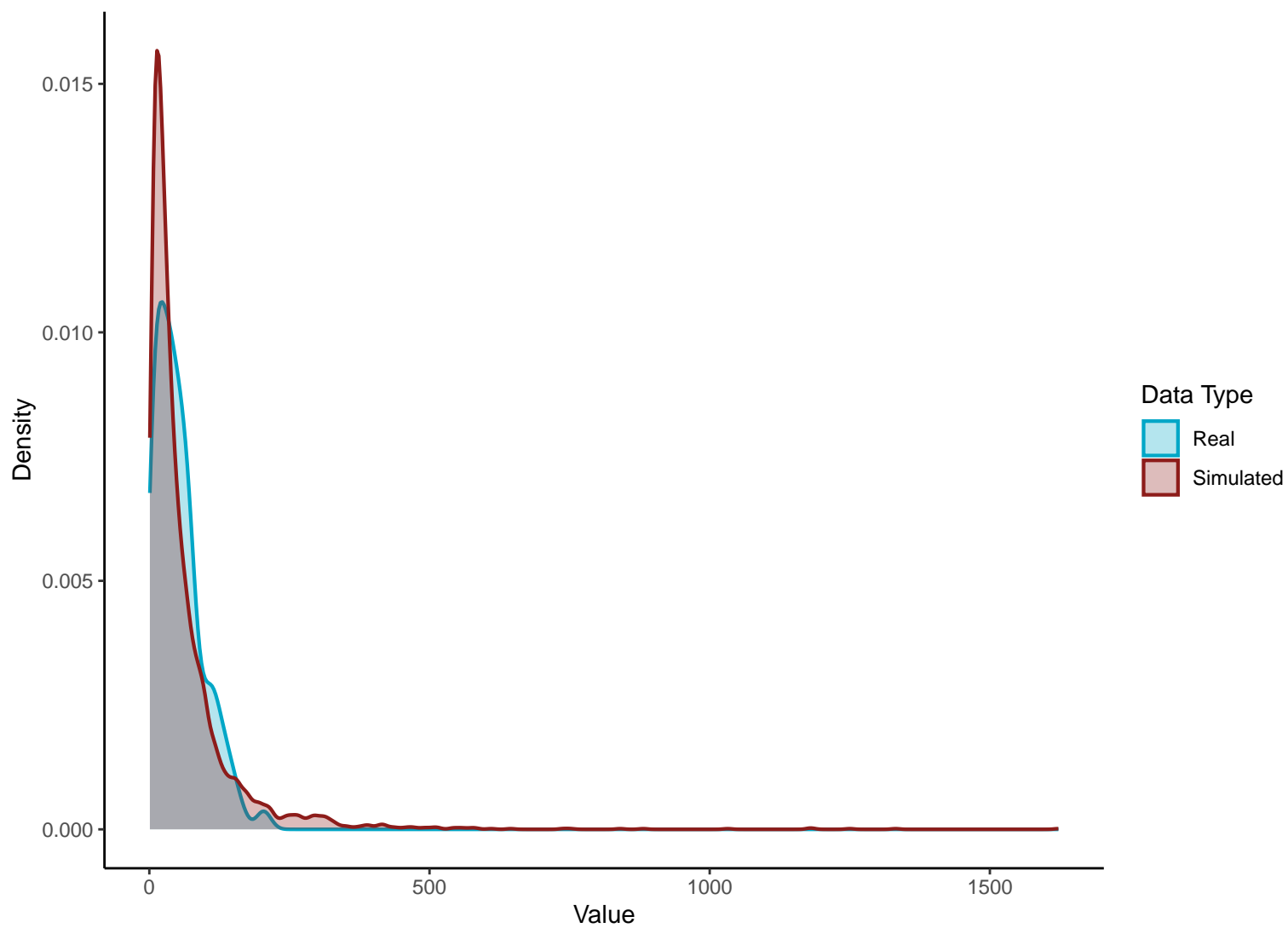
Megamonas



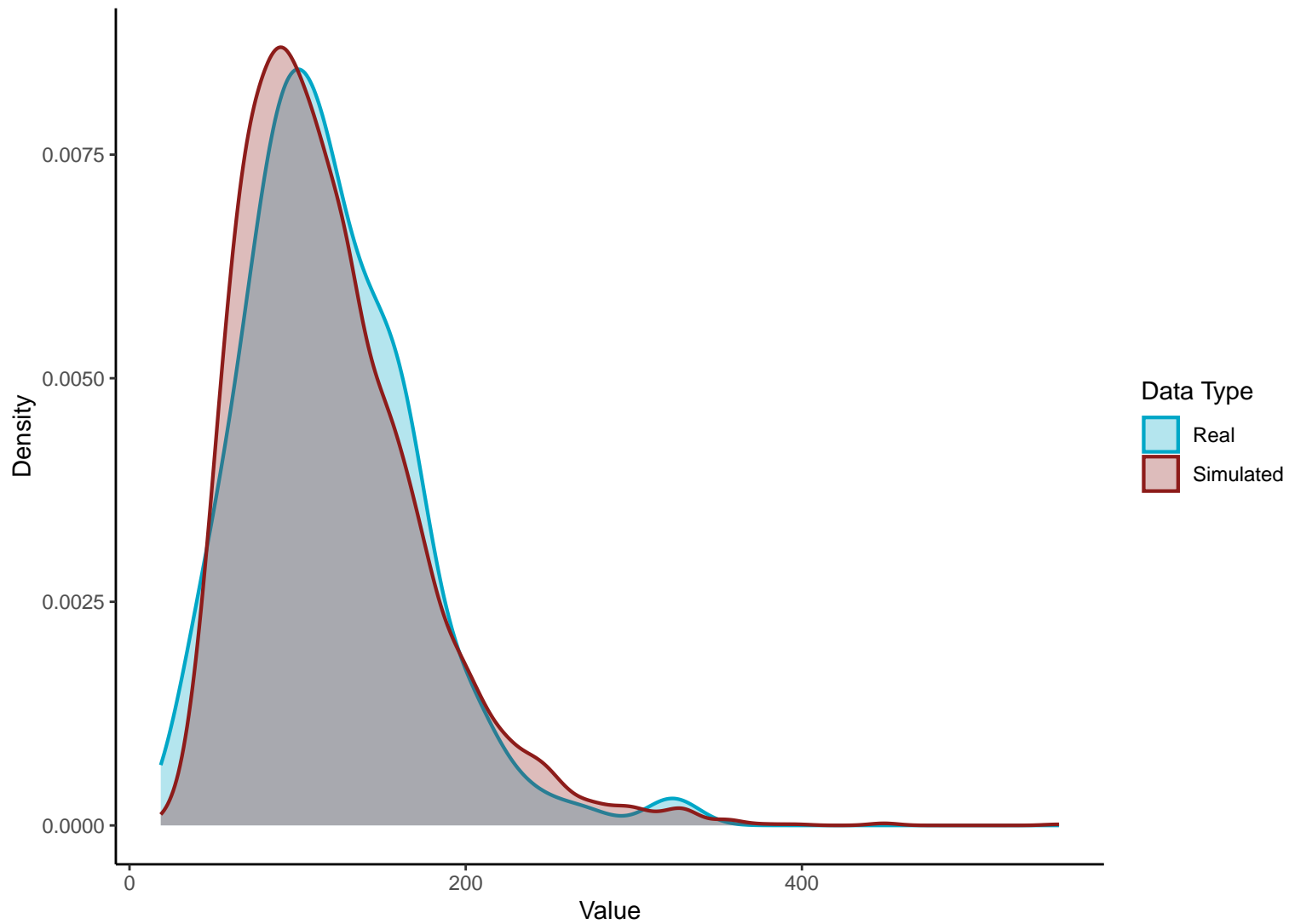
X.Eubacterium..nodatum.group



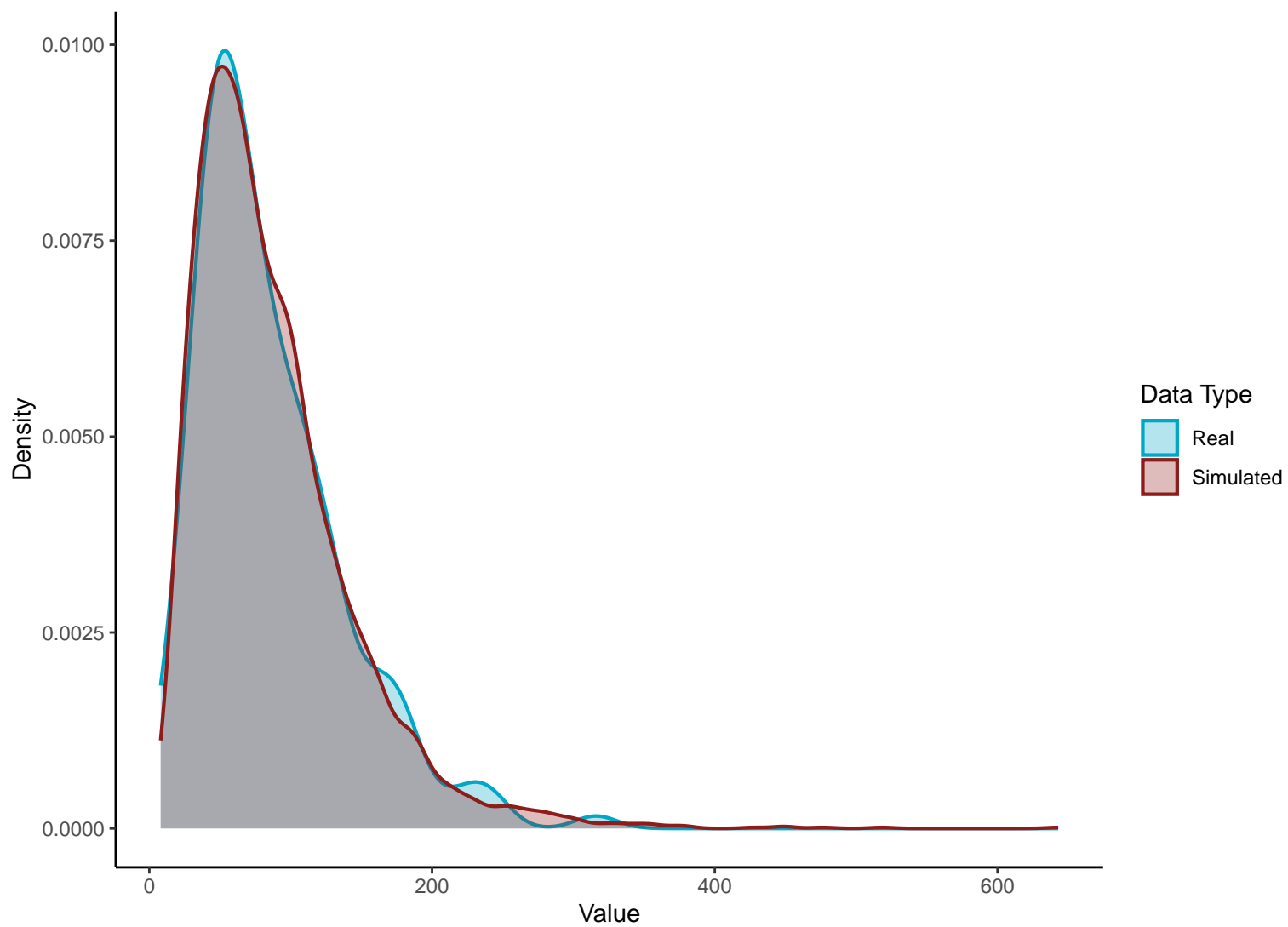
Lachnospiraceae.NK3A20.group



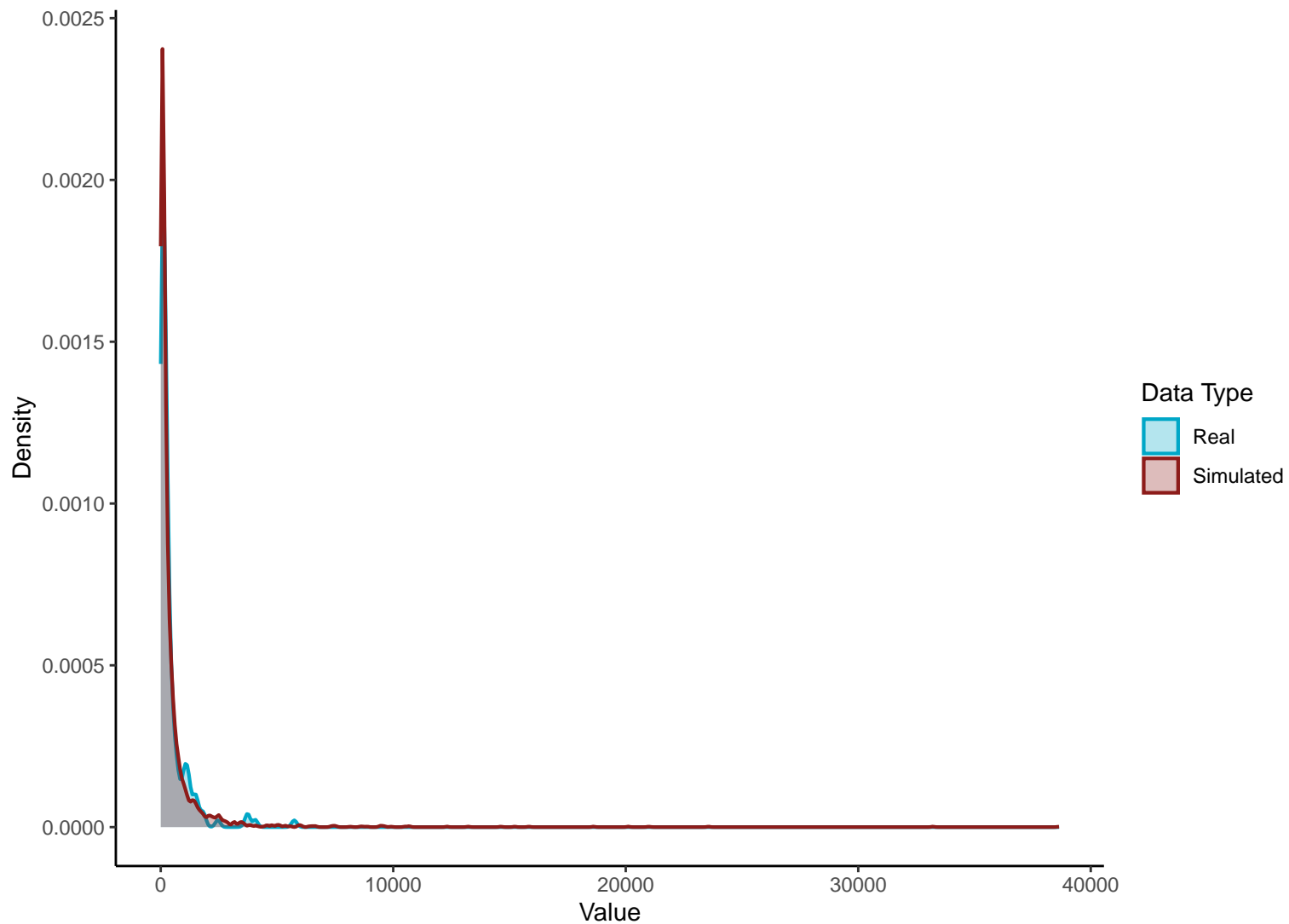
Lachnospiraceae.FCS020.group



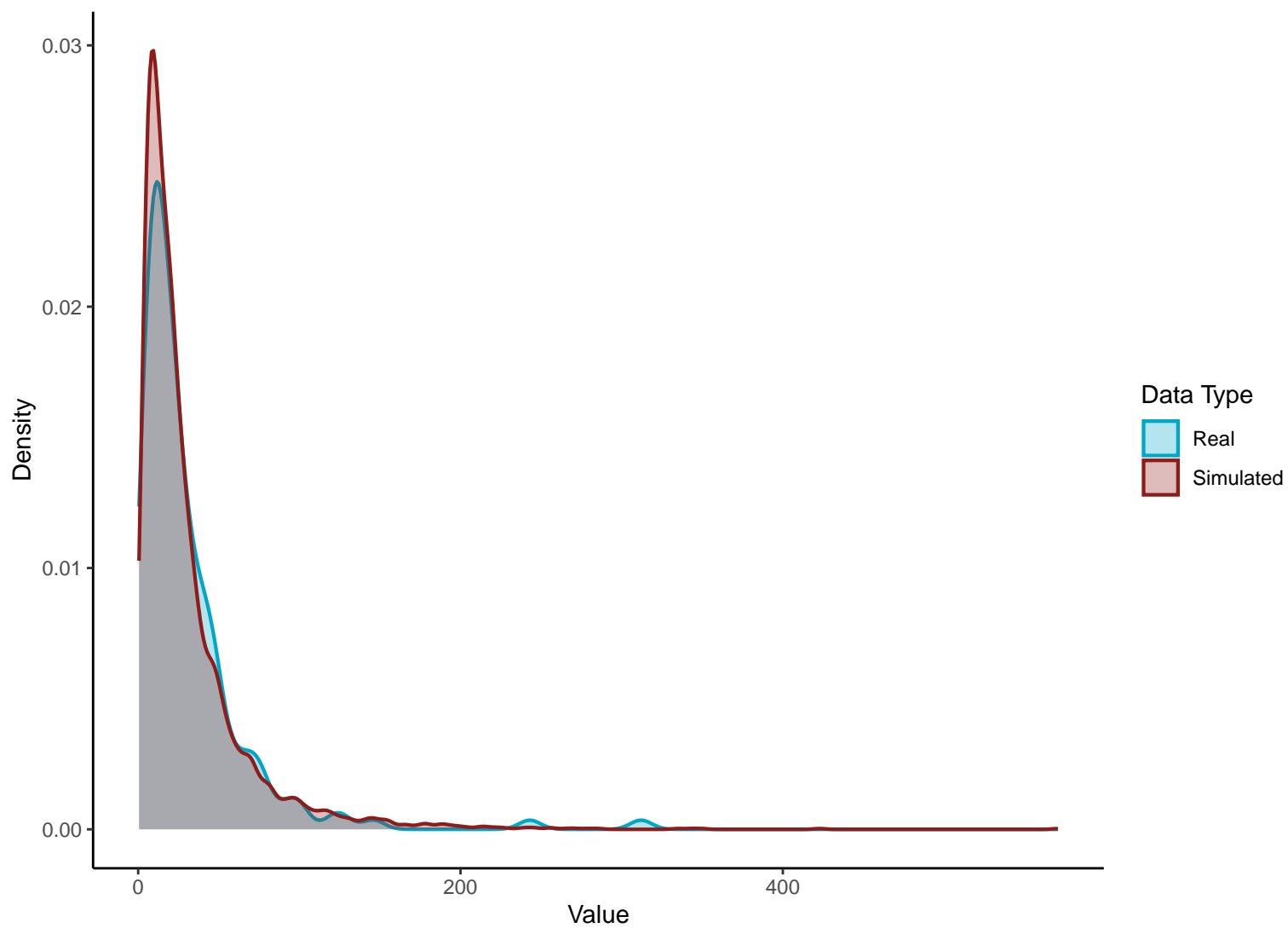
Incertae.Sedis



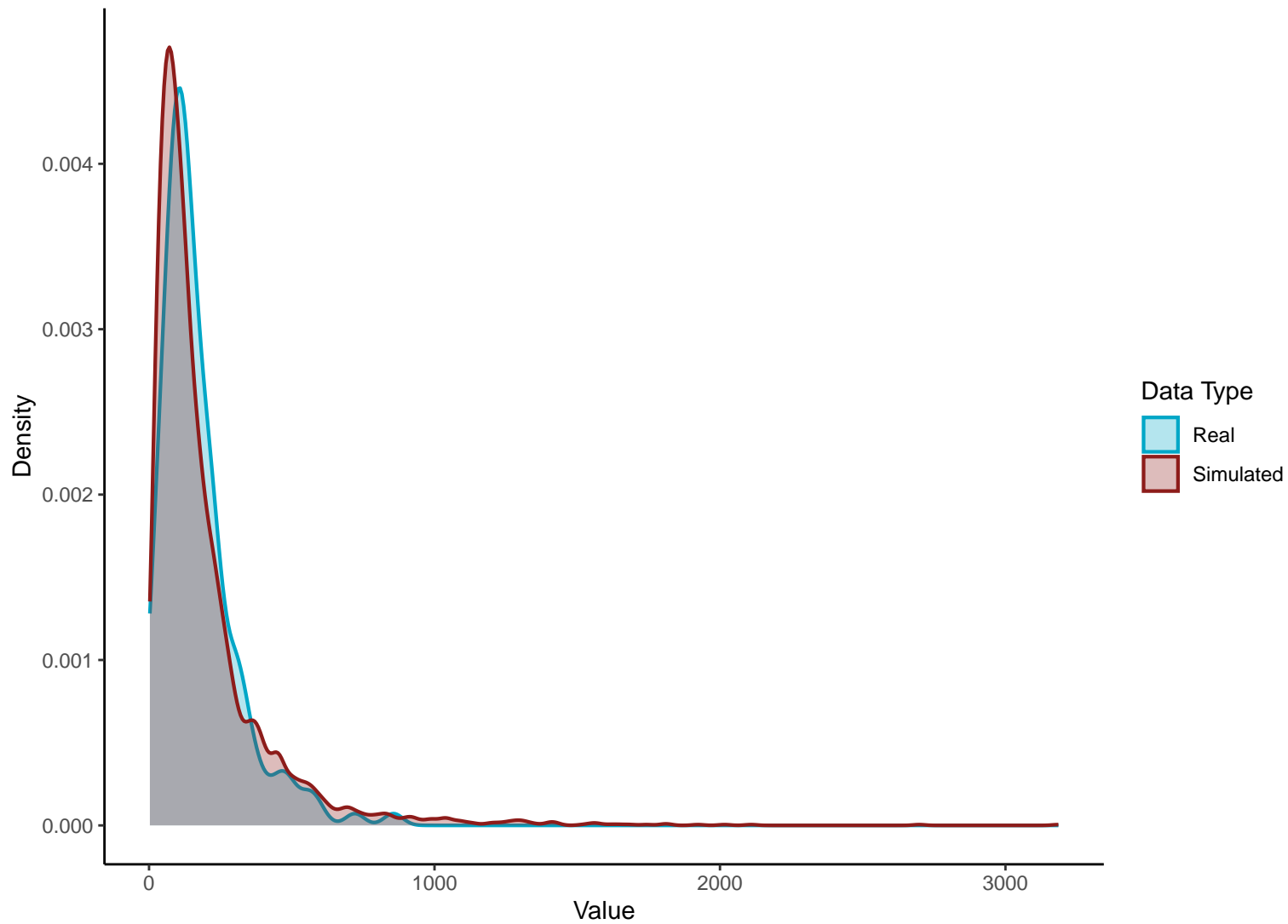
Limosilactobacillus



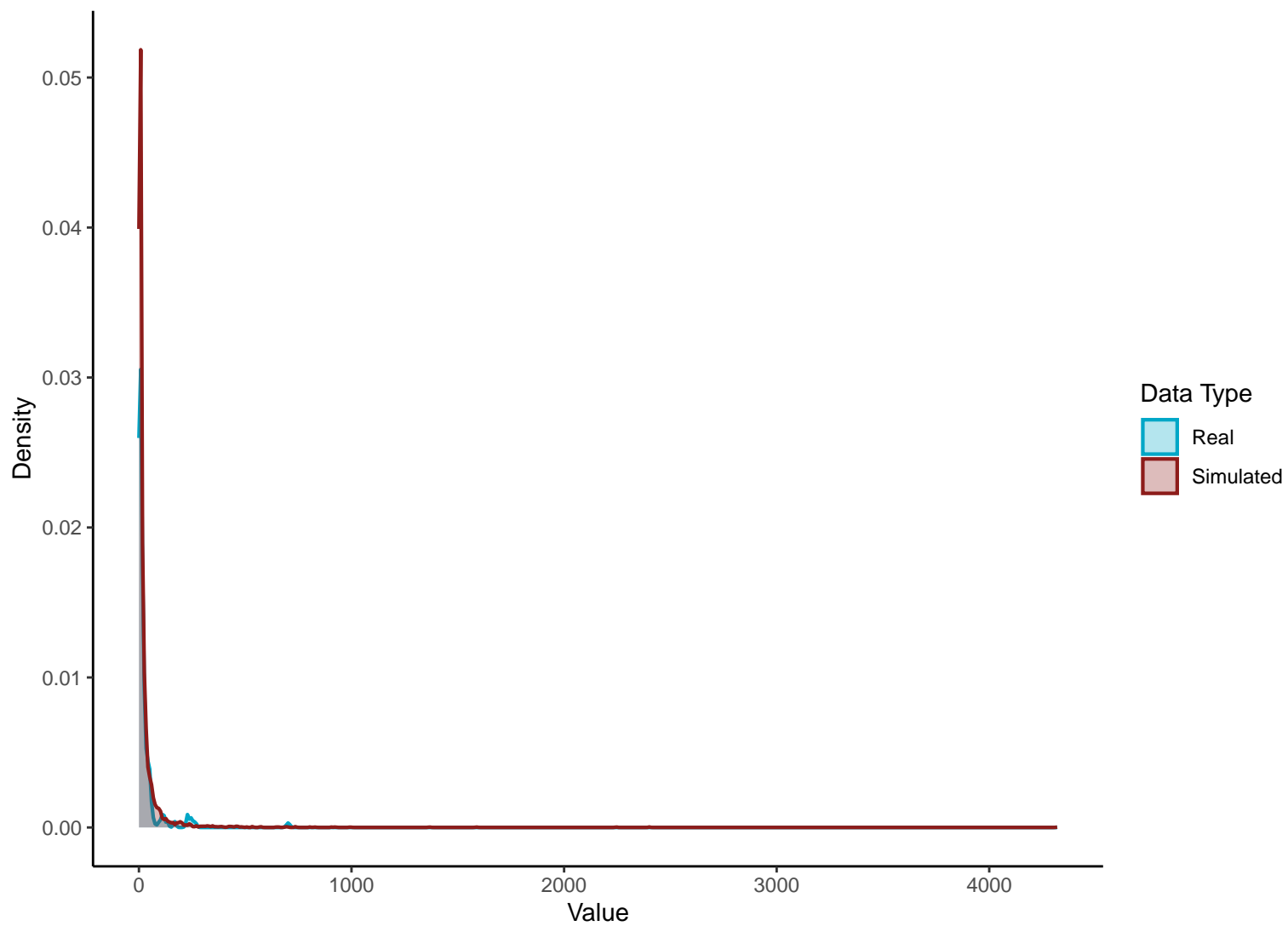
Desulfovibrio



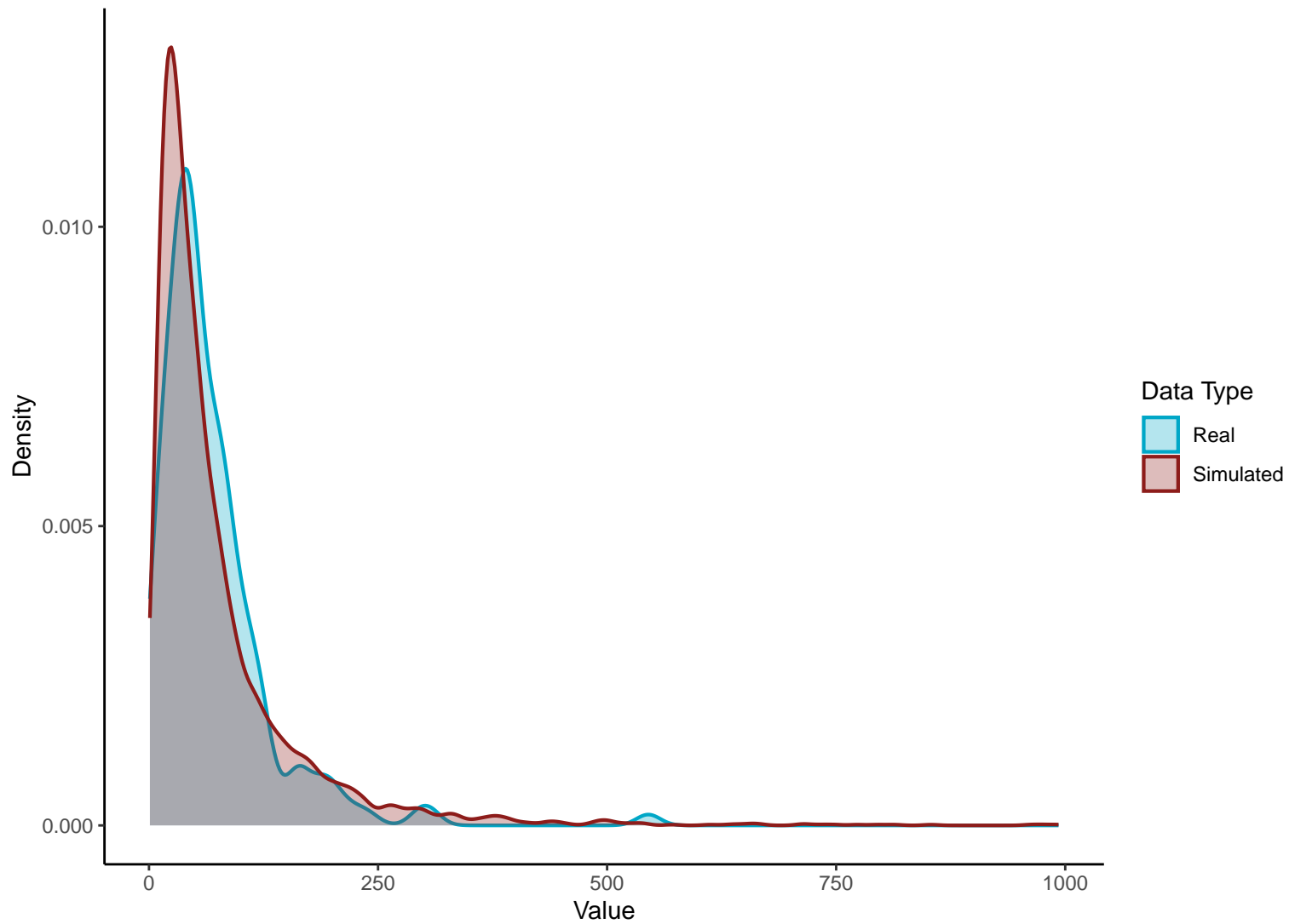
X.Eubacterium..ruminantium.group



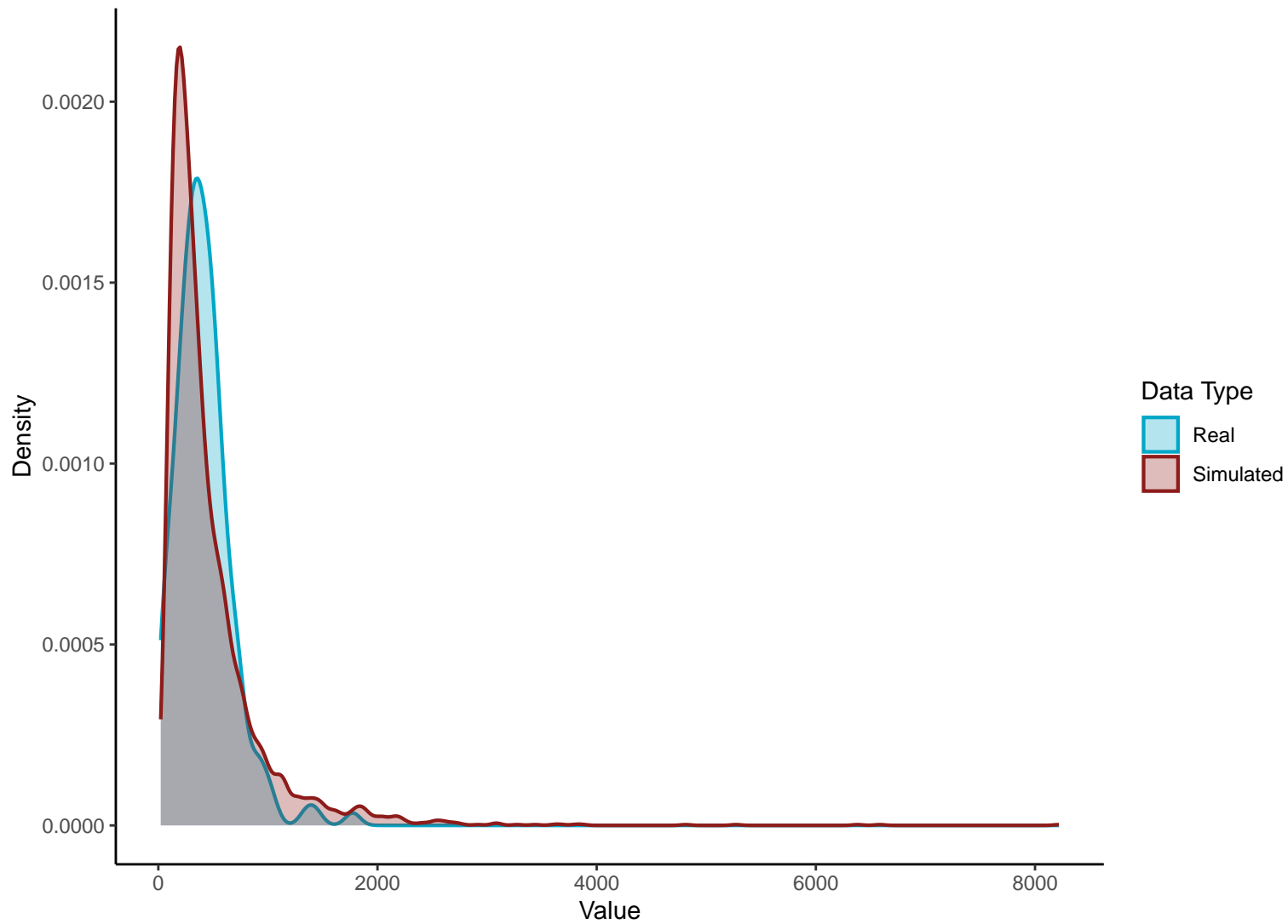
Prevotellaceae.UGC.001



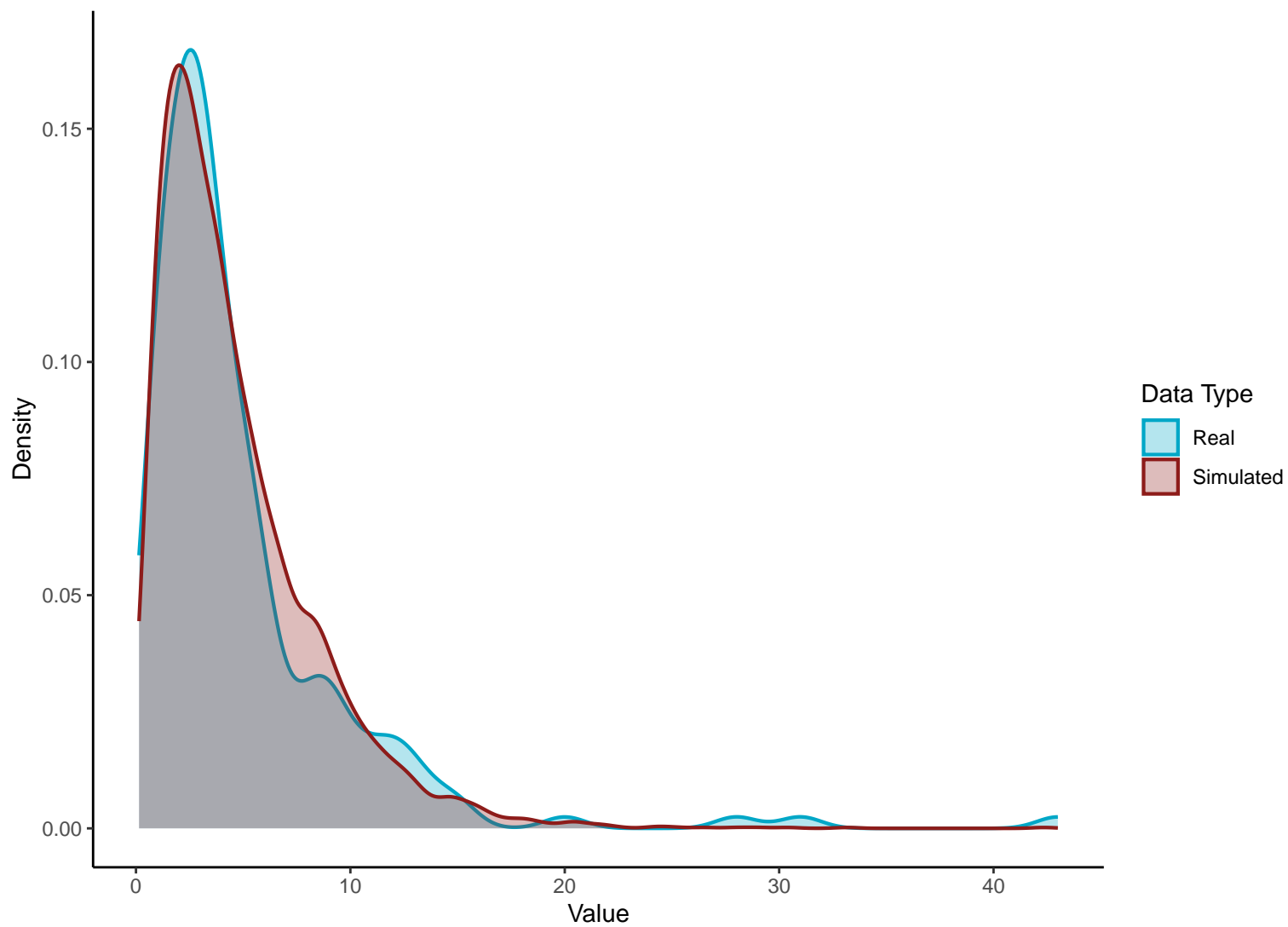
Lachnospiraceae.NK4B4.group



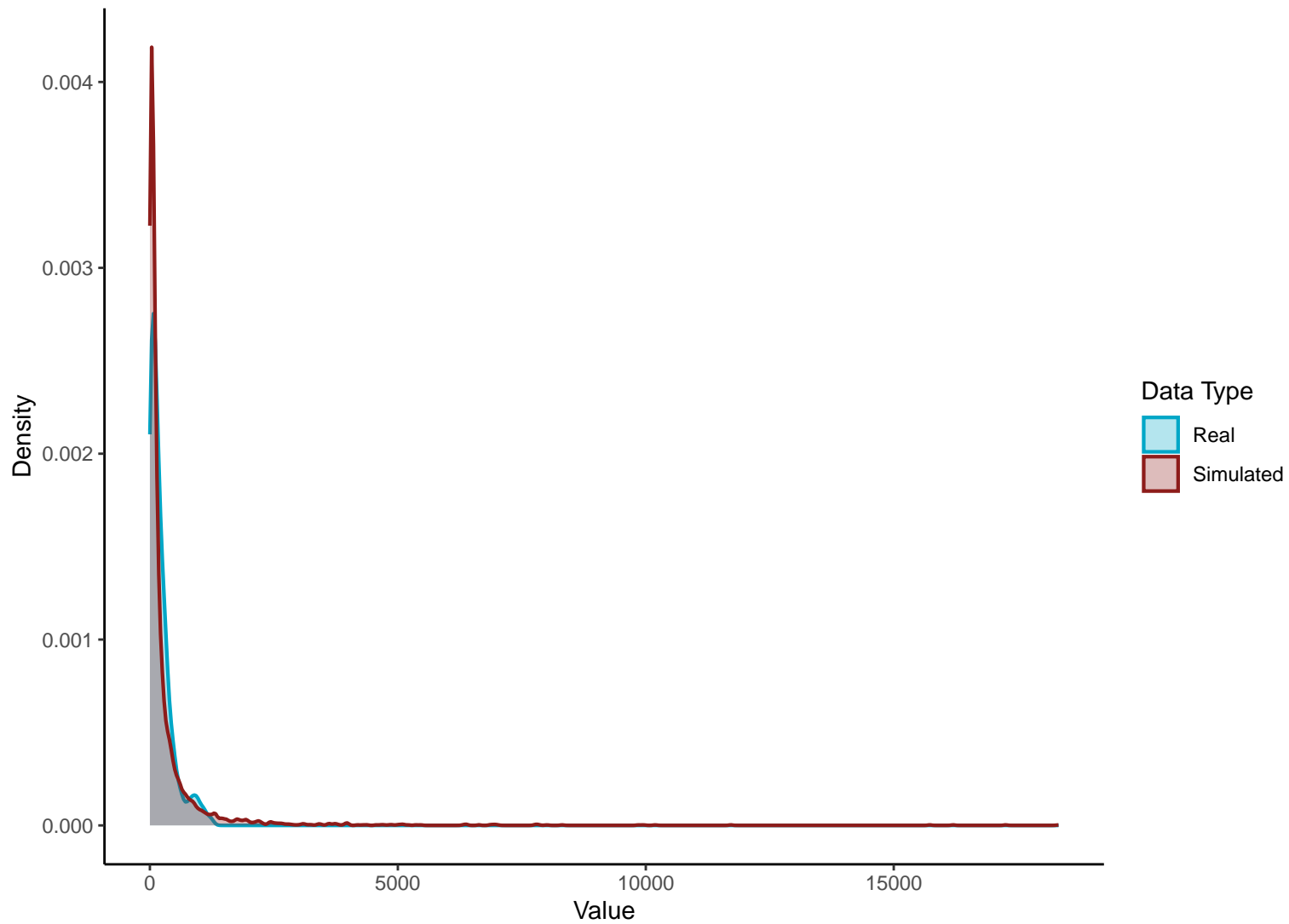
Holdemanella



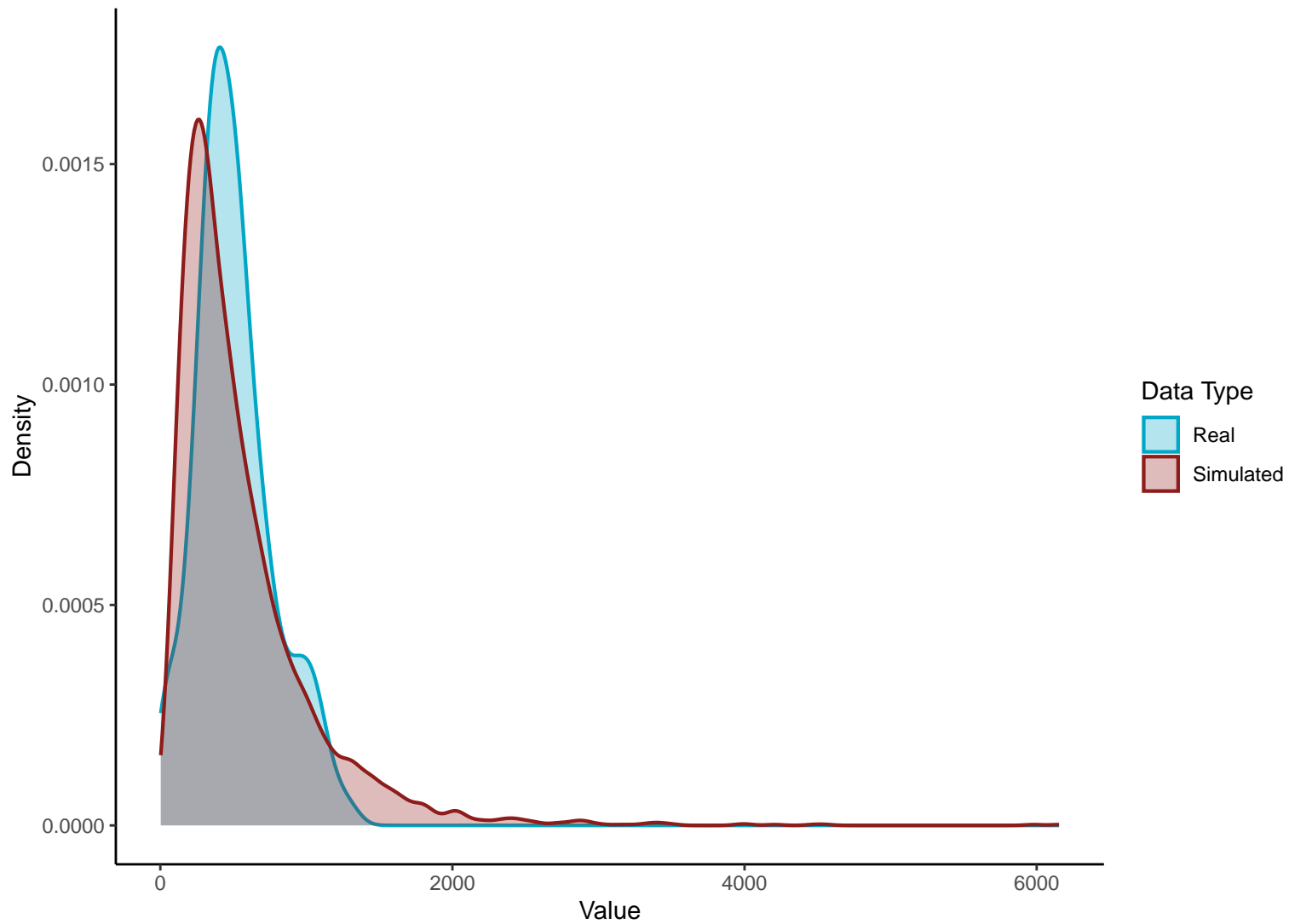
Papillibacter



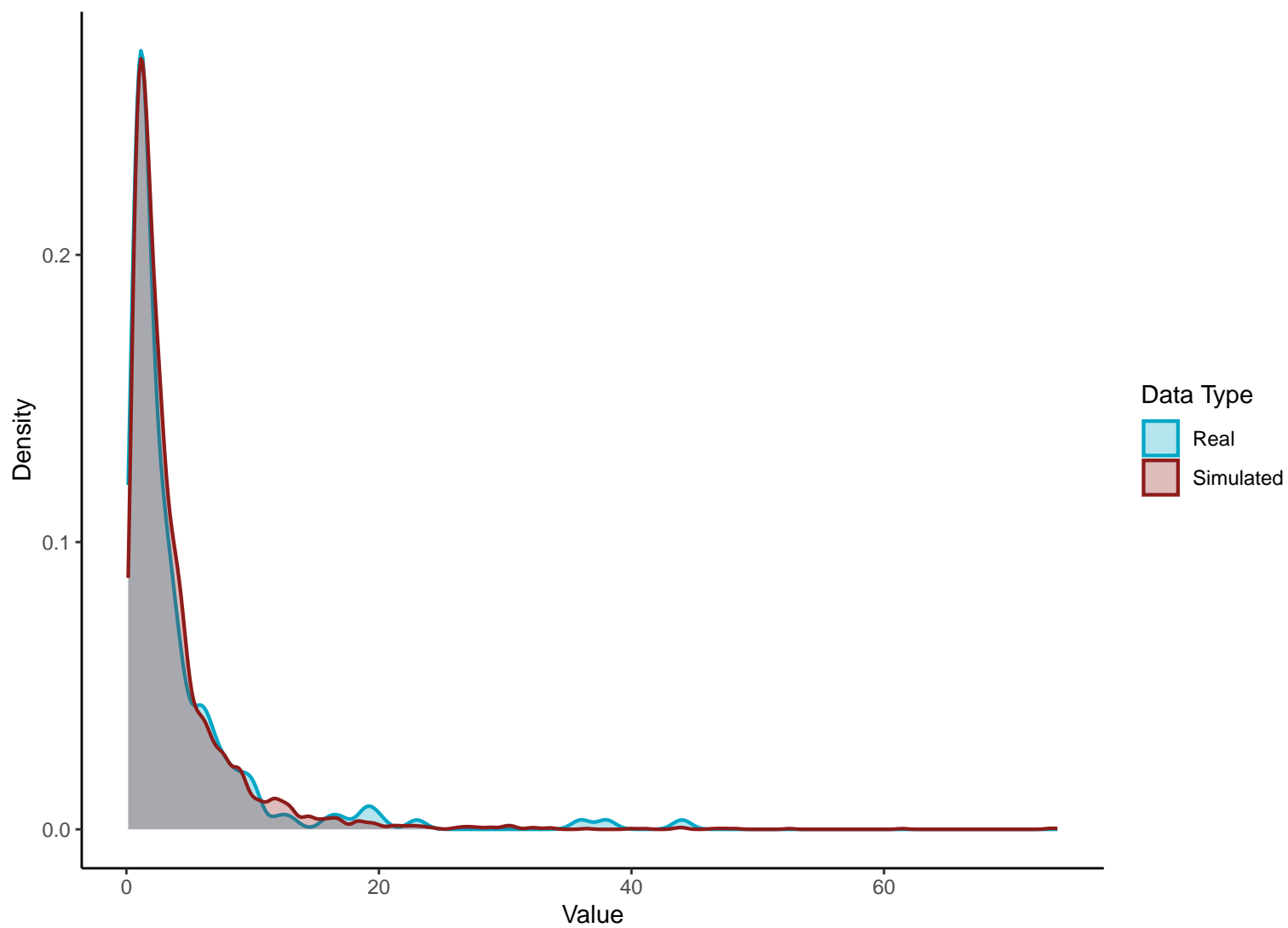
Lachnospiraceae.AC2044.group



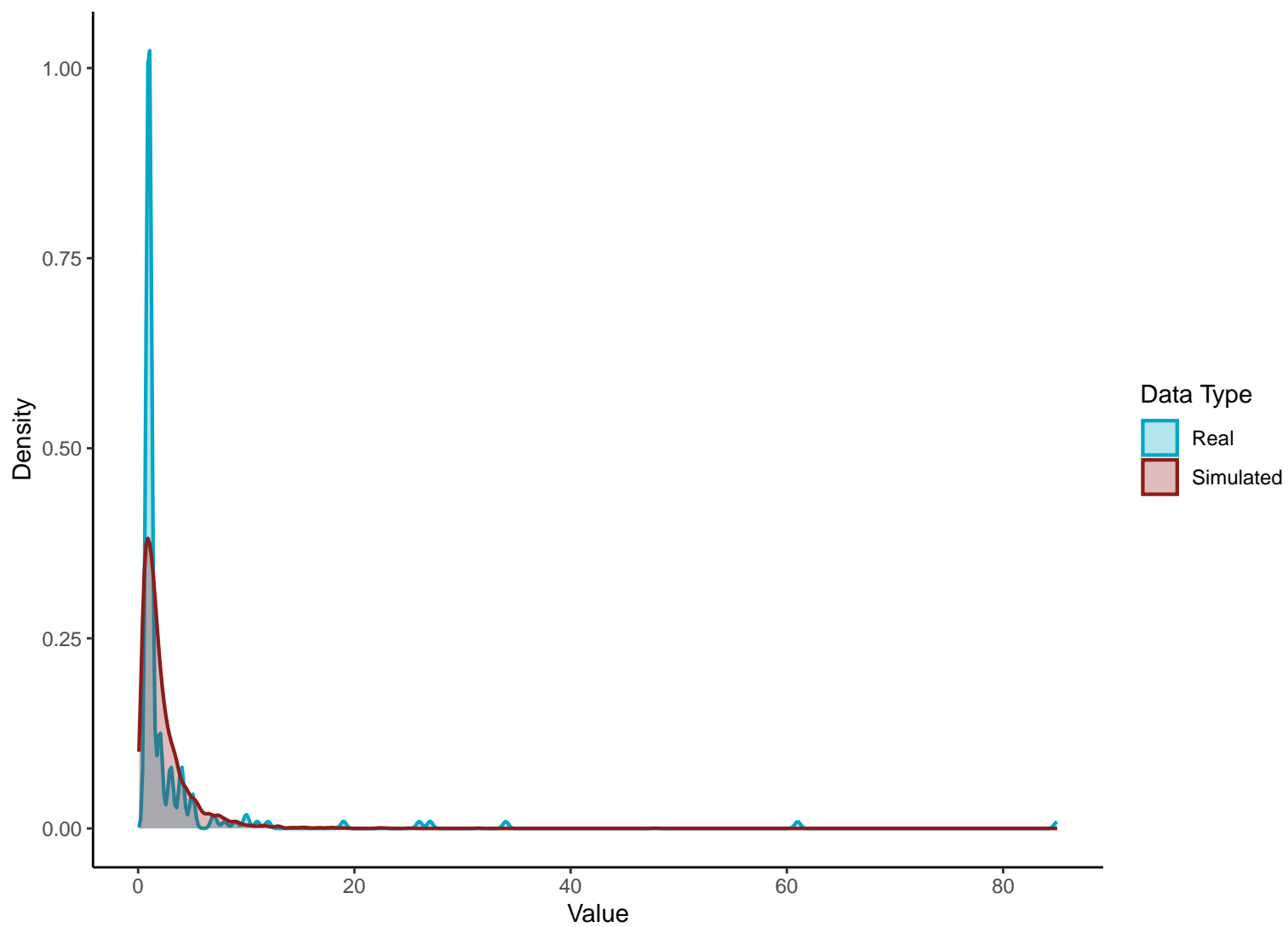
Phascolarctobacterium



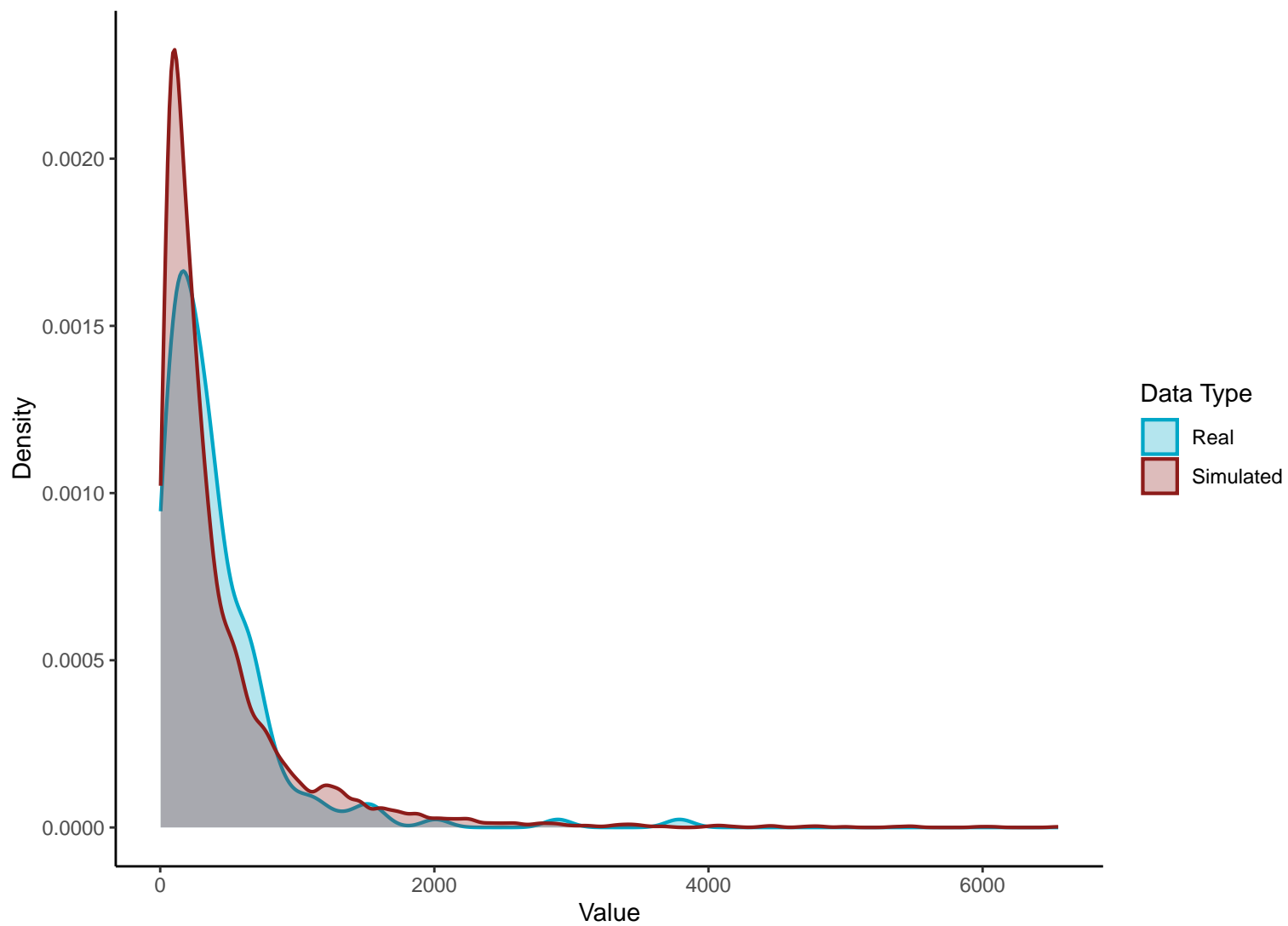
Fibrobacter



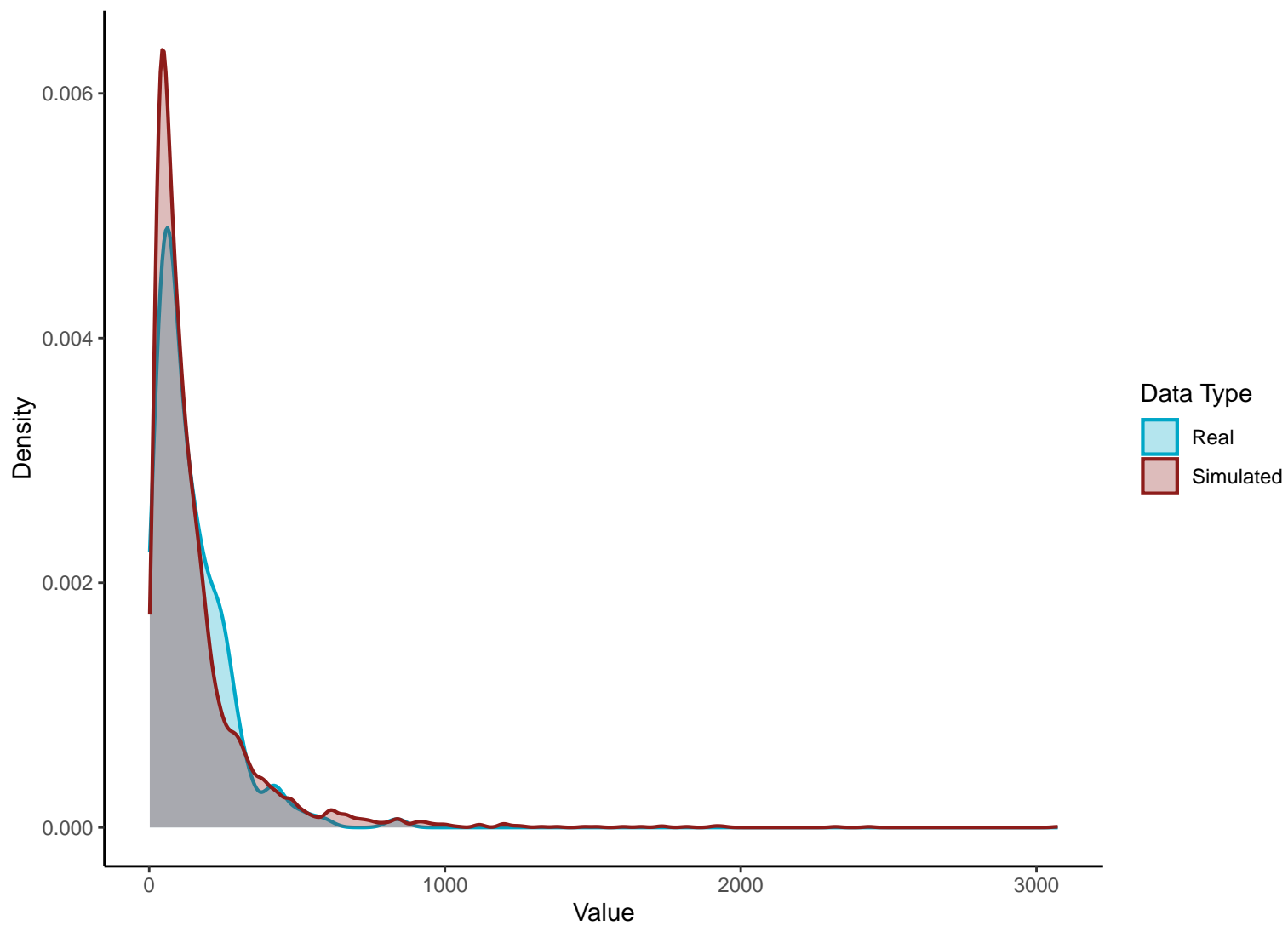
Akkermansia



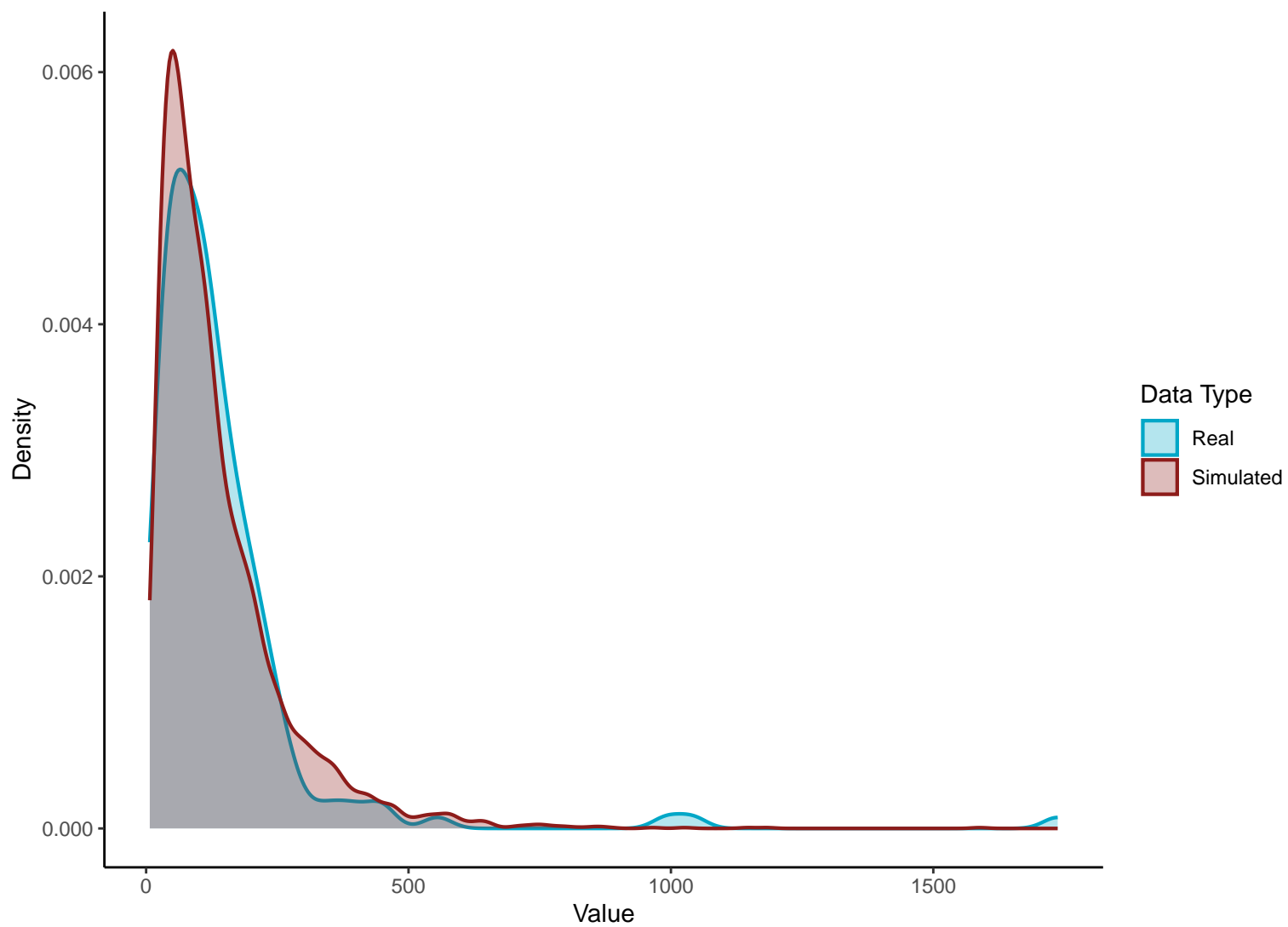
UCG.002



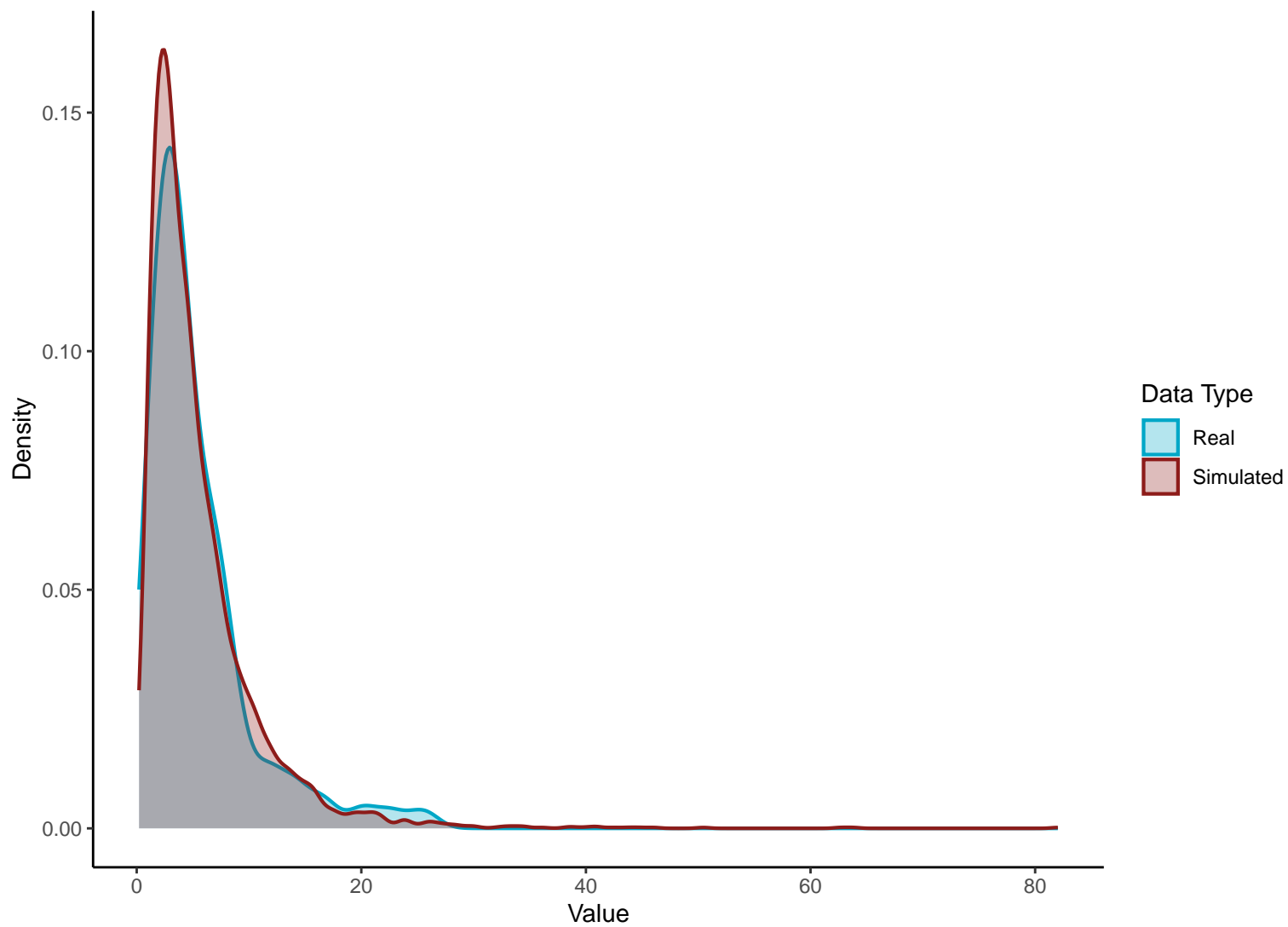
Olsenella



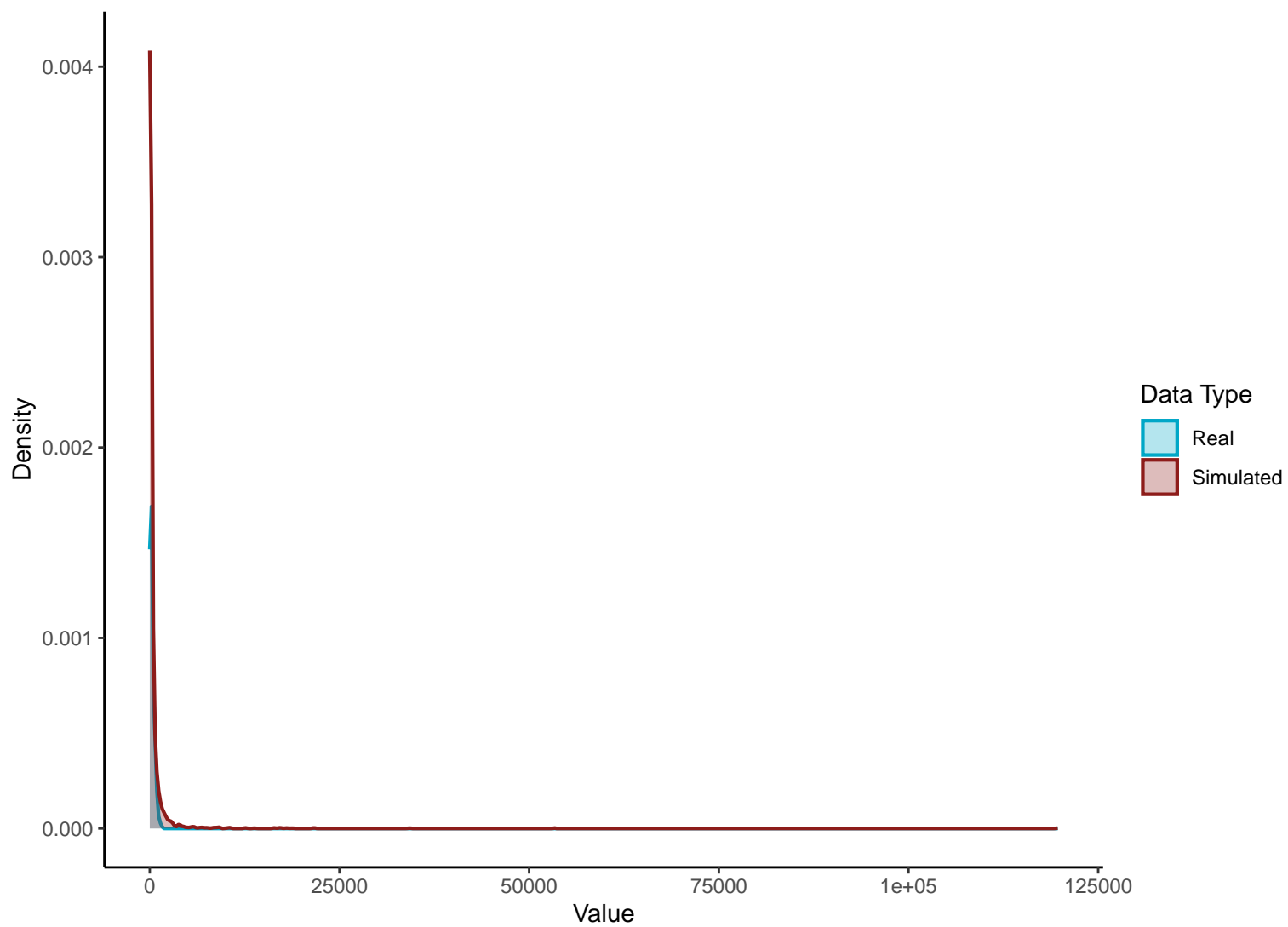
Shuttleworthia



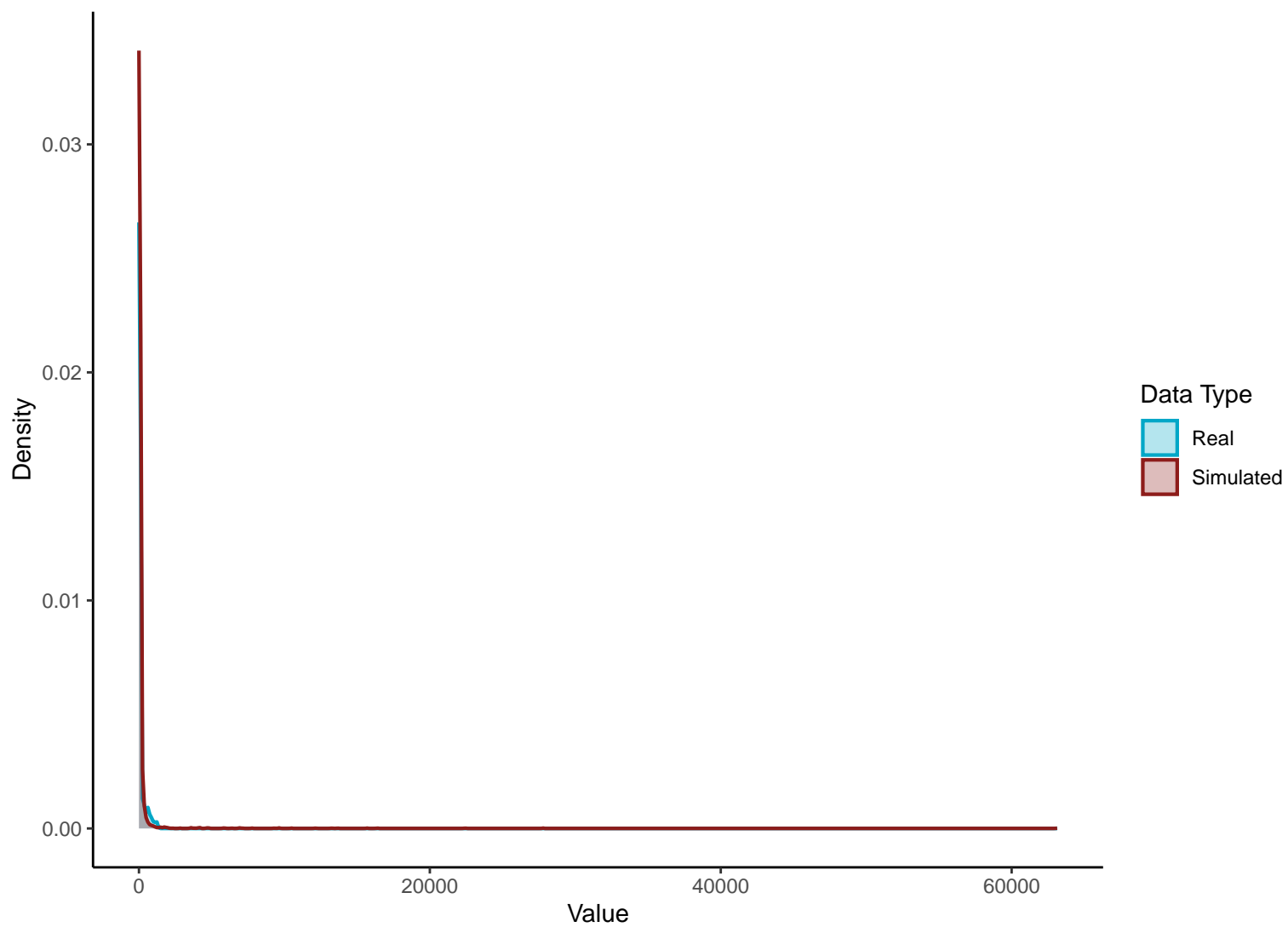
Pygmaibacter



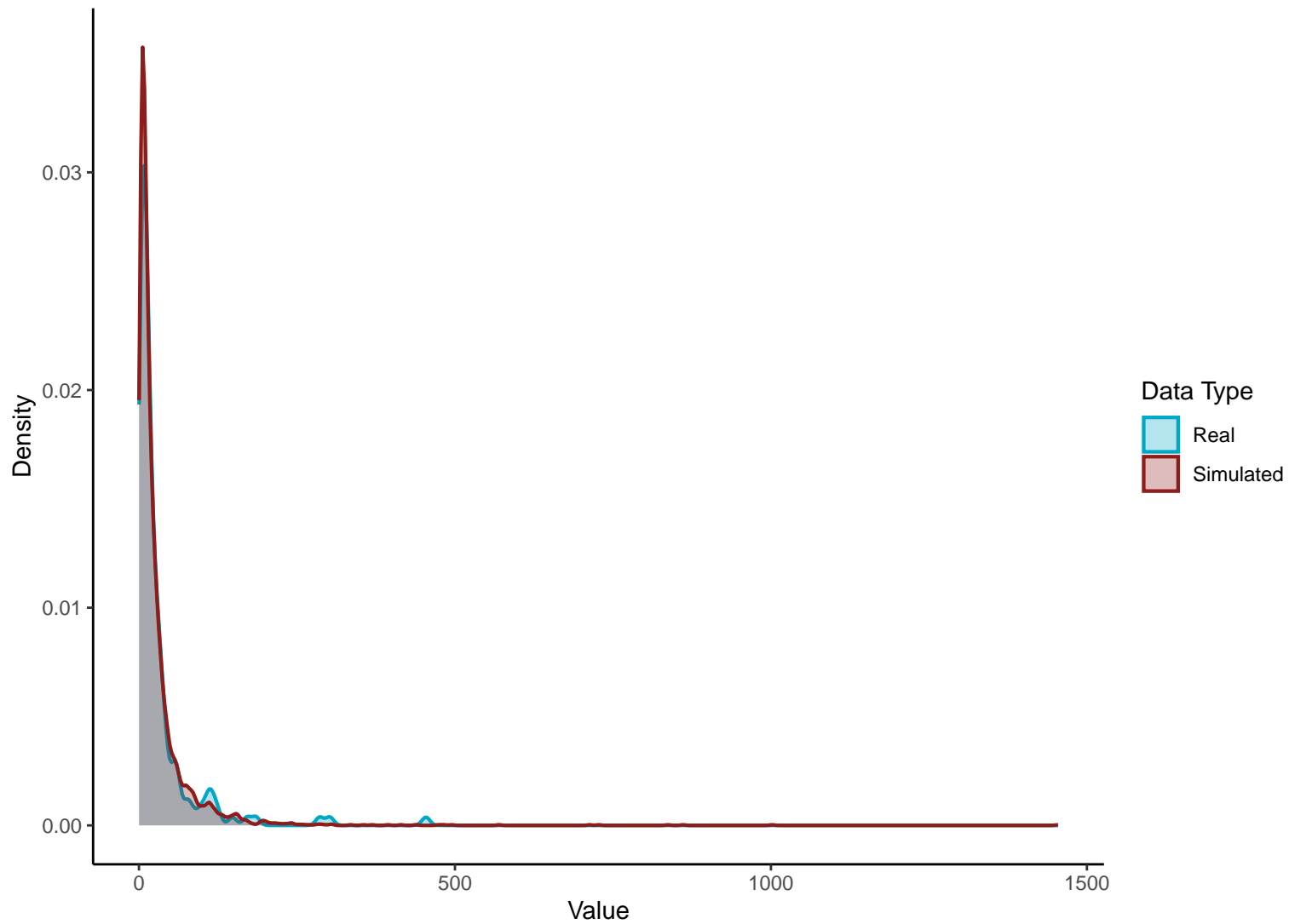
Dialister



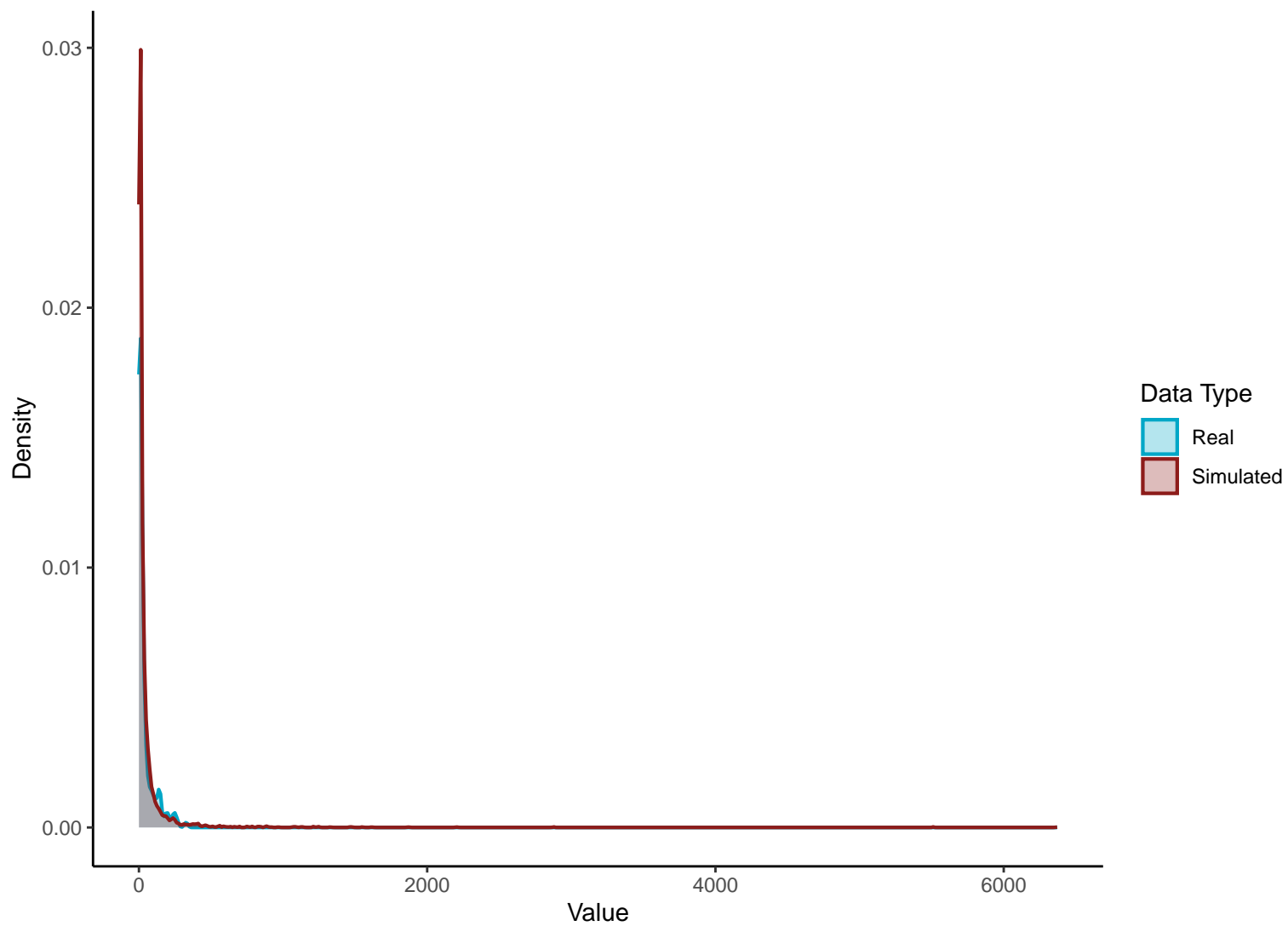
Acetitomaculum



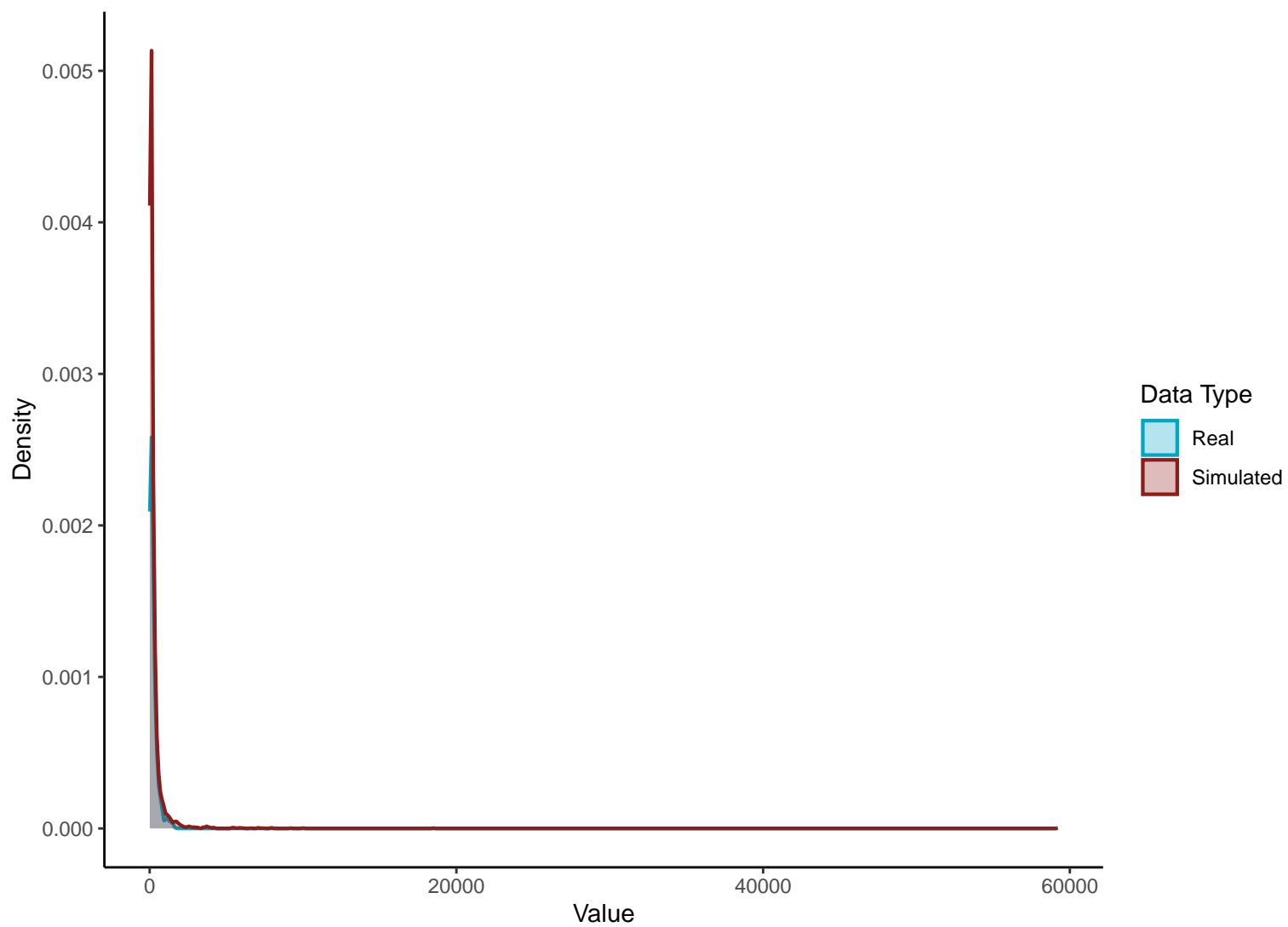
Campylobacter



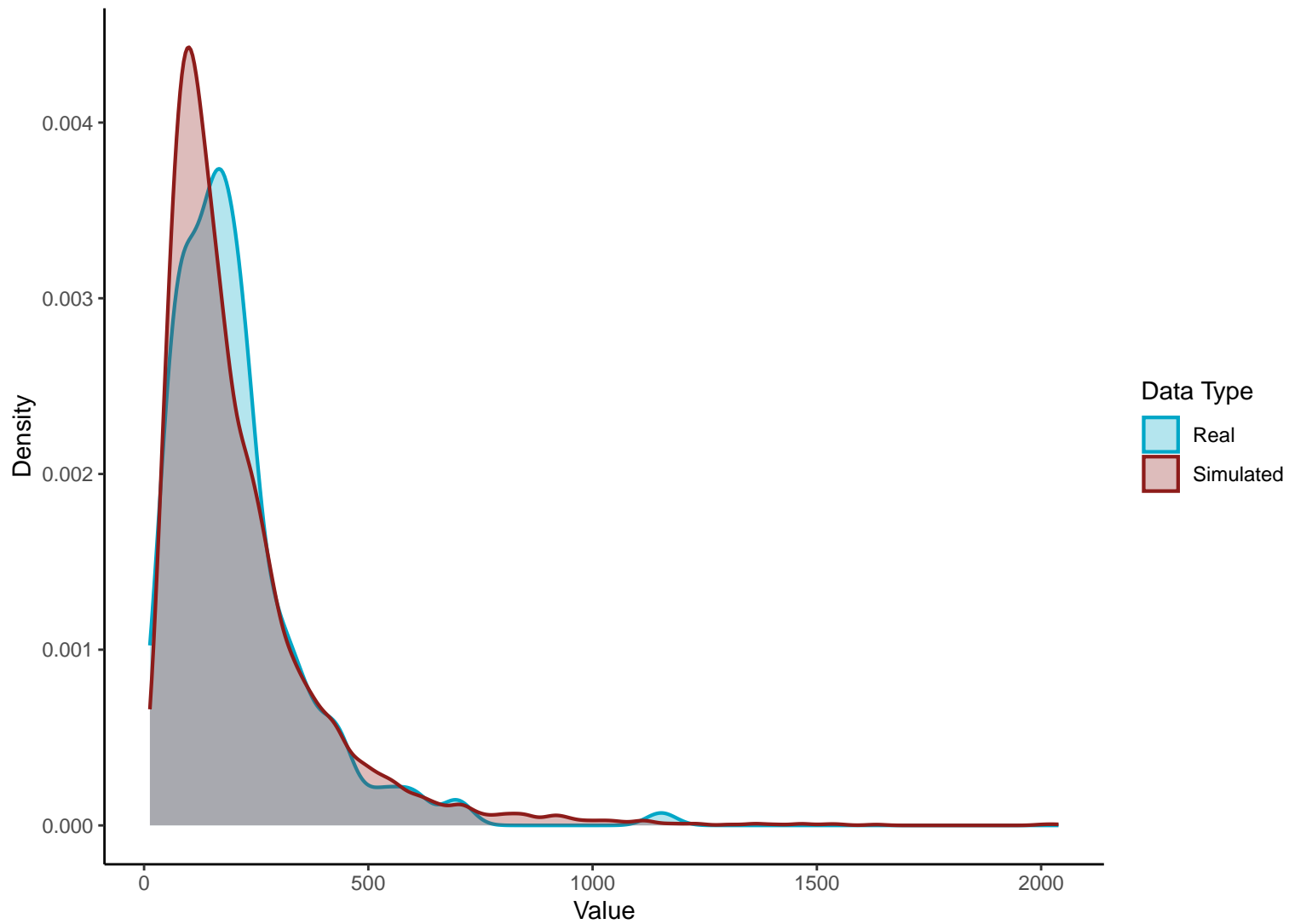
Anaerosporobacter



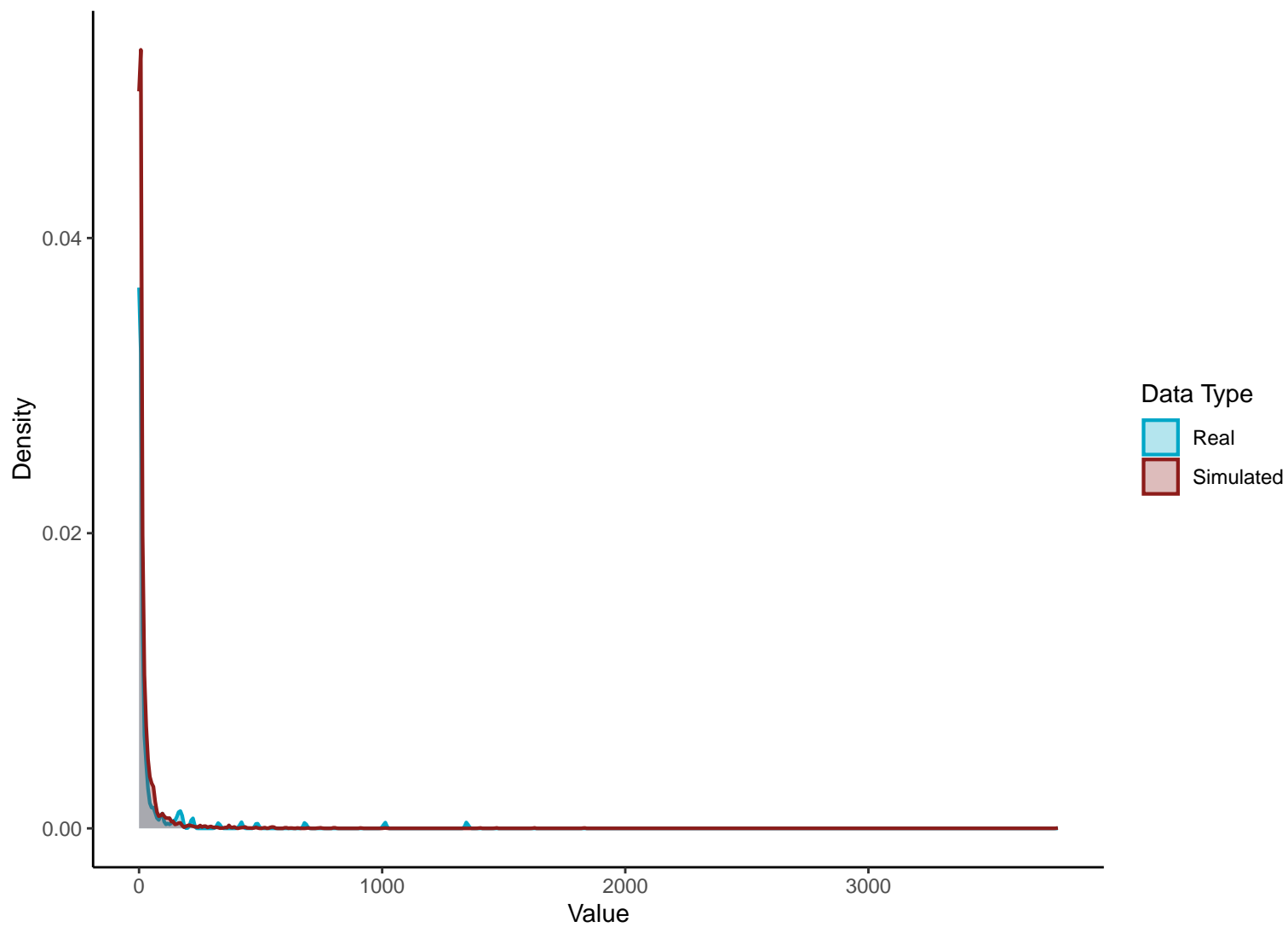
Anaerostipes



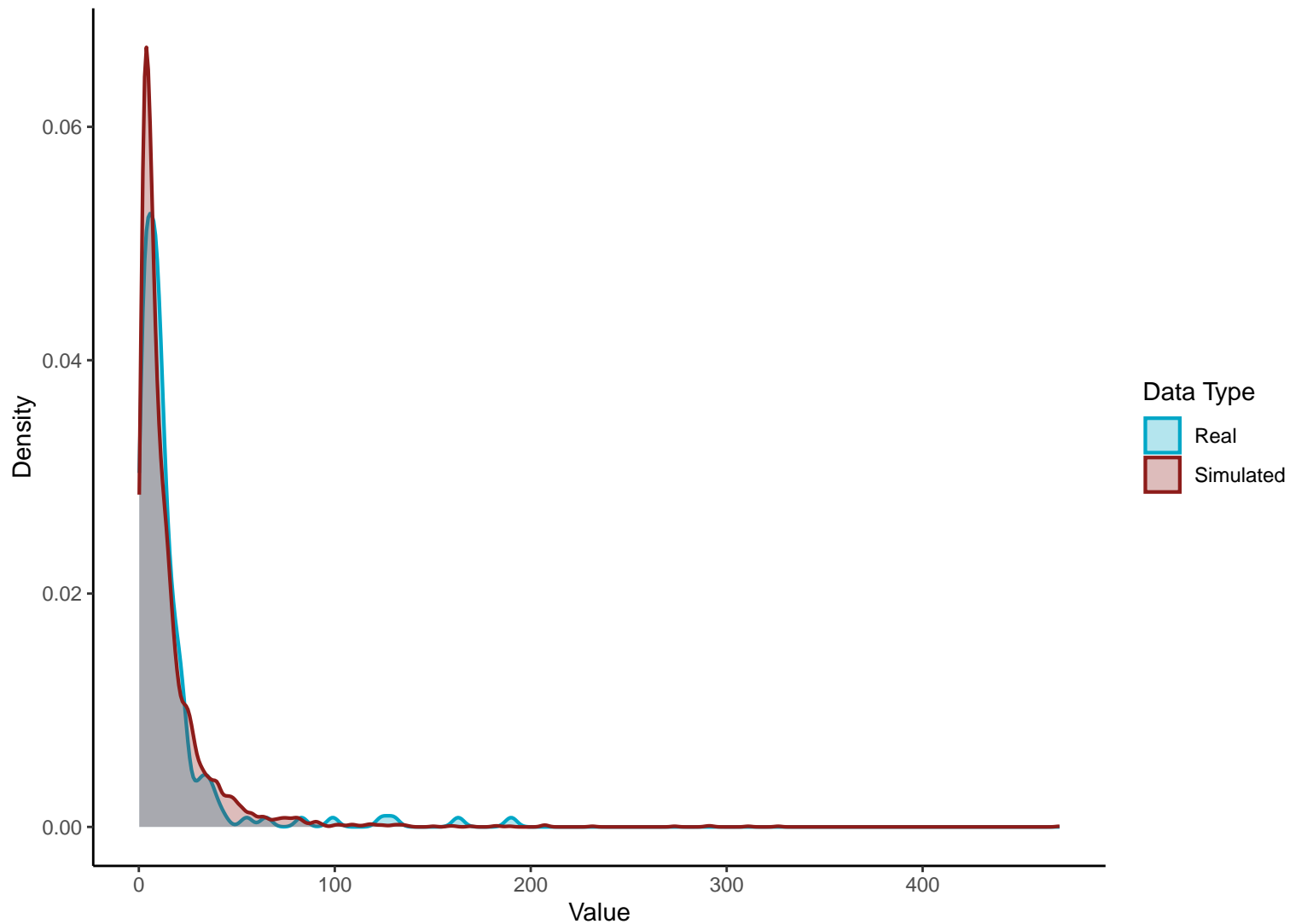
Collinsella



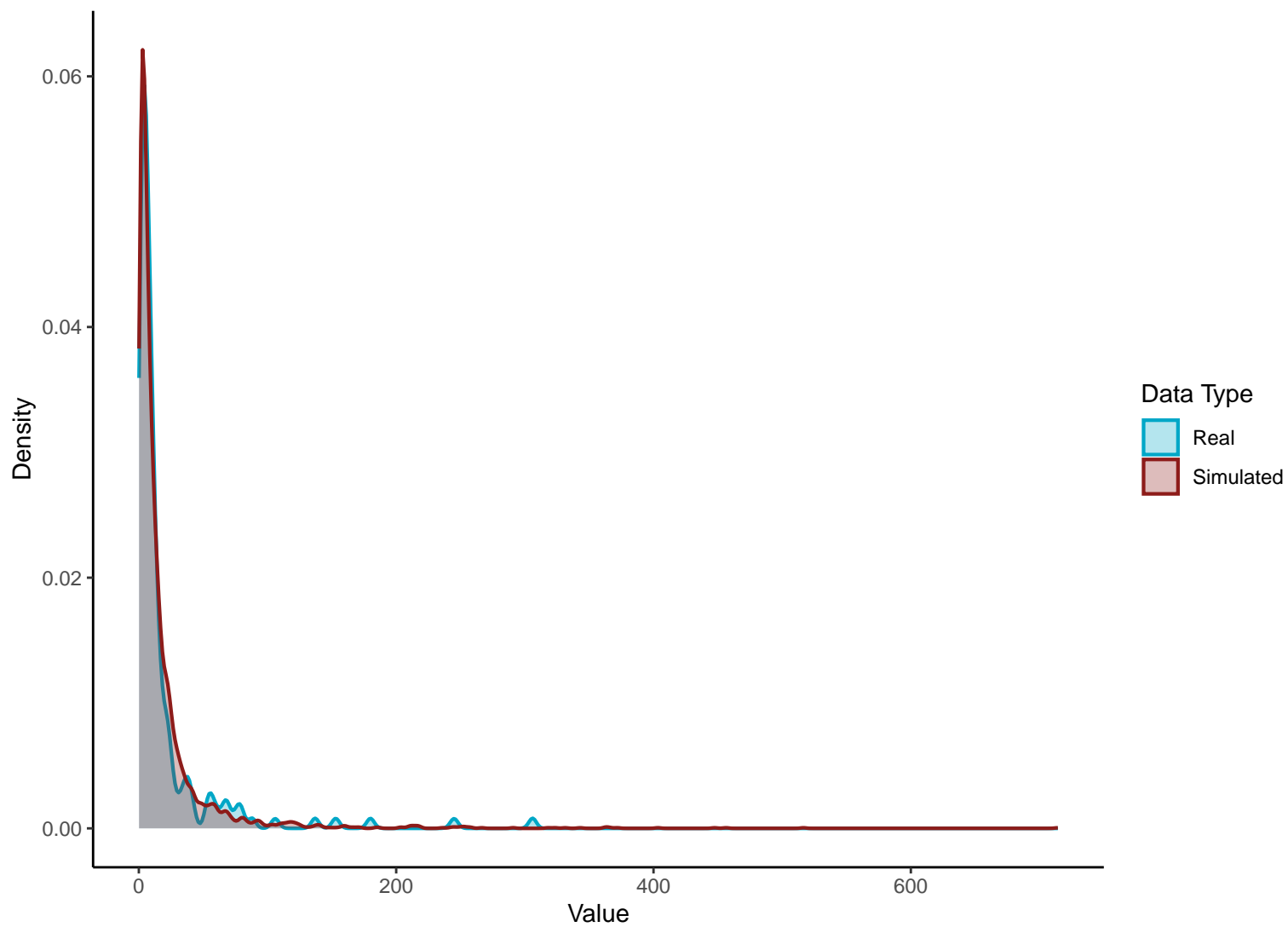
Sarcina



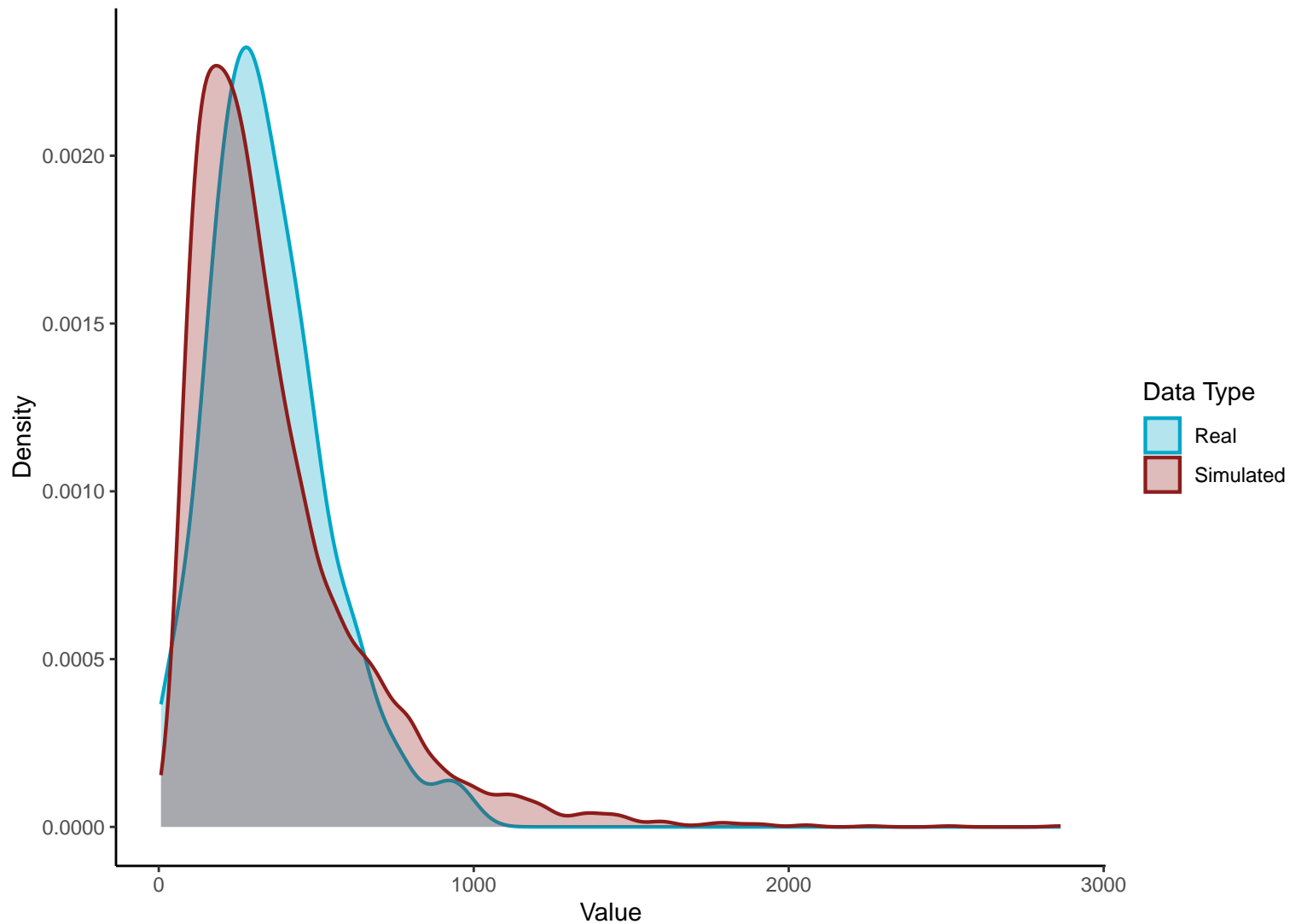
X.Eubacterium..eligens.group



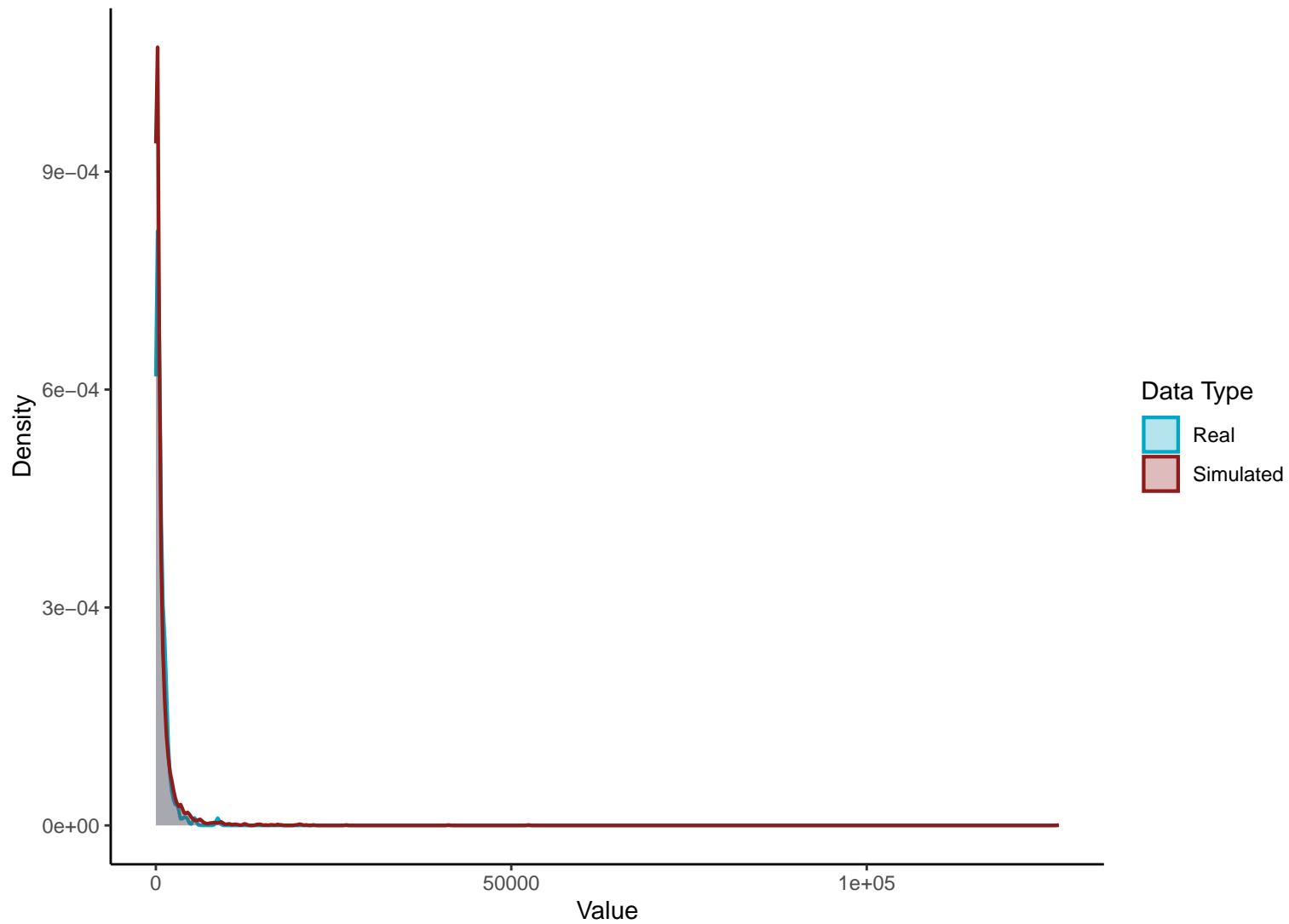
Corynebacterium



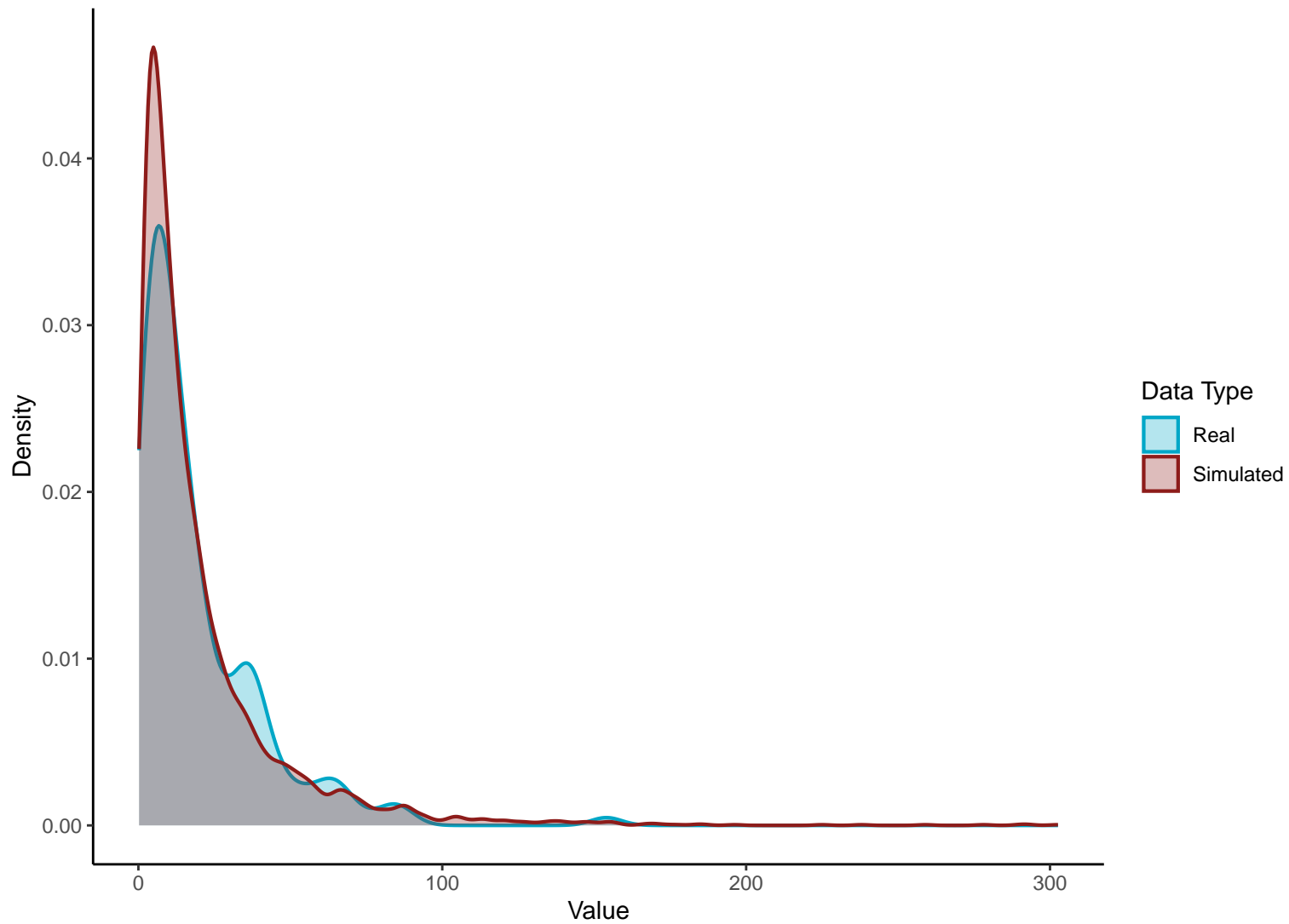
X.Ruminococcus..gauvreauii.group



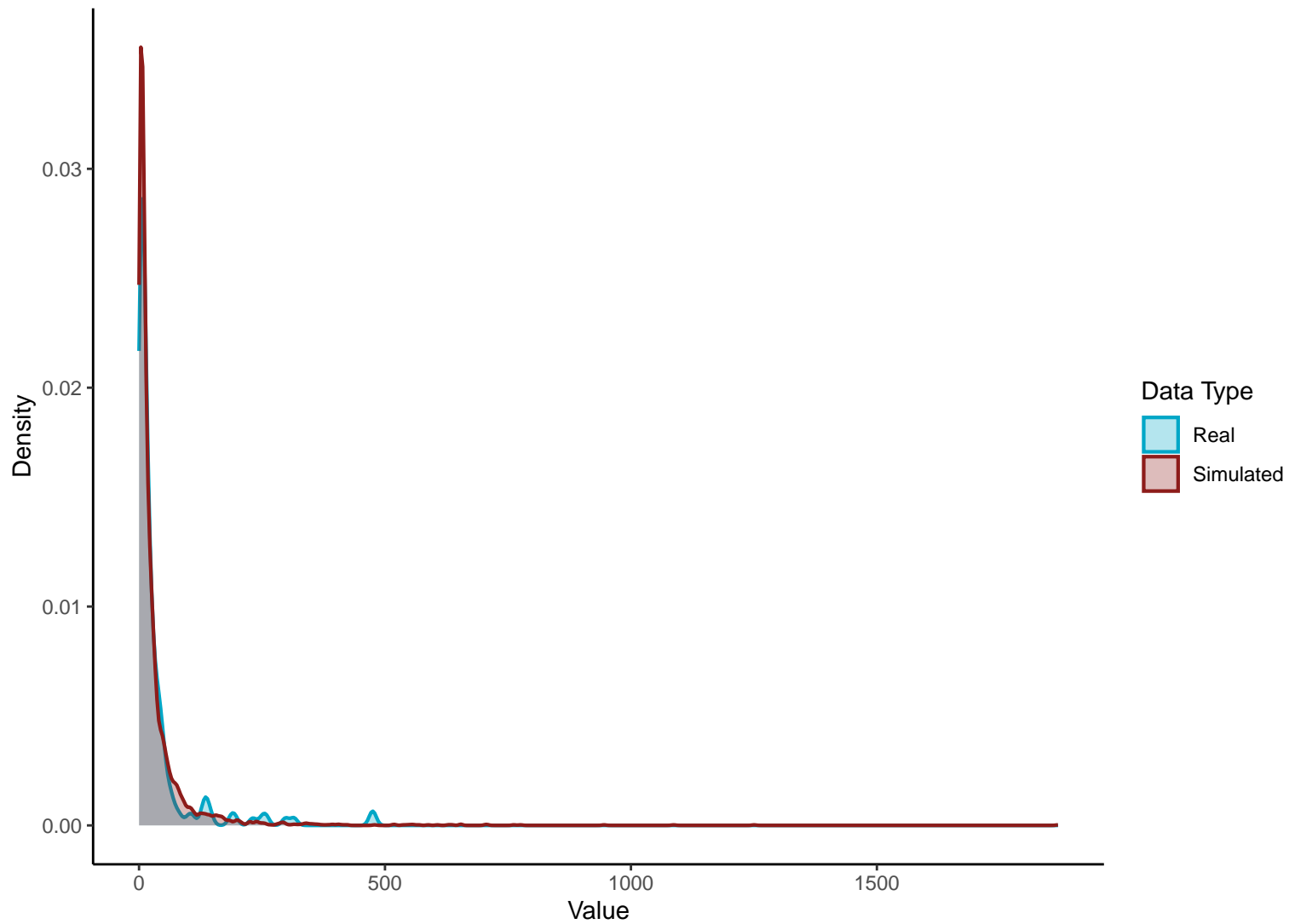
Megasphaera



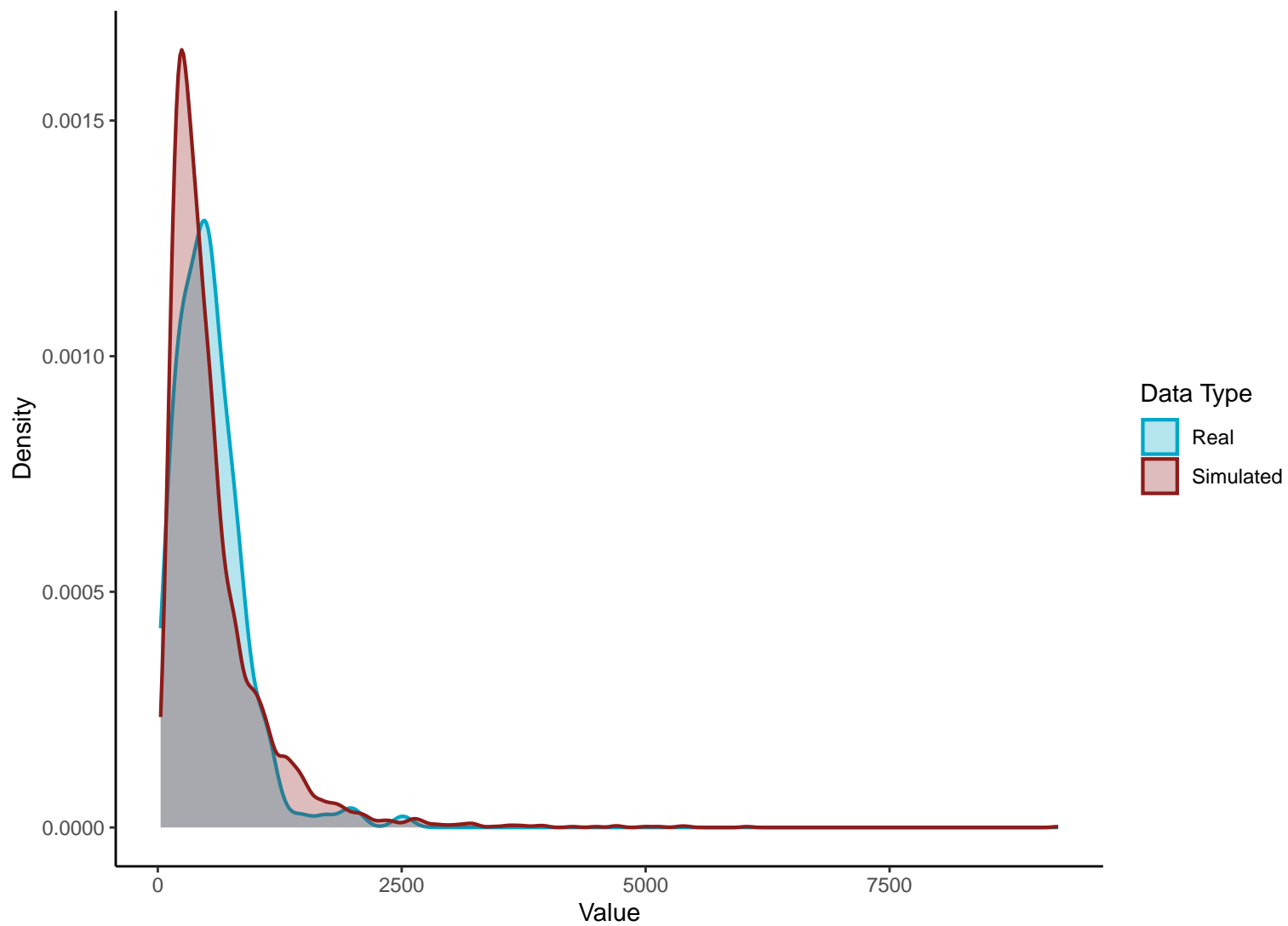
Candidatus.Saccharimonas



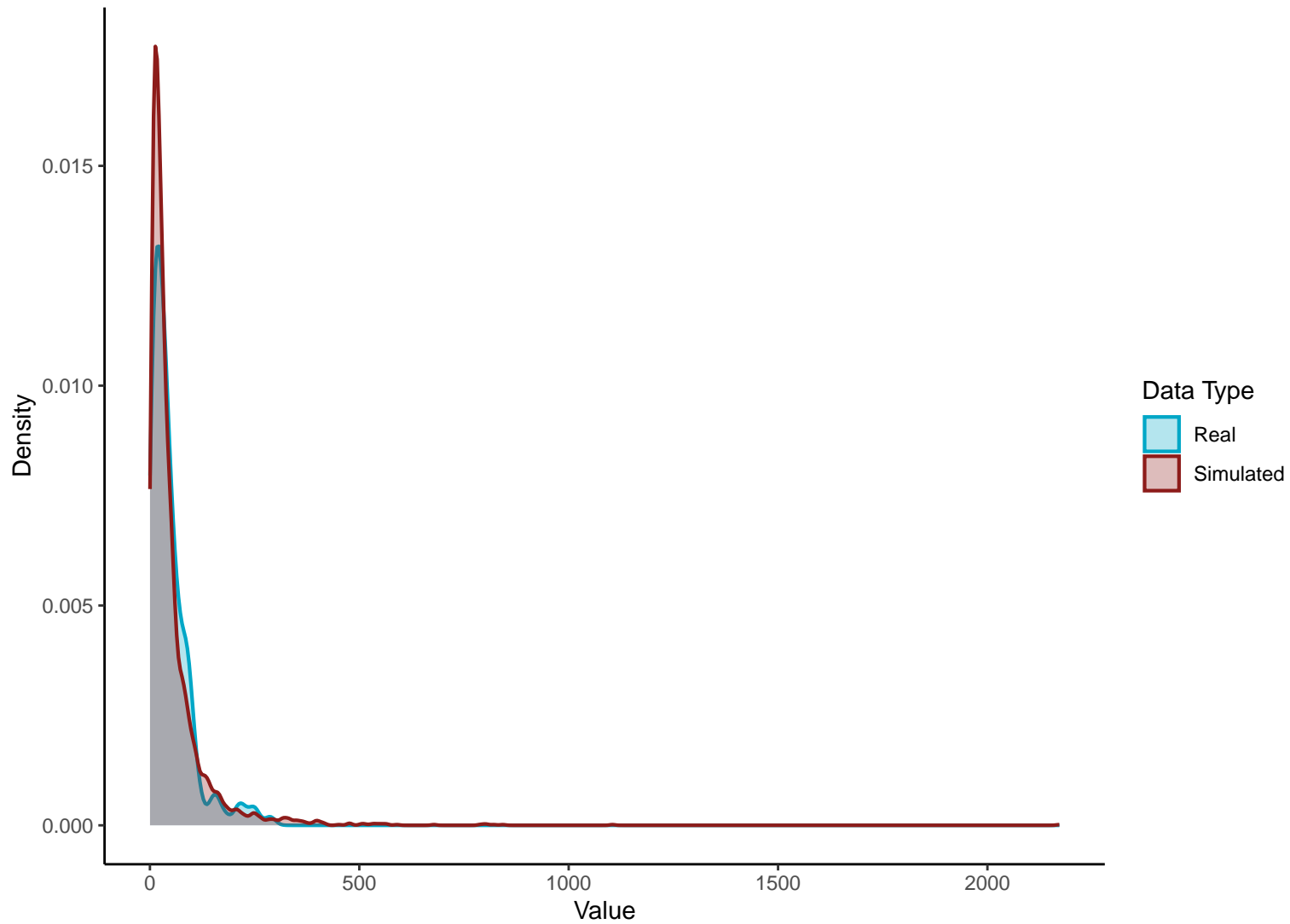
Lachnospira



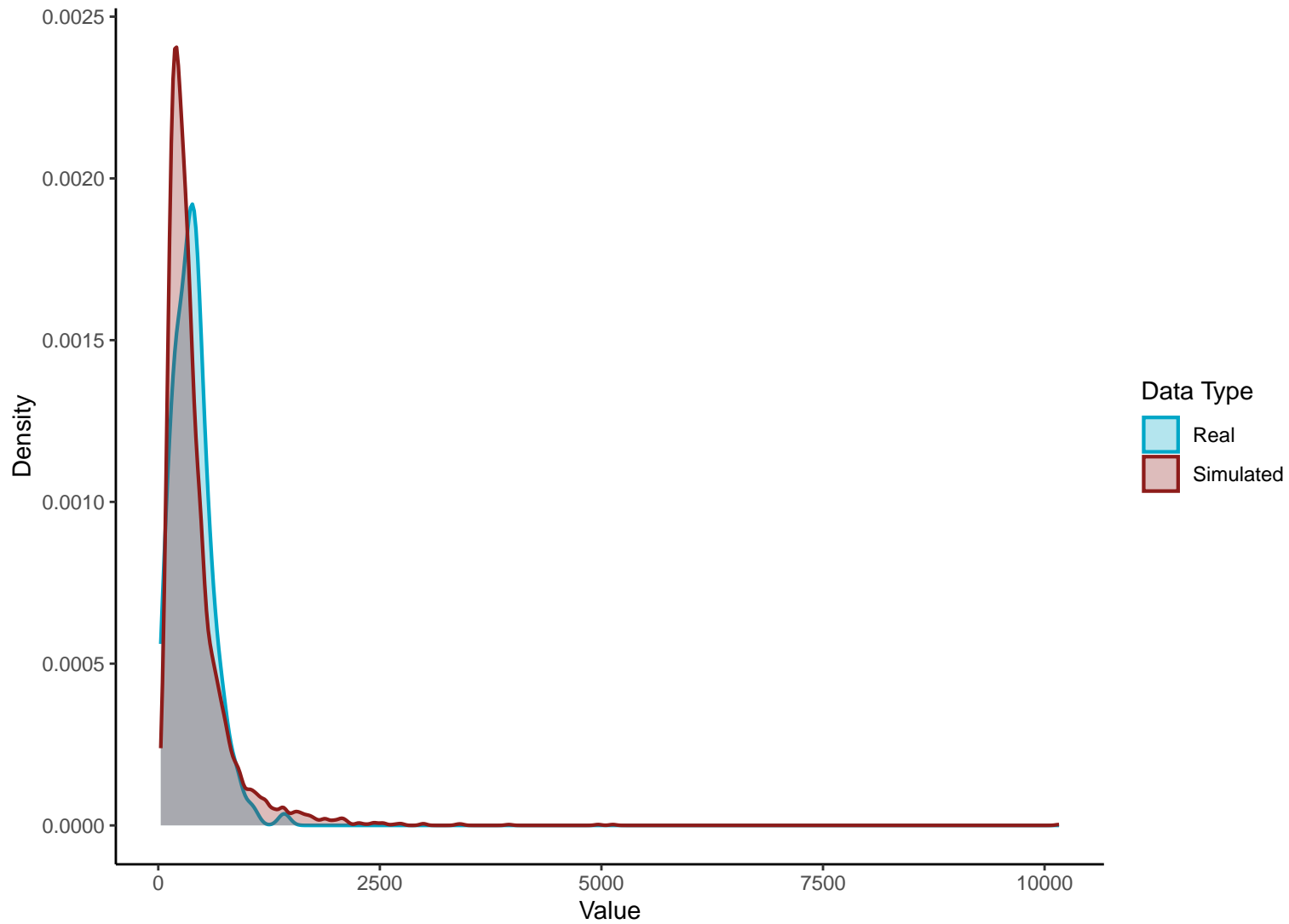
Dorea



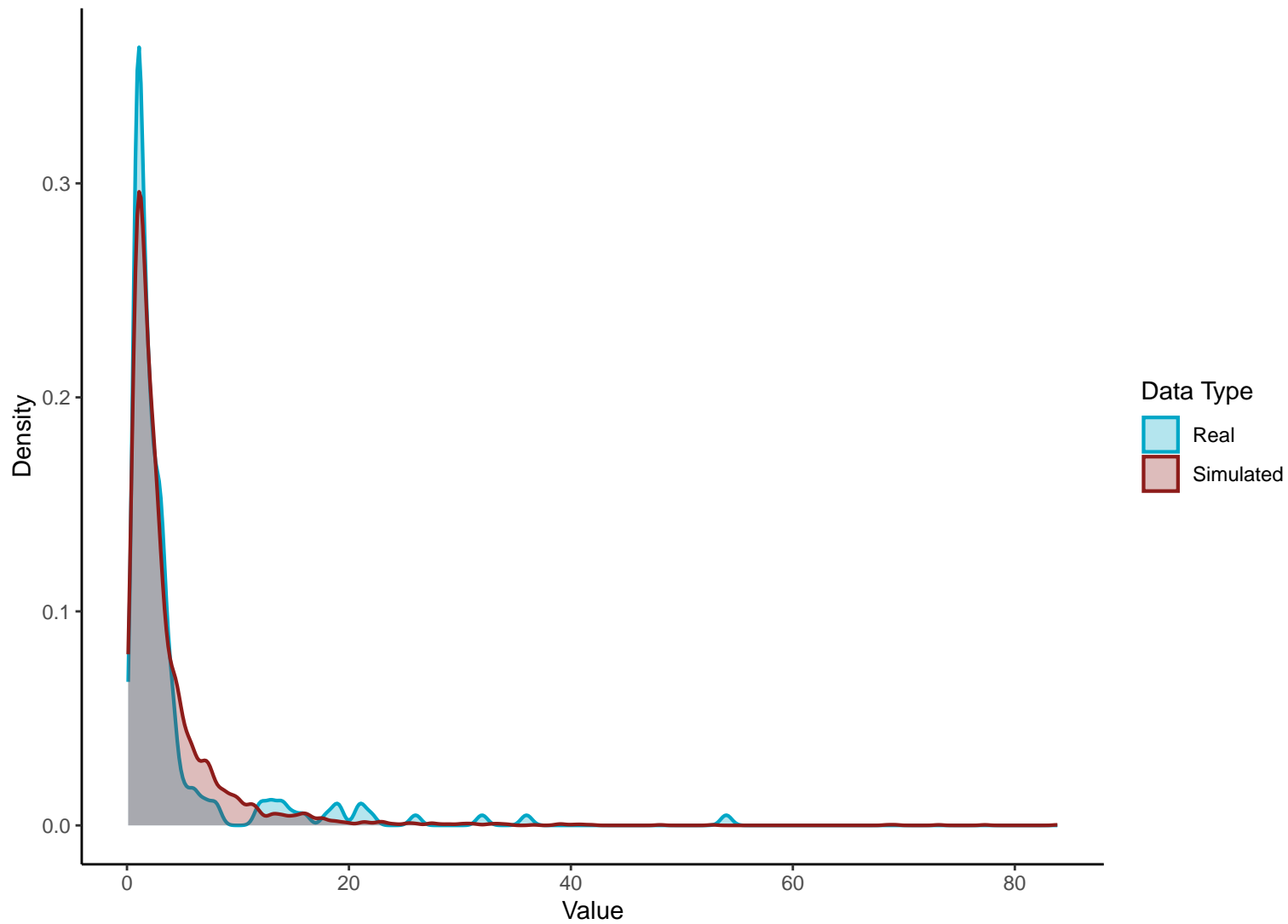
Candidatus.Soleaferrea



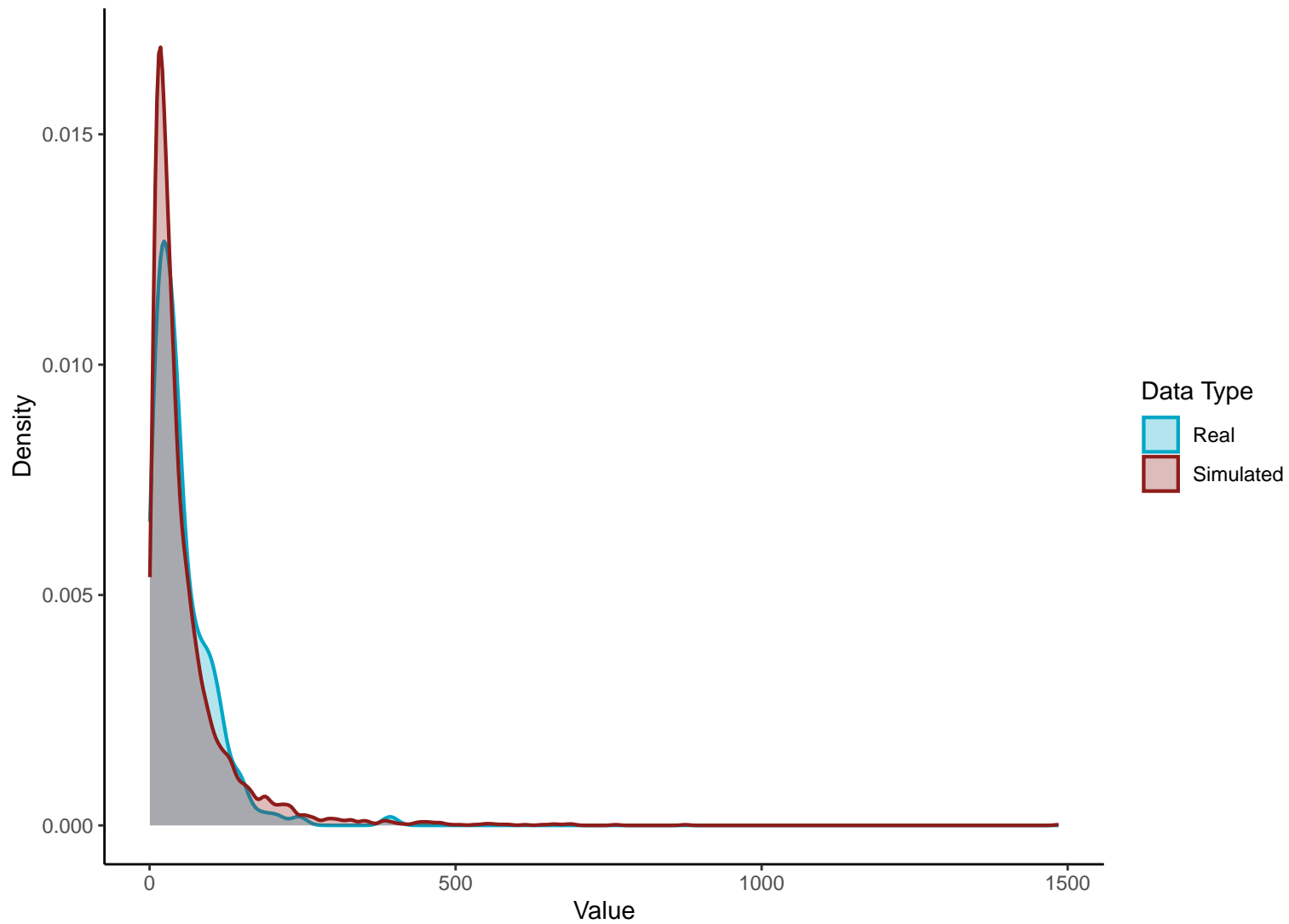
Oribacterium



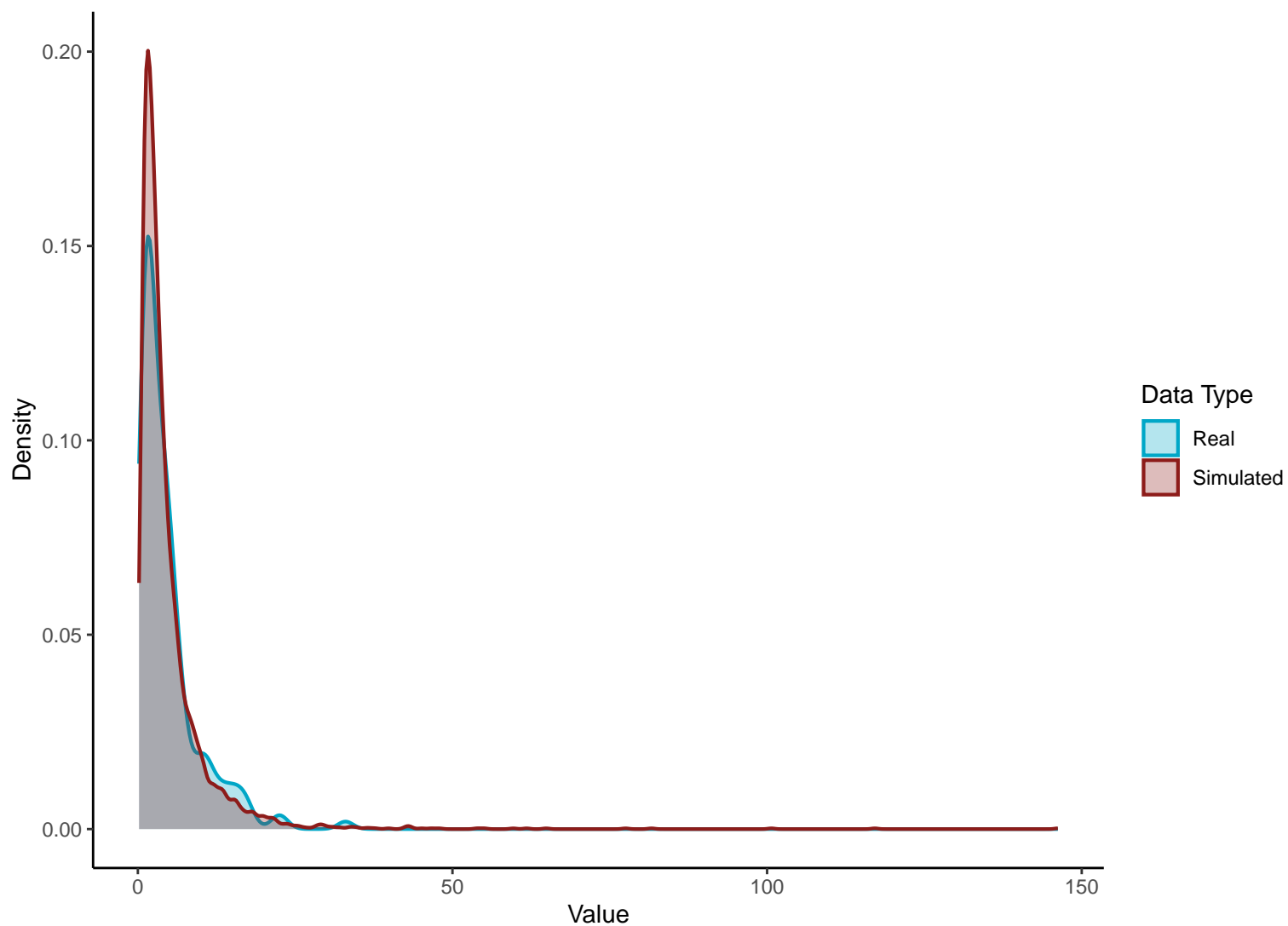
Helicobacter



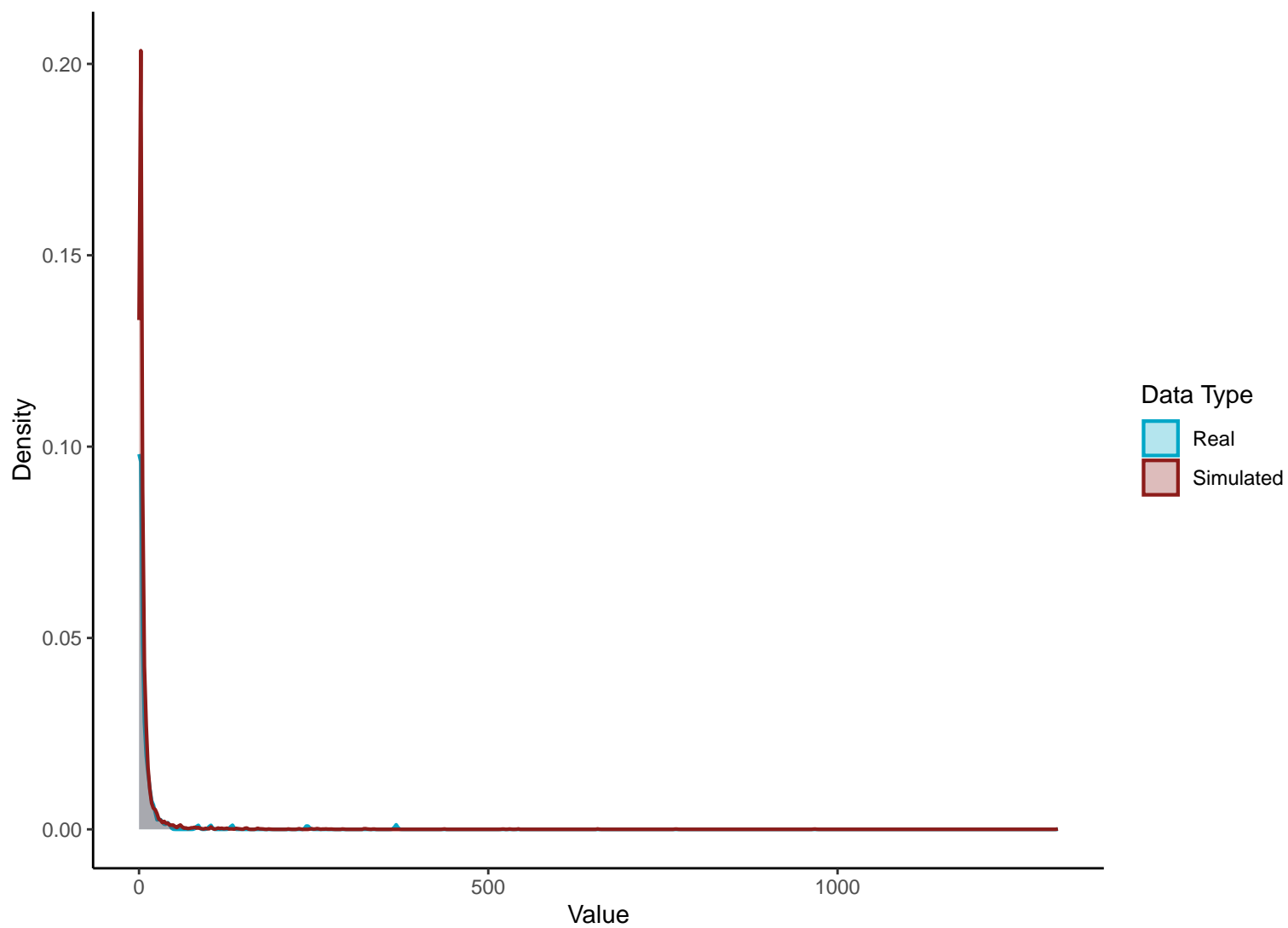
Oscillospira



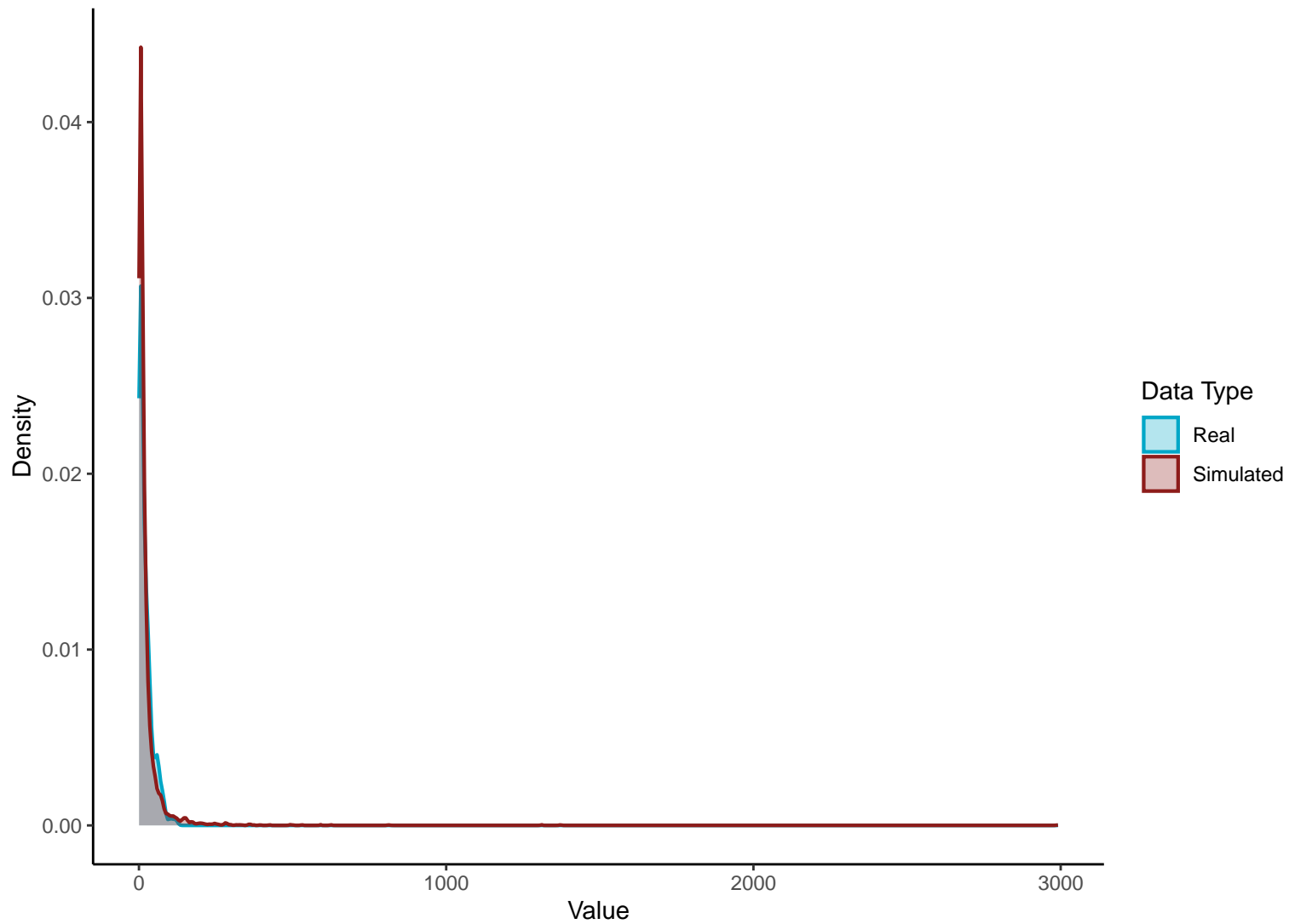
Mailhella



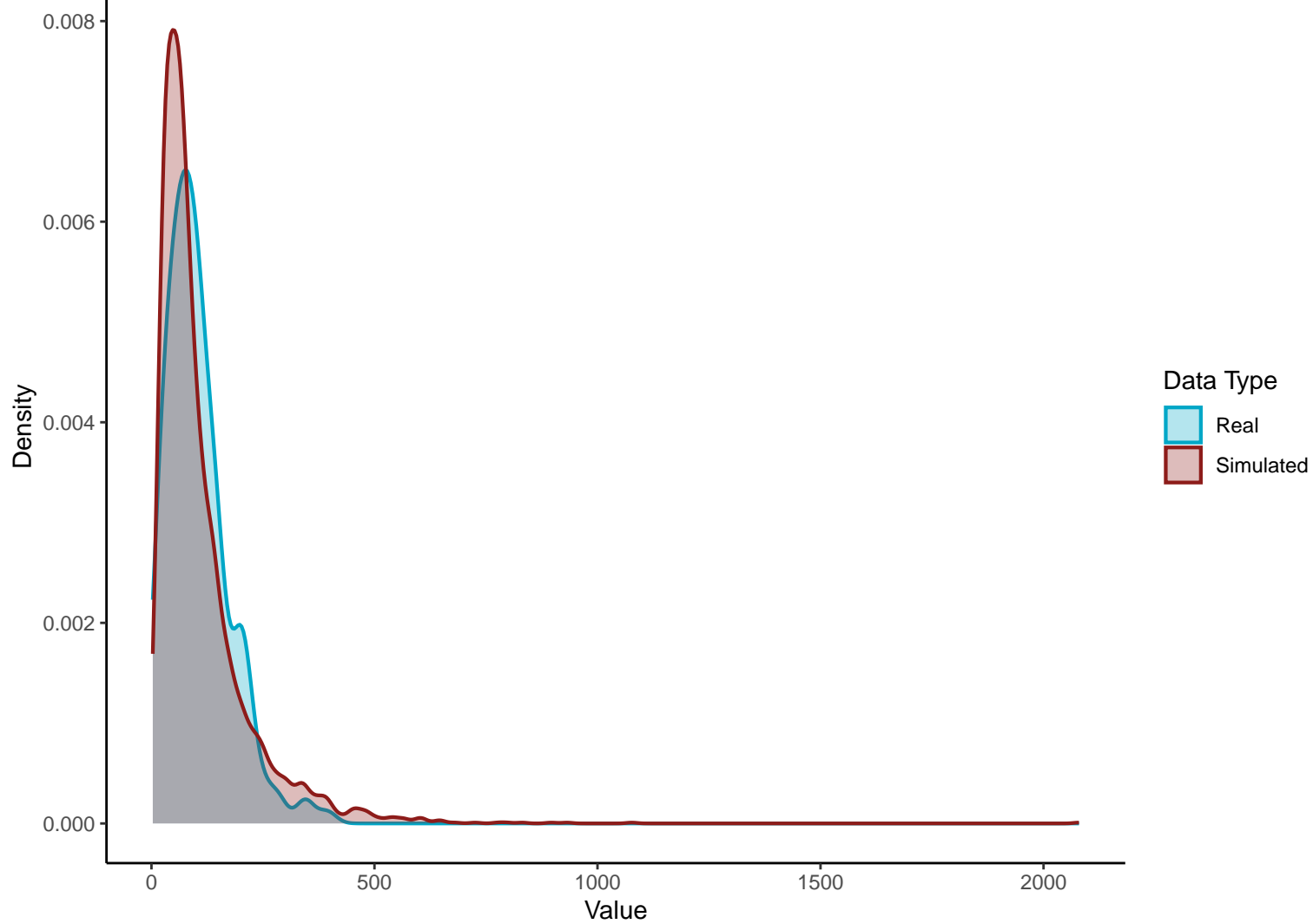
Negativibacillus



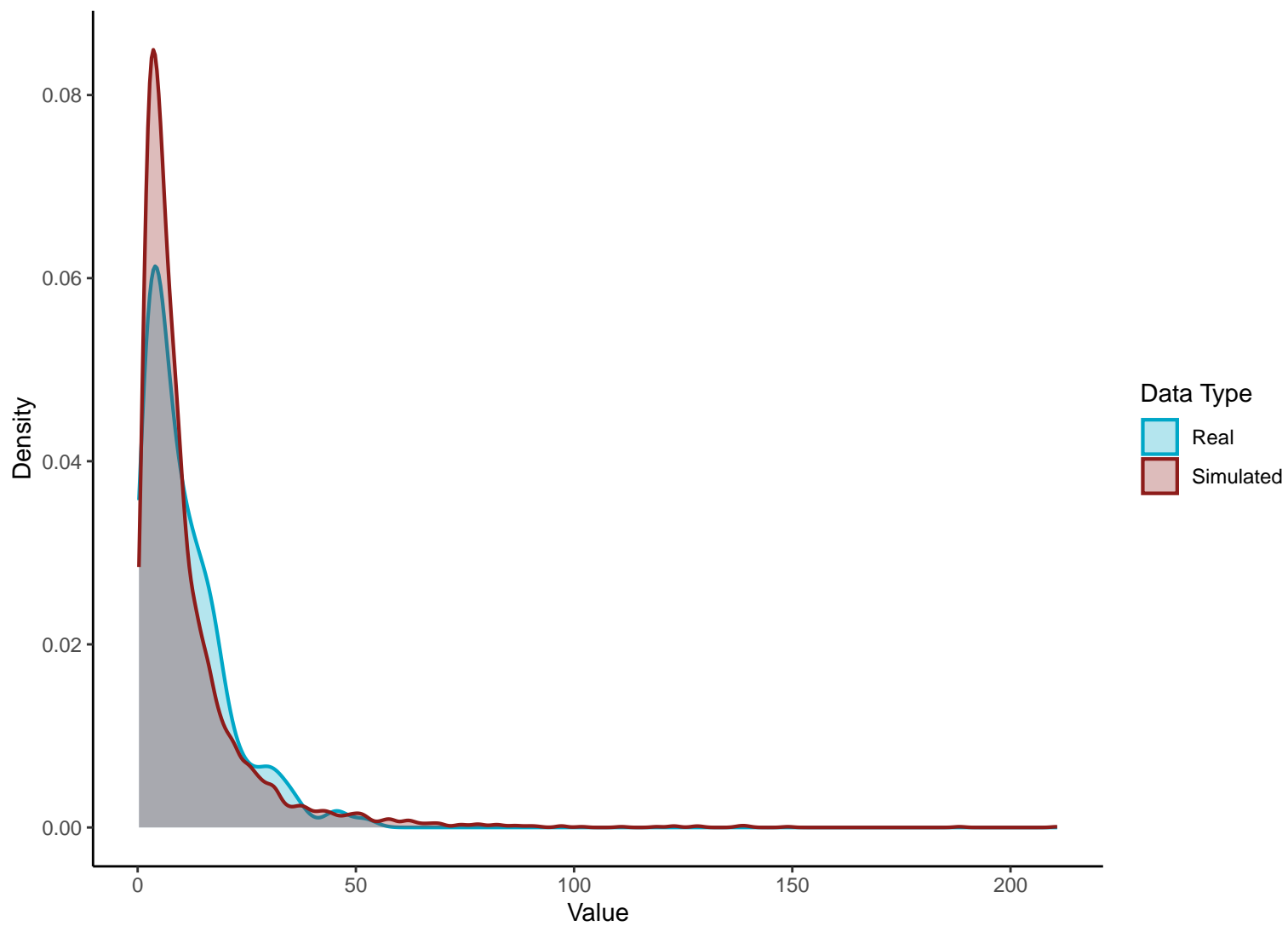
Succinivibrio



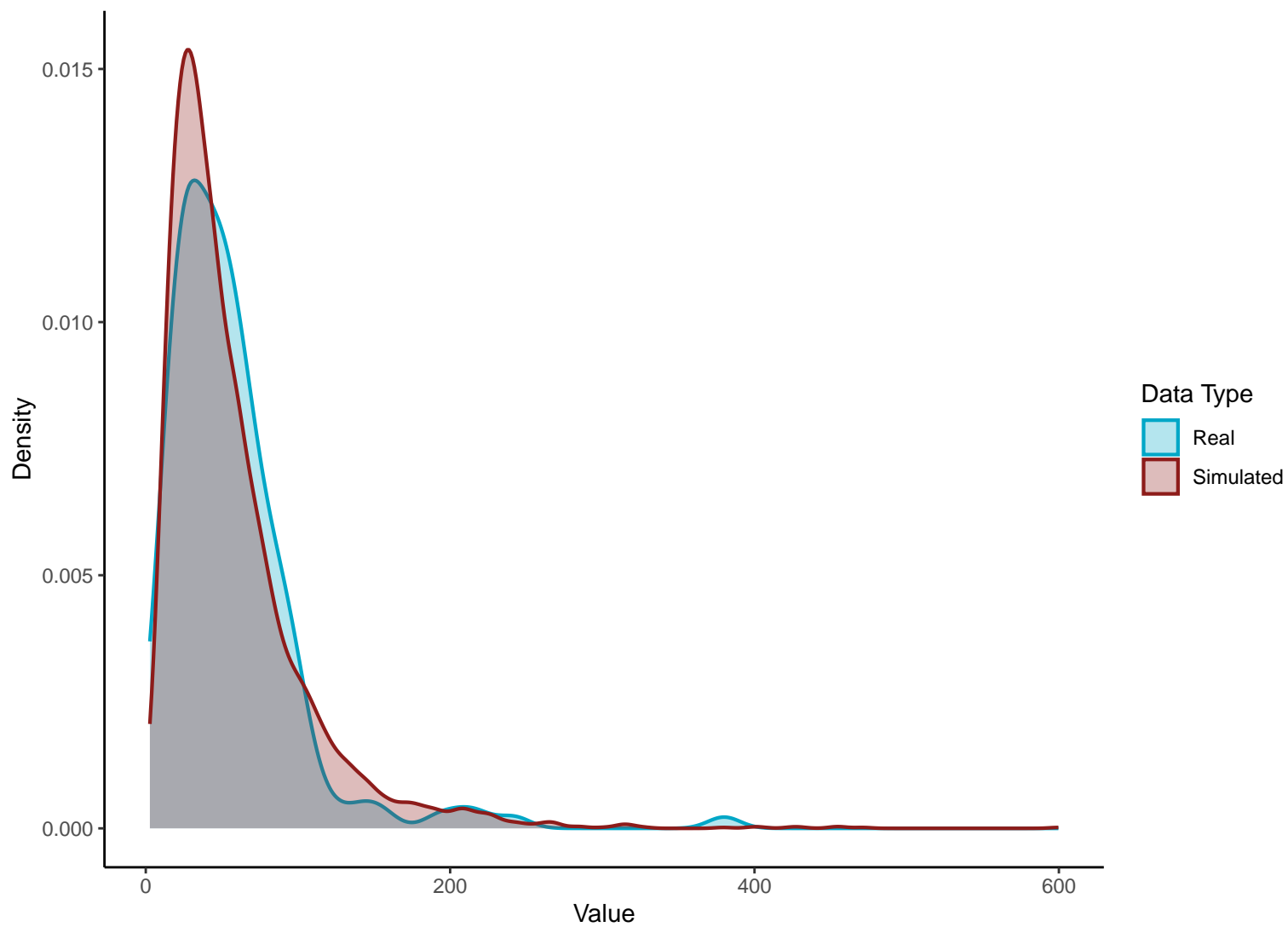
Peptococcus



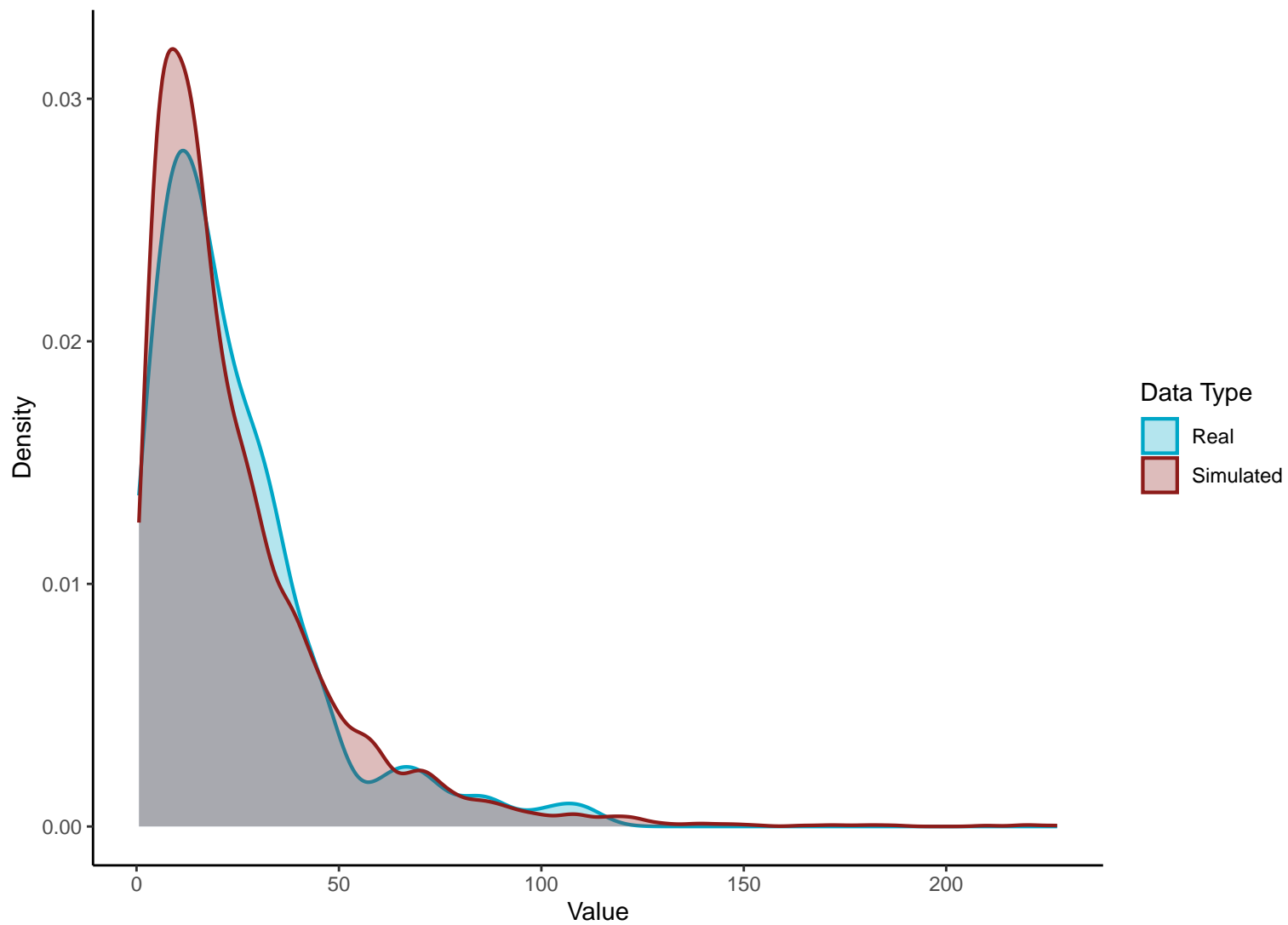
UCG.003



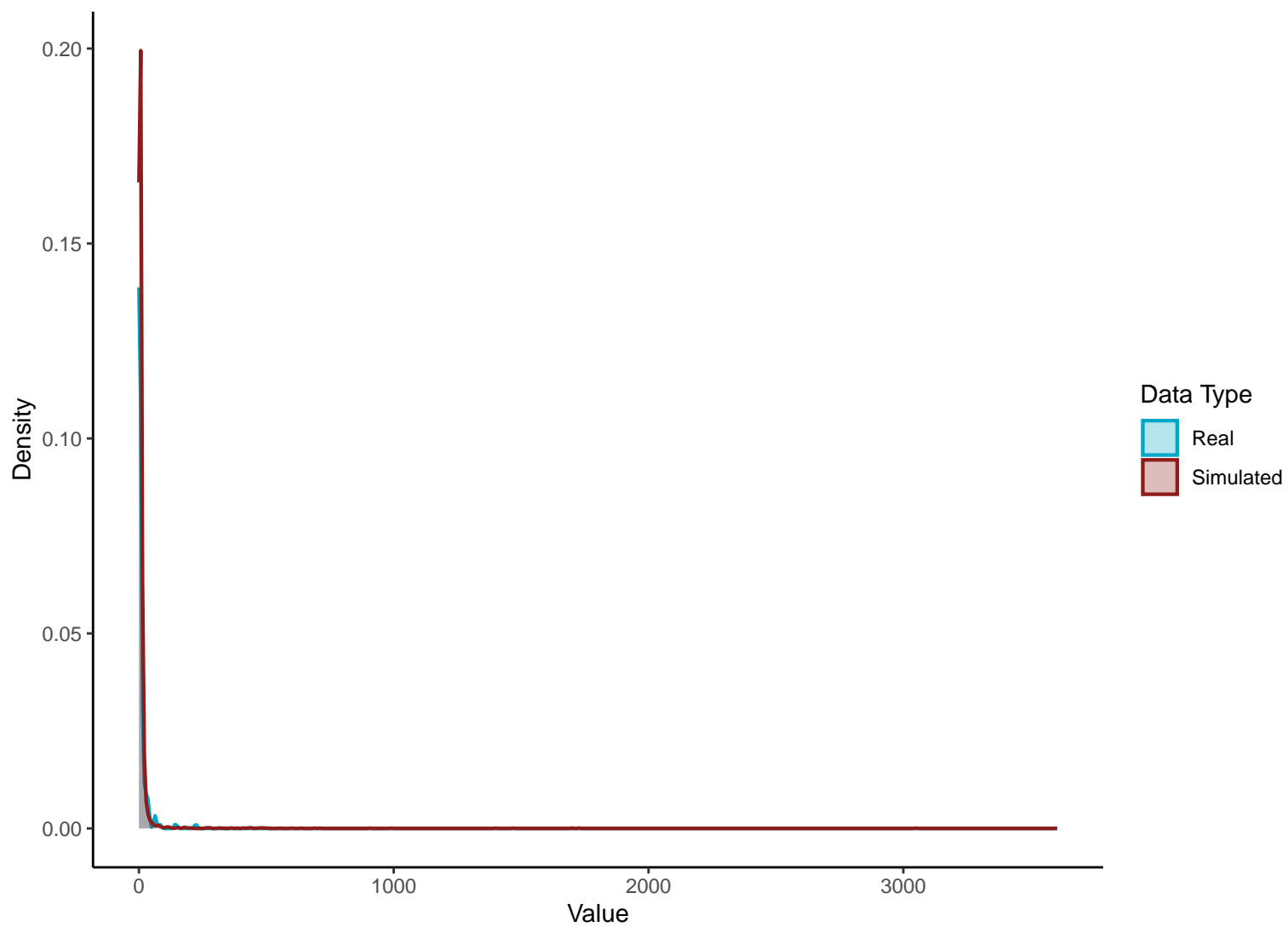
Lachnoclostridium



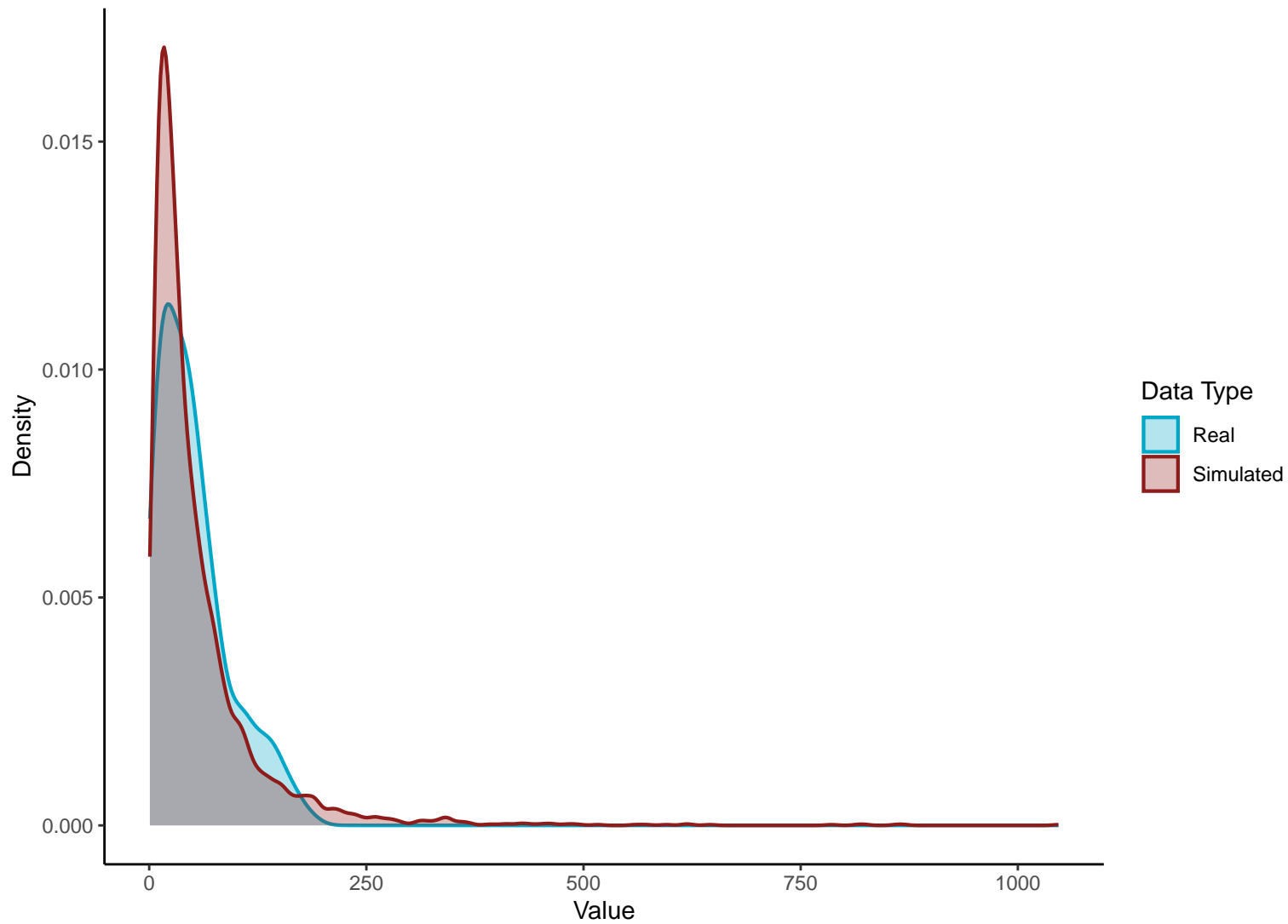
X.Eubacterium..ventriosum.group



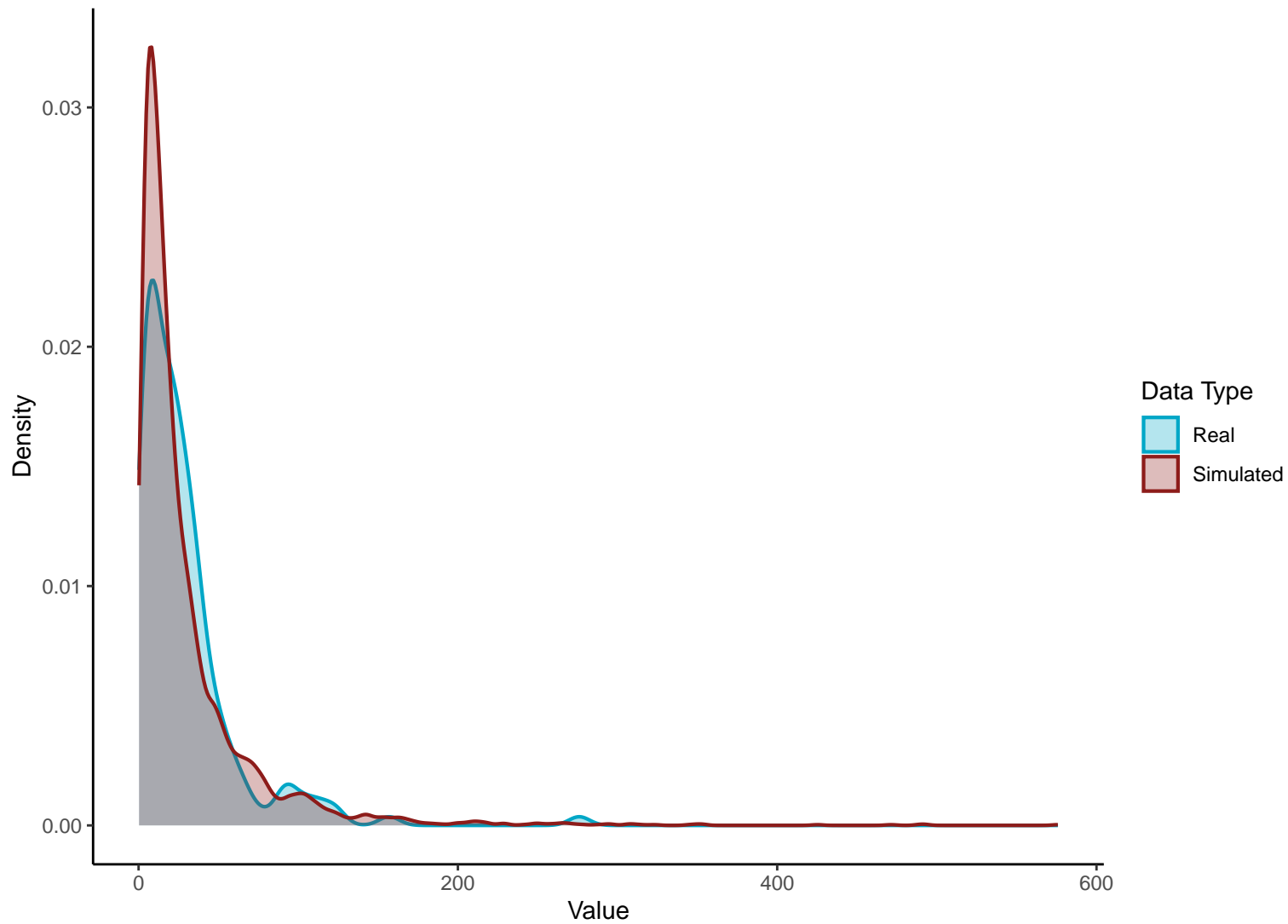
Anaerococcus



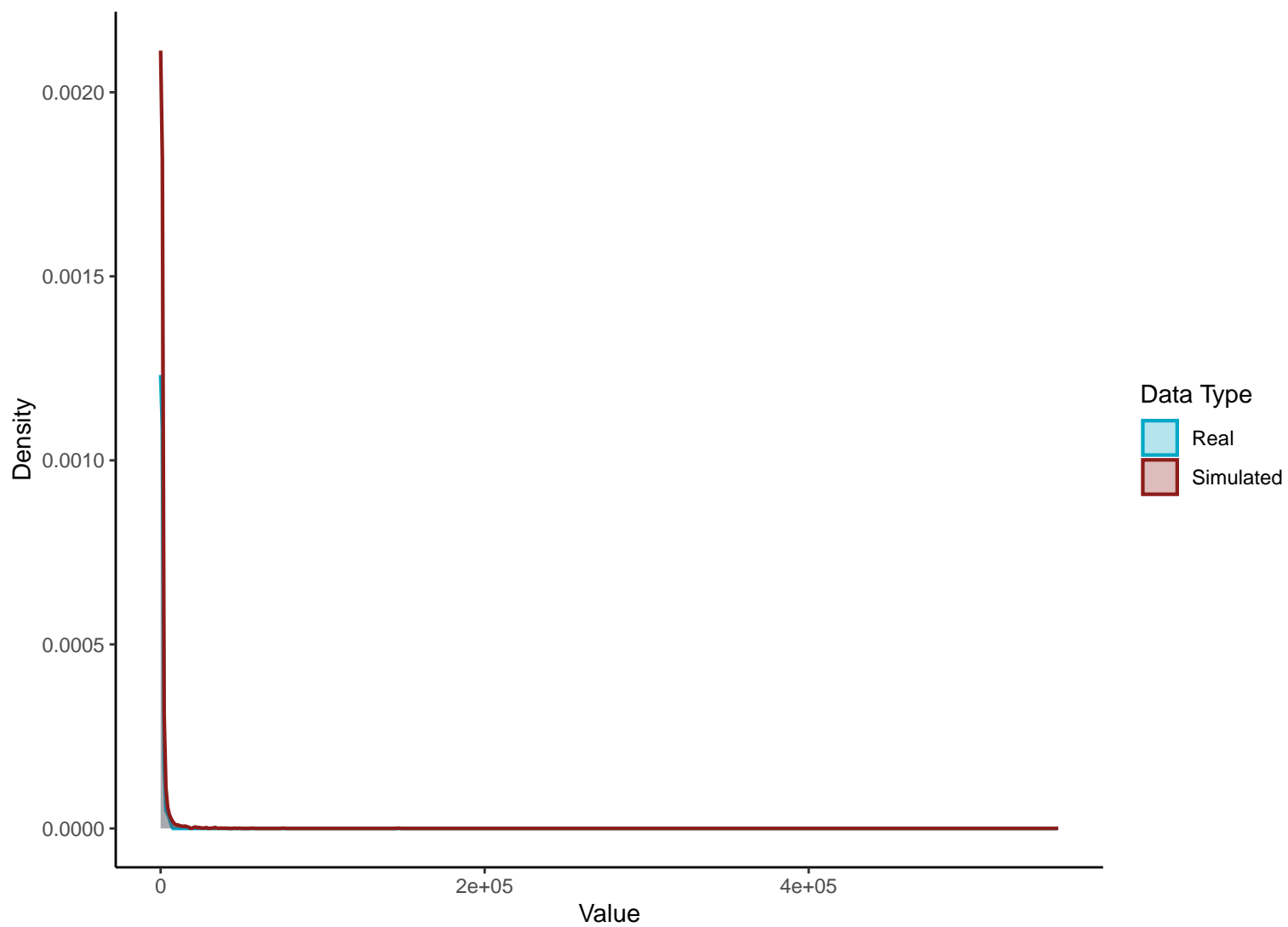
Enterorhabdus



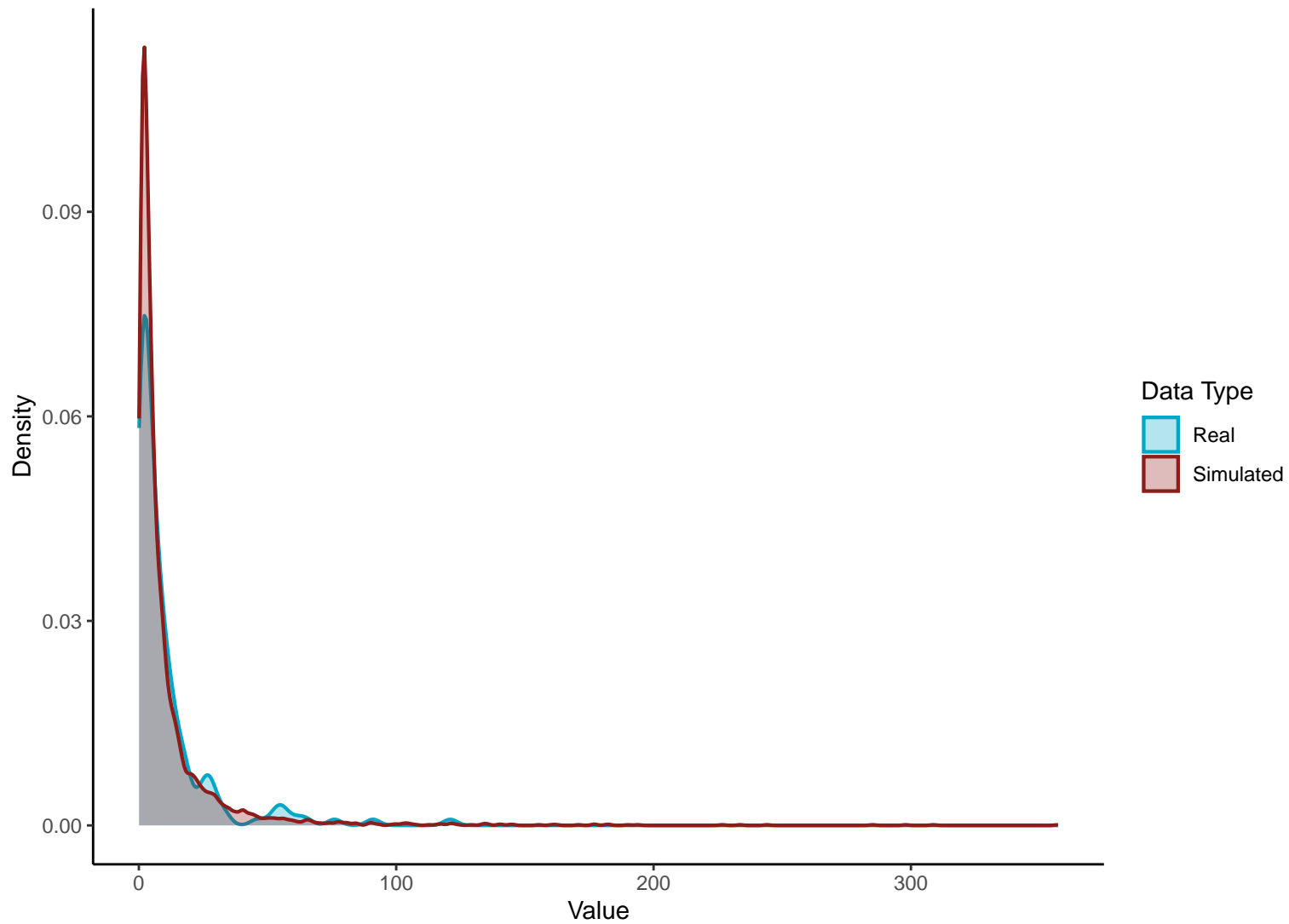
Libanicoccus



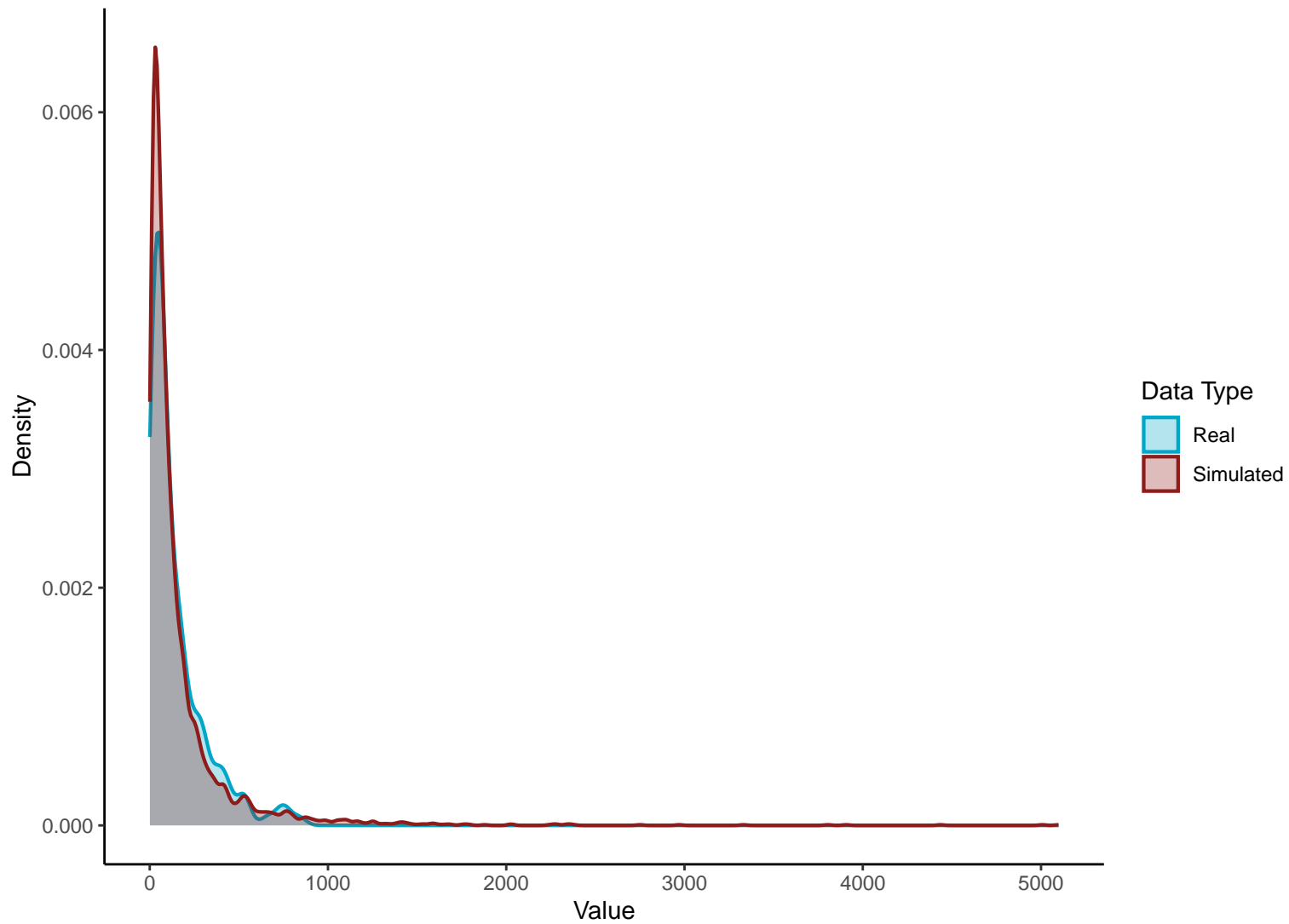
Turicibacter



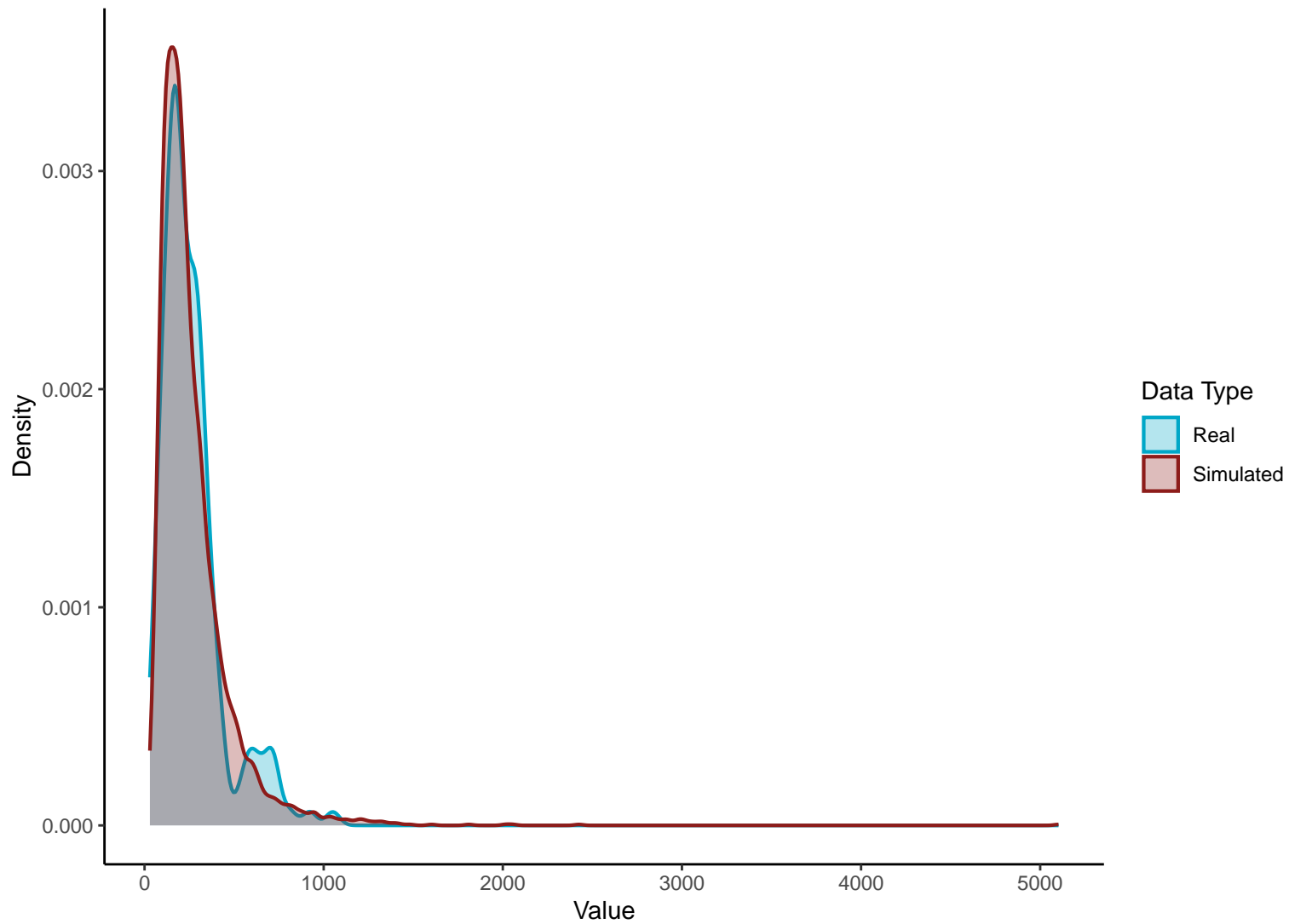
XBB1006



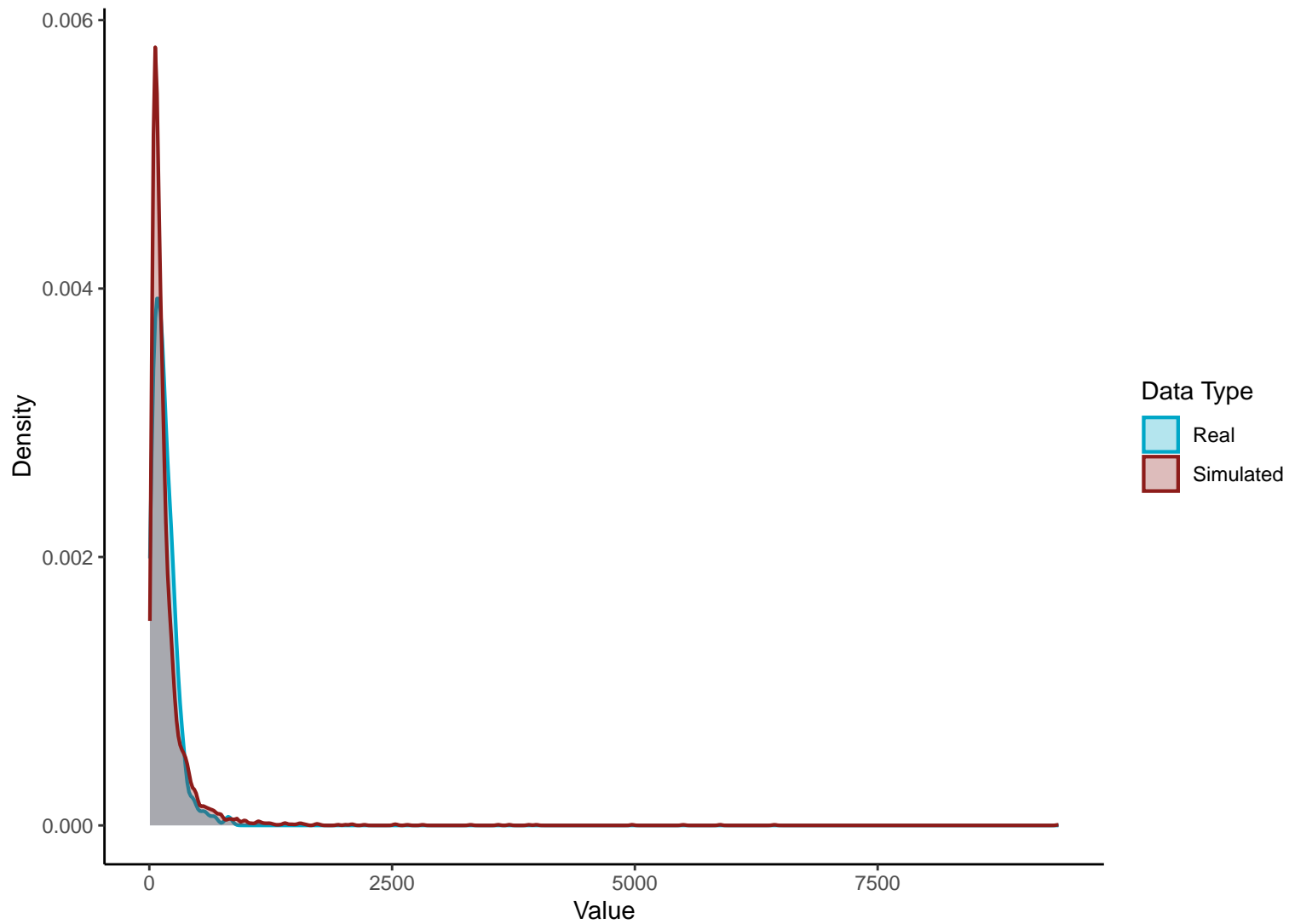
UCG.008



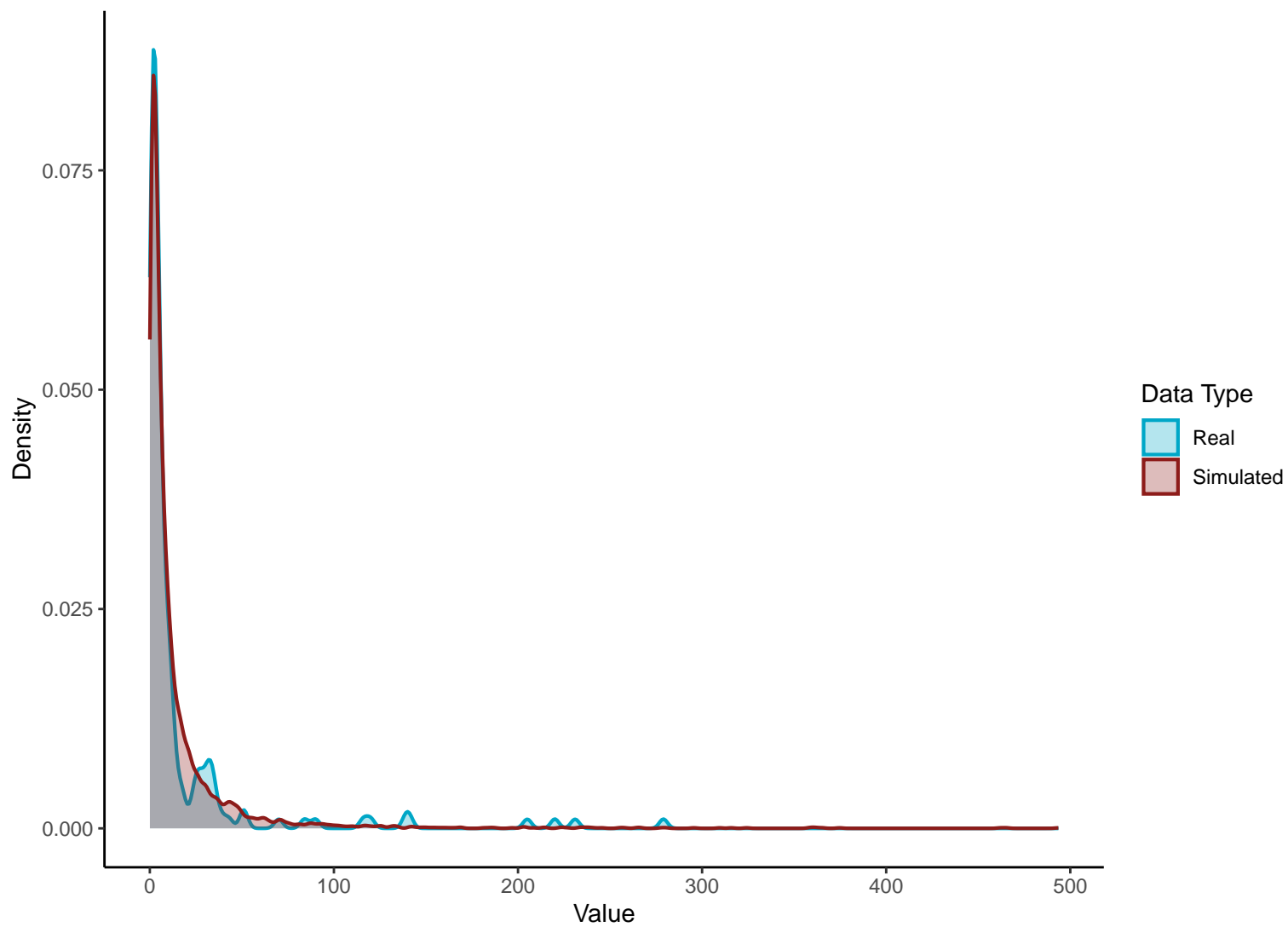
Intestinibacter



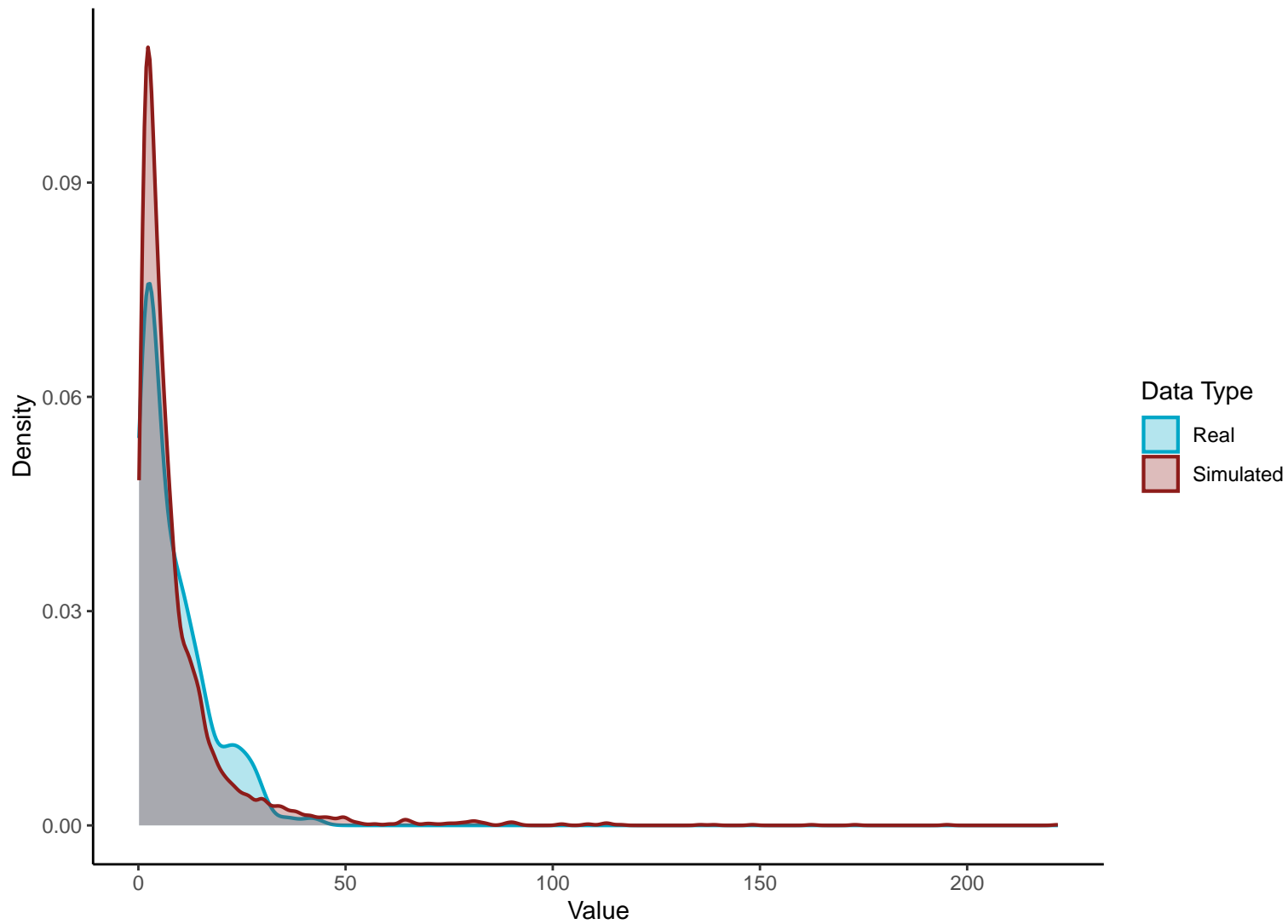
Fusicatenibacter



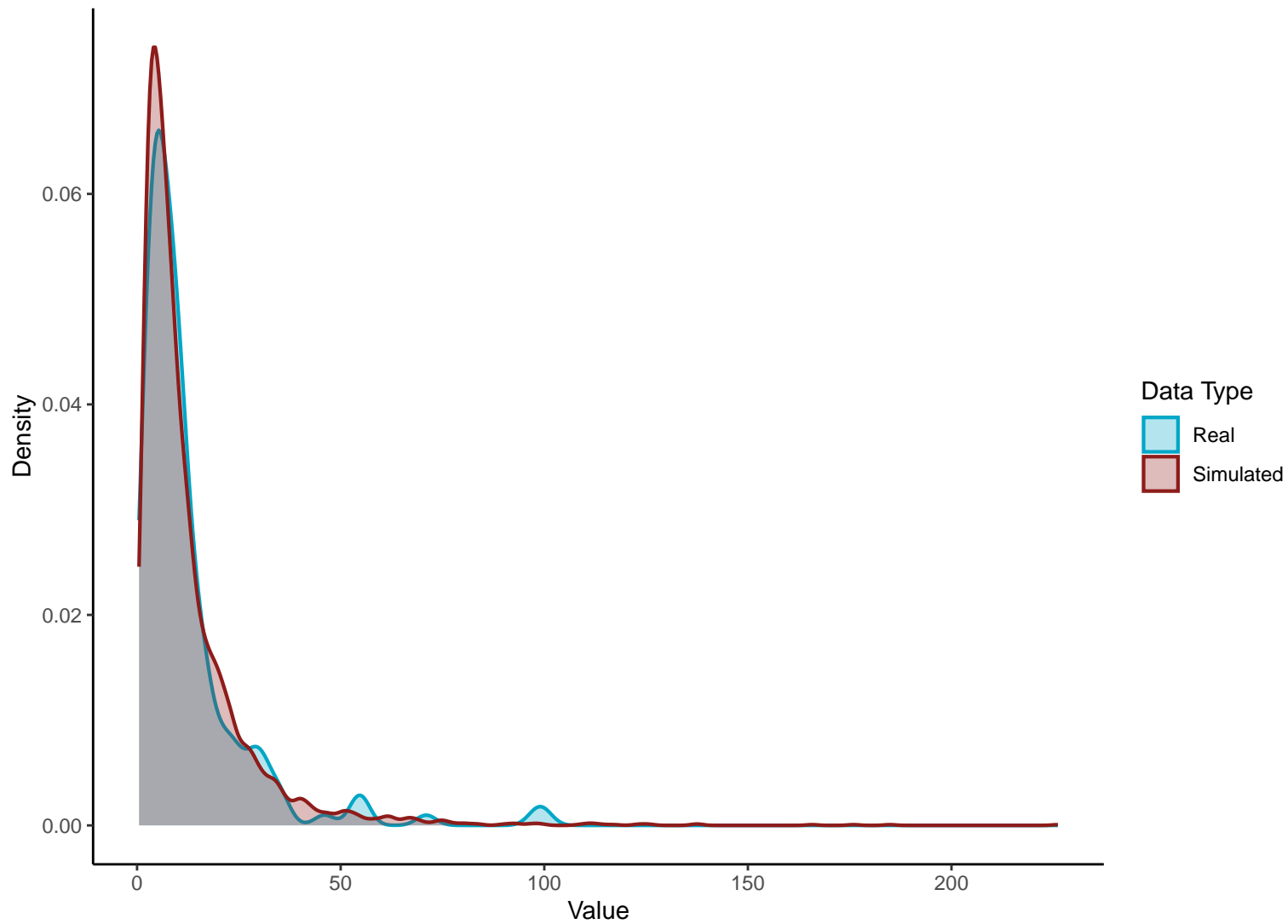
X28.4



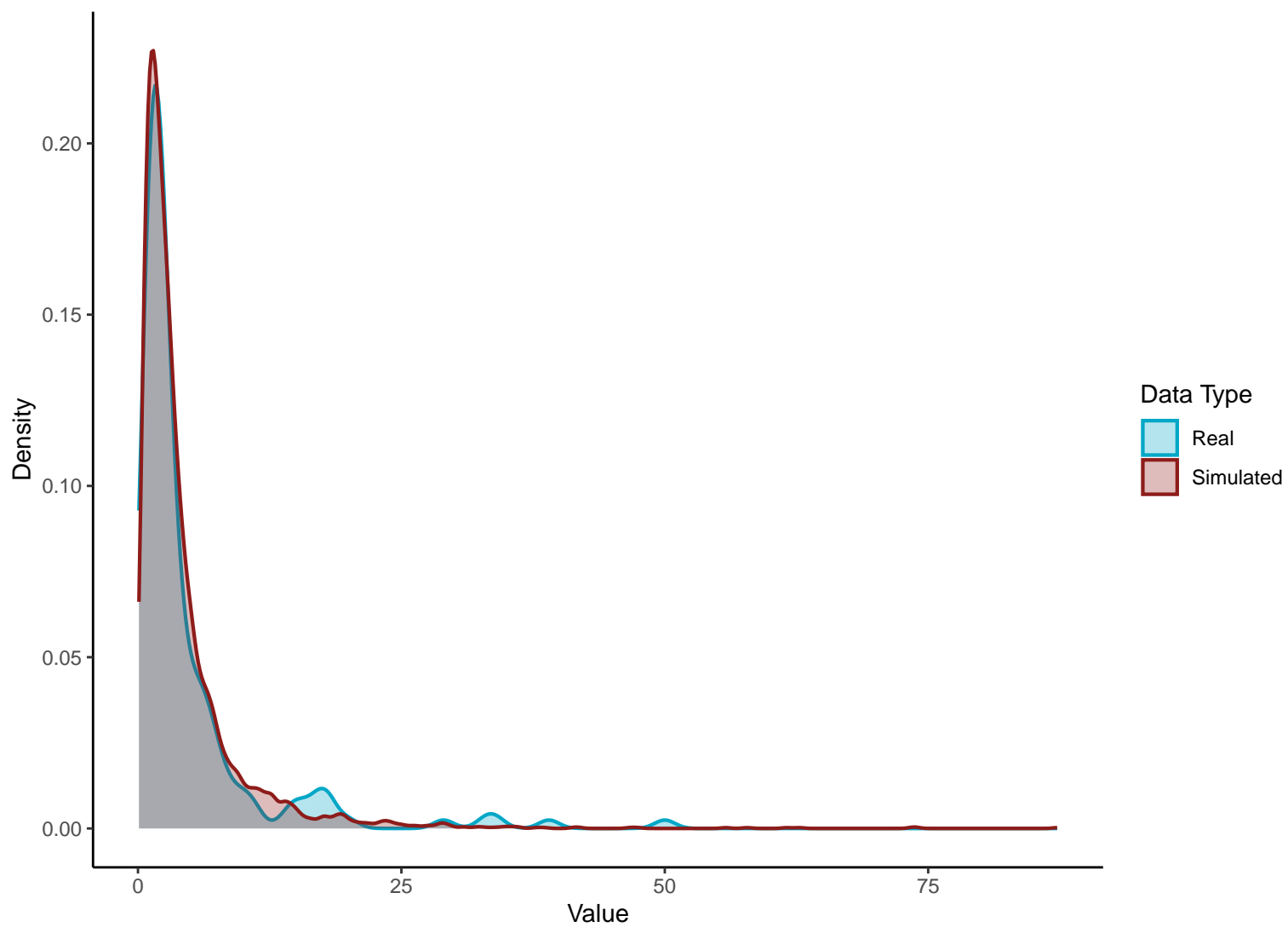
Howardella



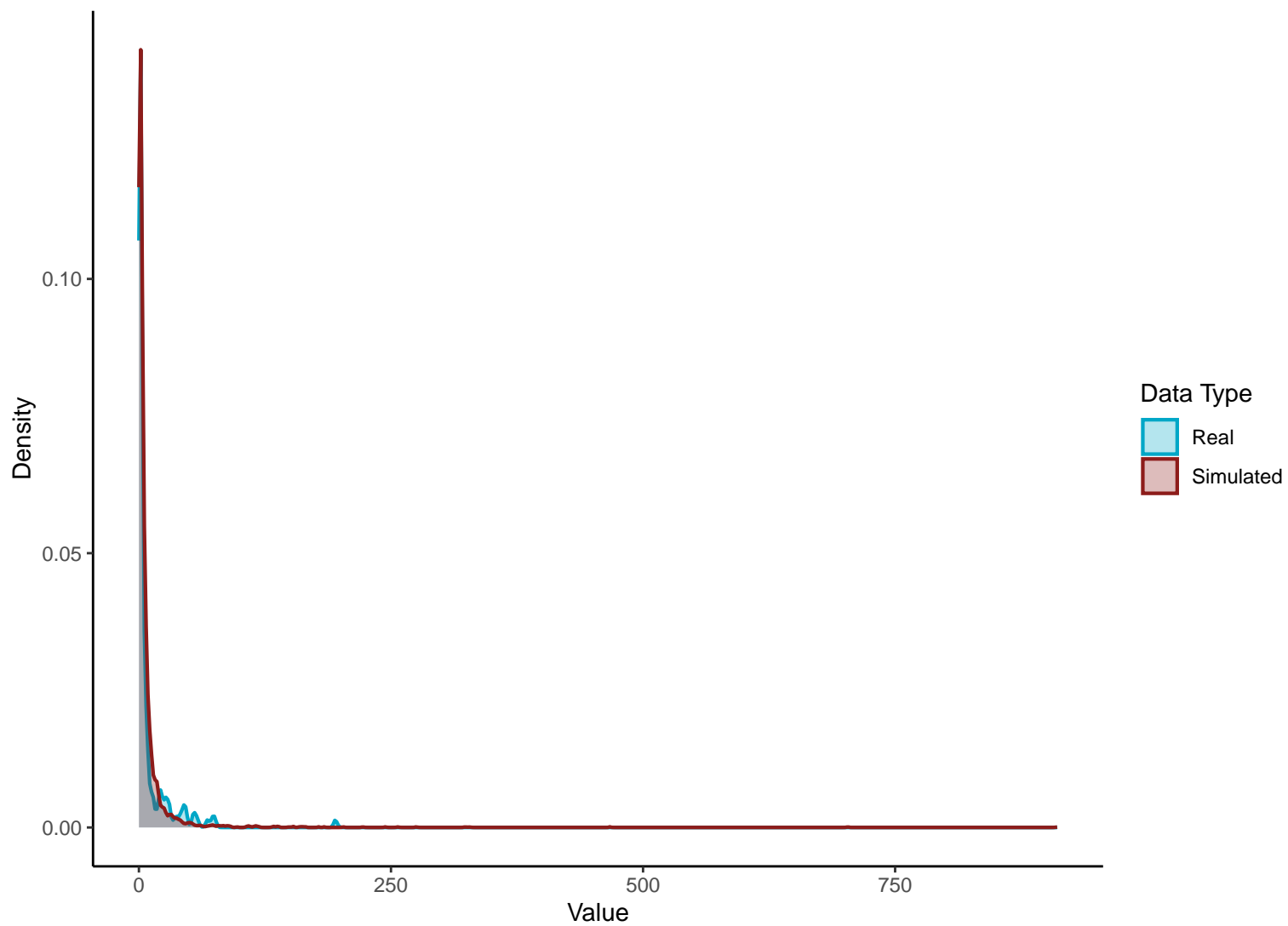
Paludicola



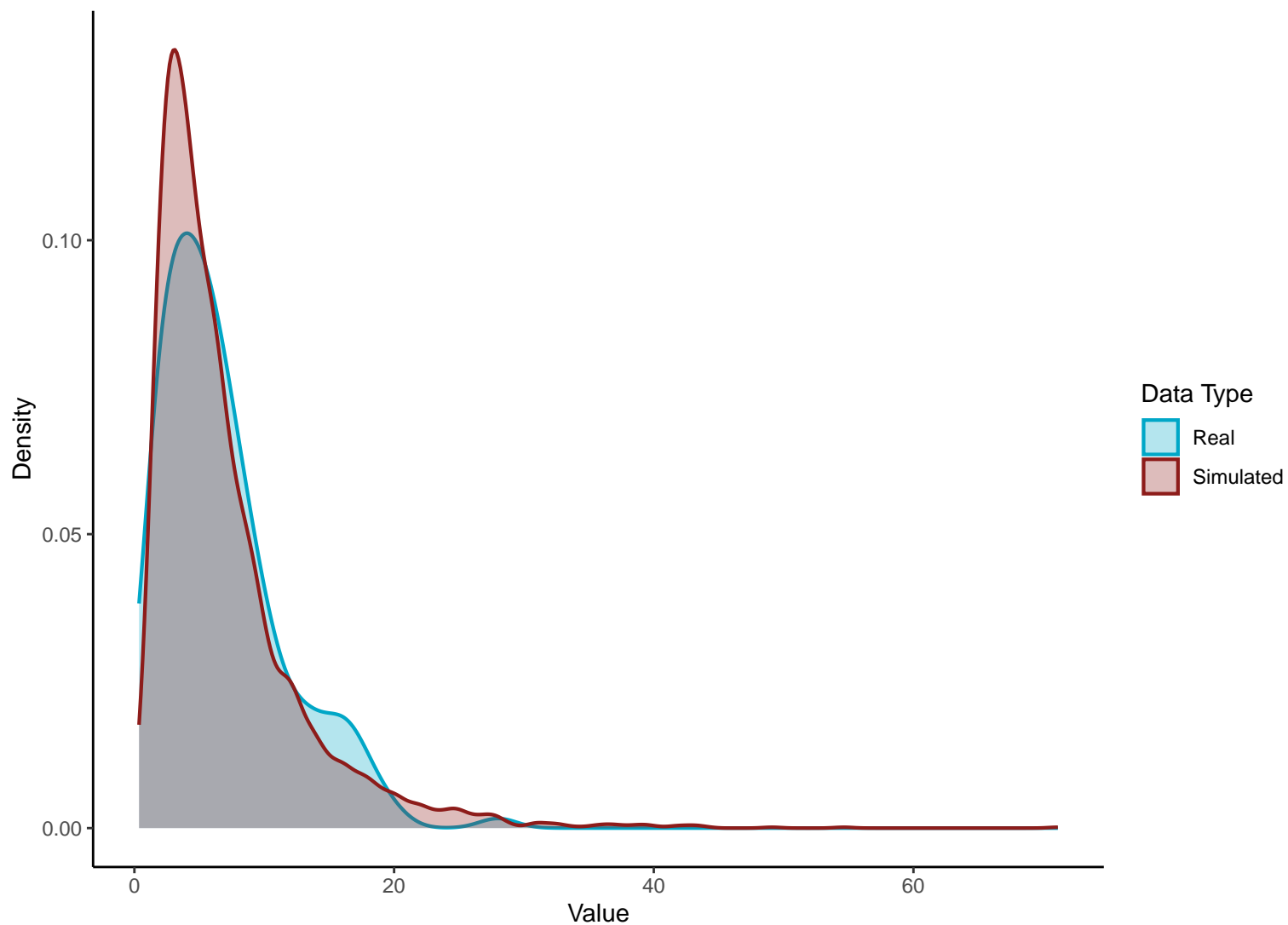
Tyzzerella



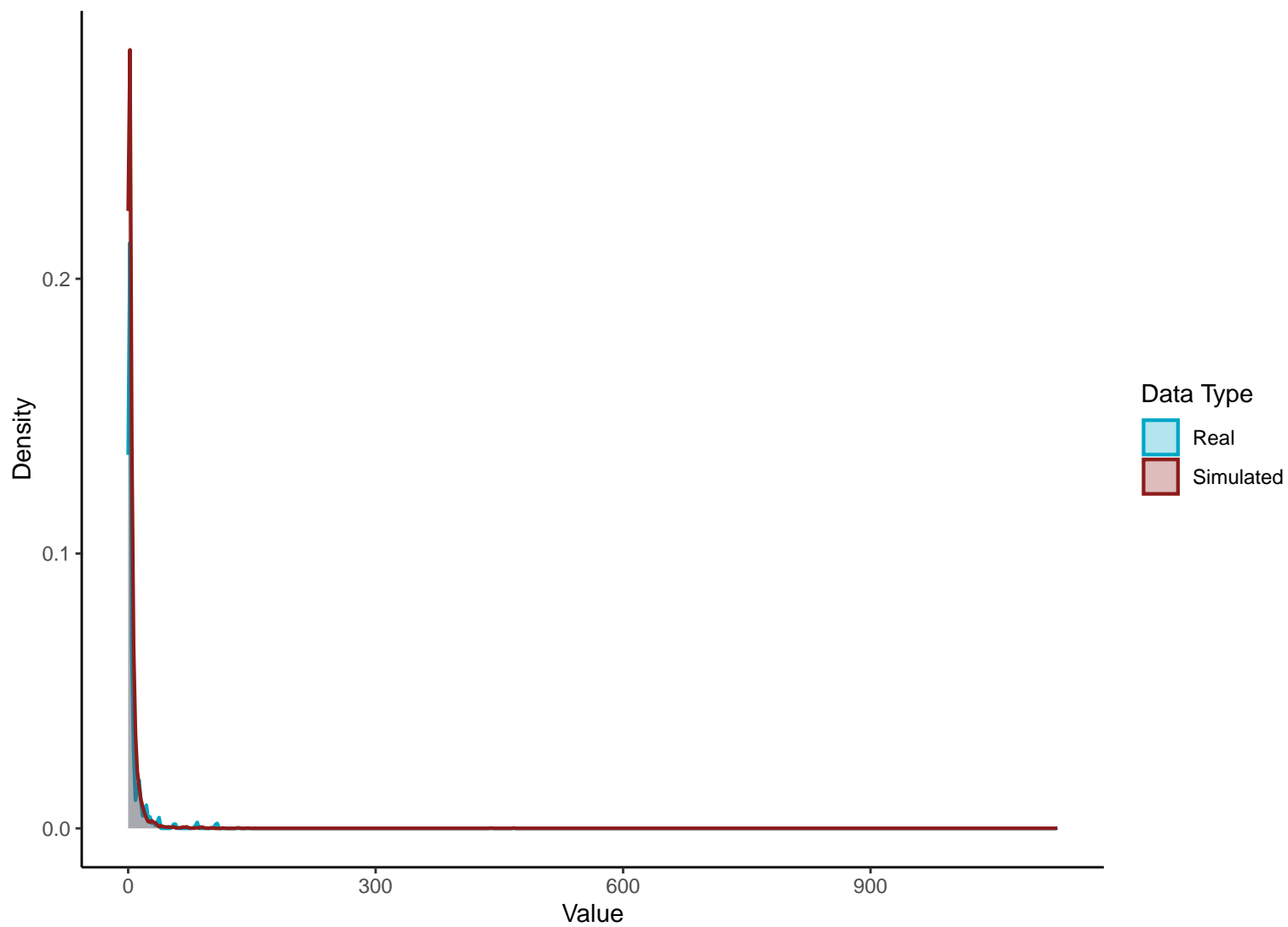
UCG.001



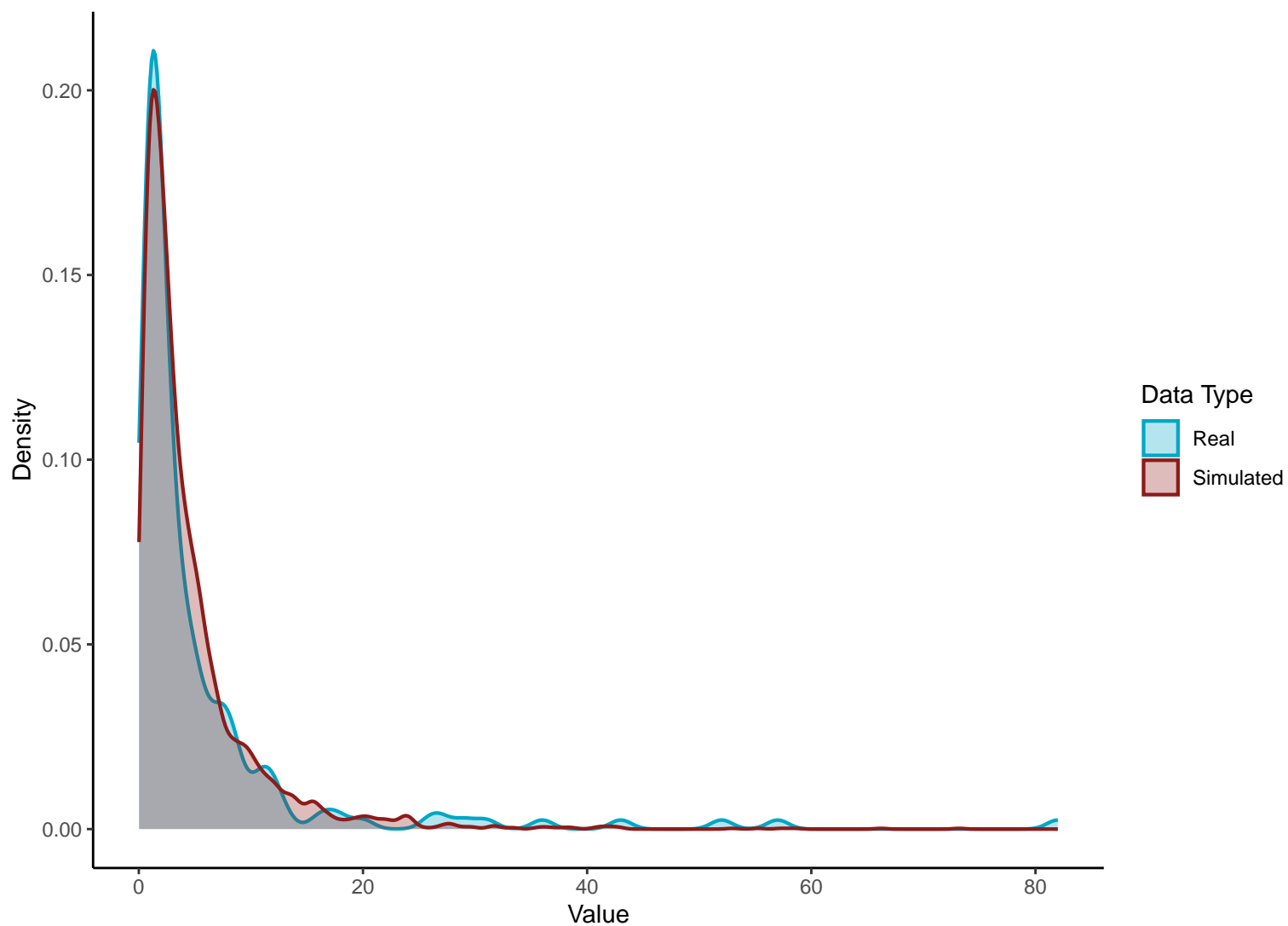
Lachnospiraceae.UGC.002



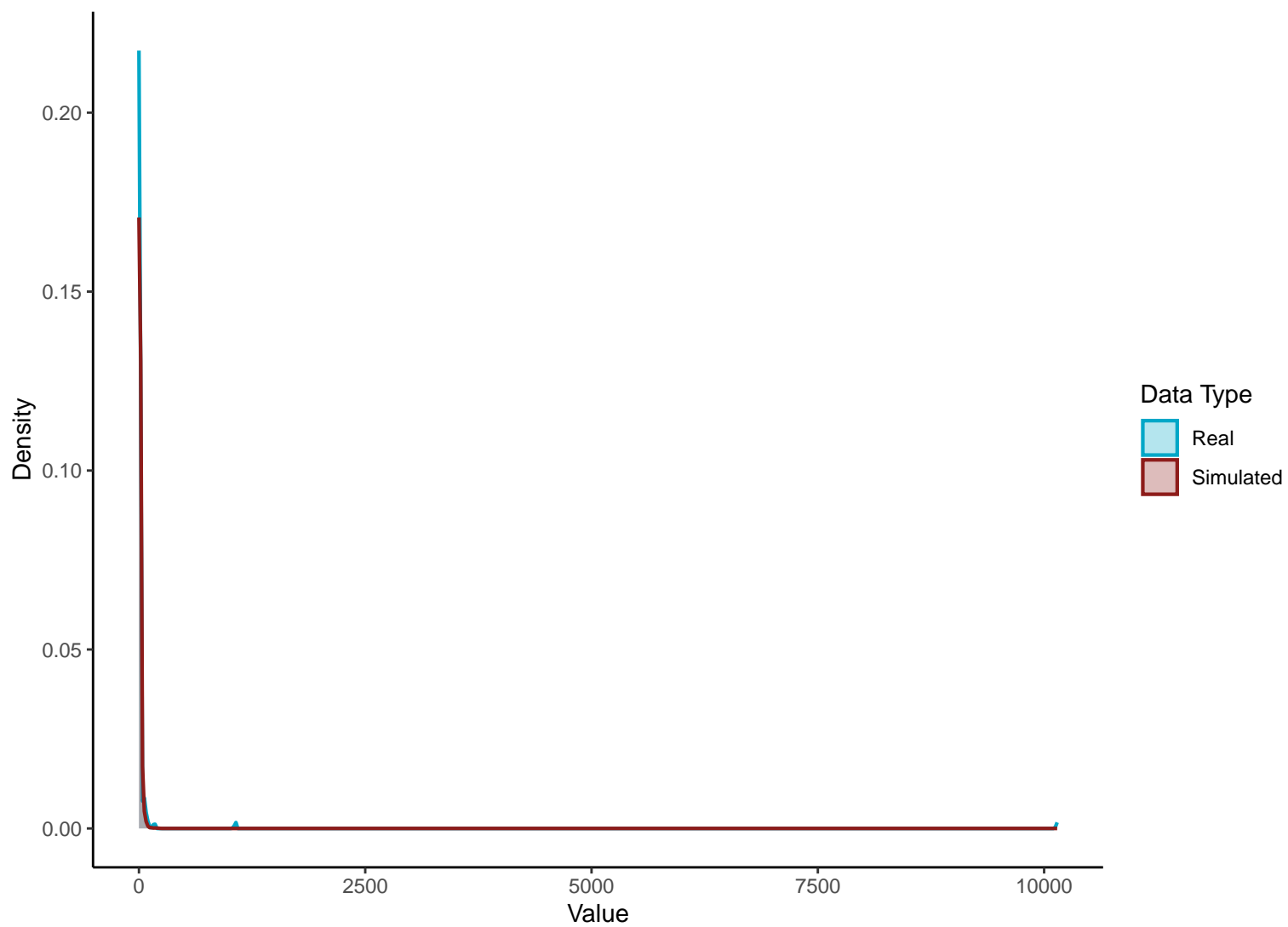
Lachnospiraceae.UGC.007



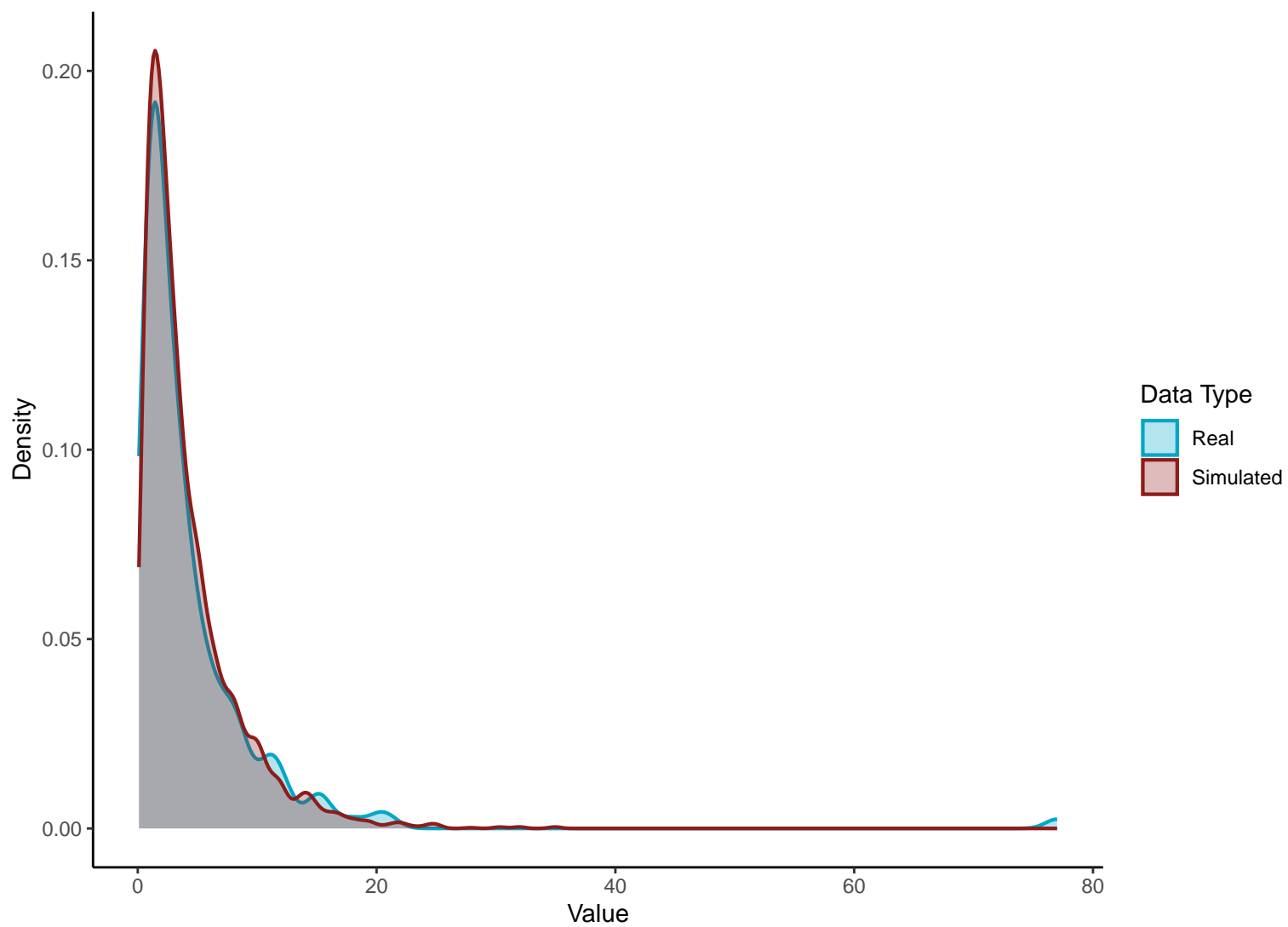
Lachnospiraceae.UGC.003



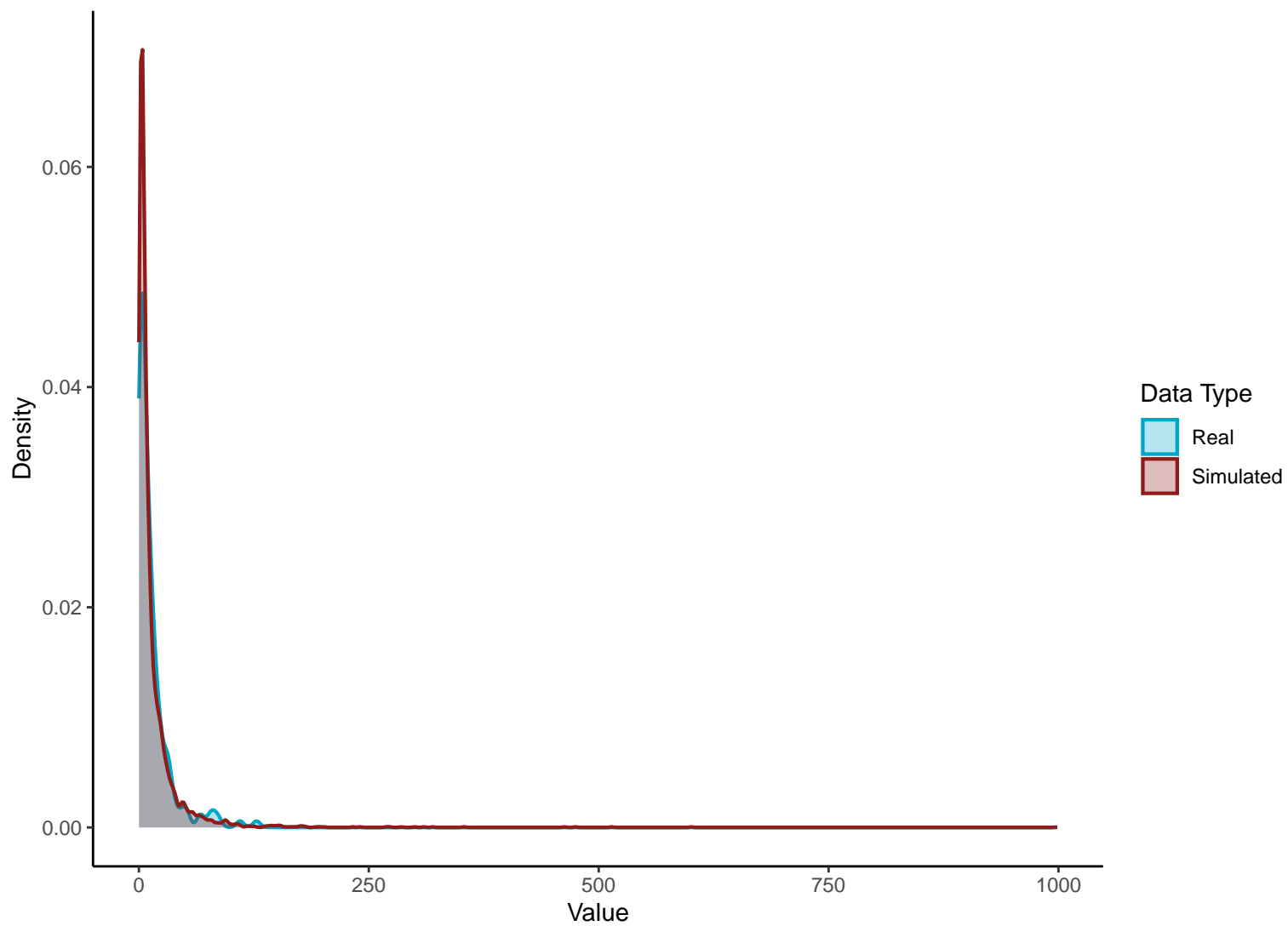
Bifidobacterium



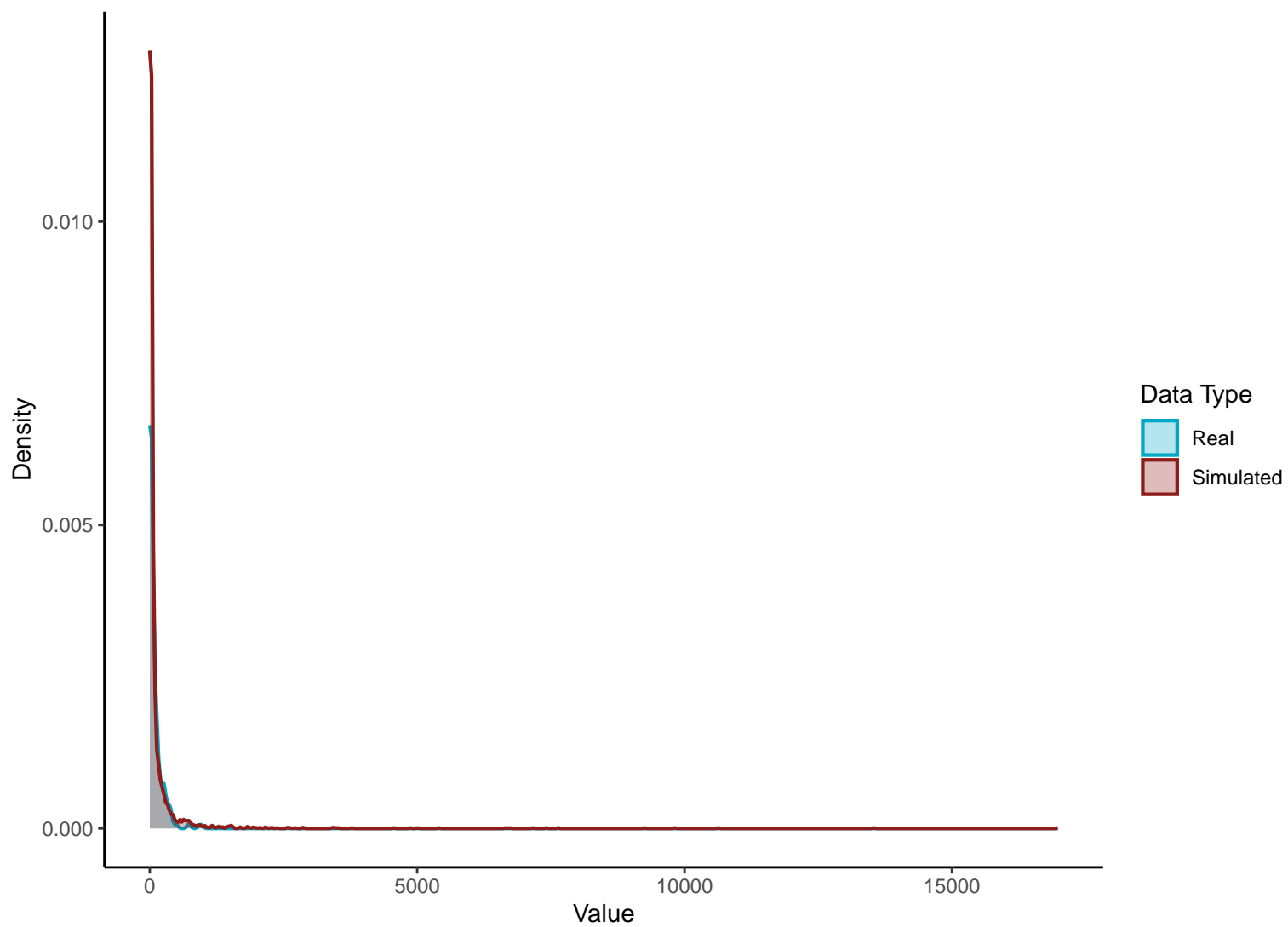
Butyrivibrio



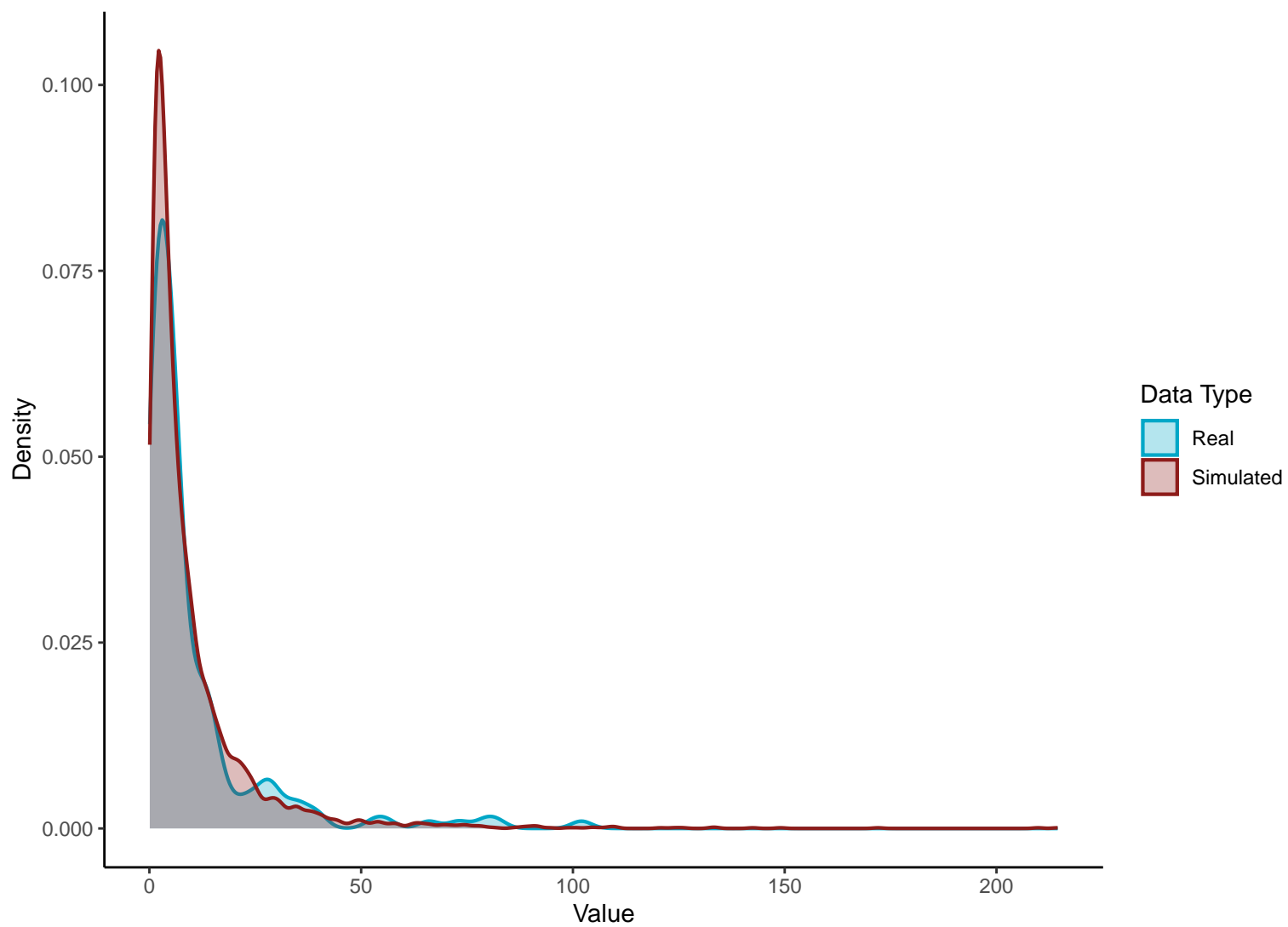
Pseudobutyrvibrio



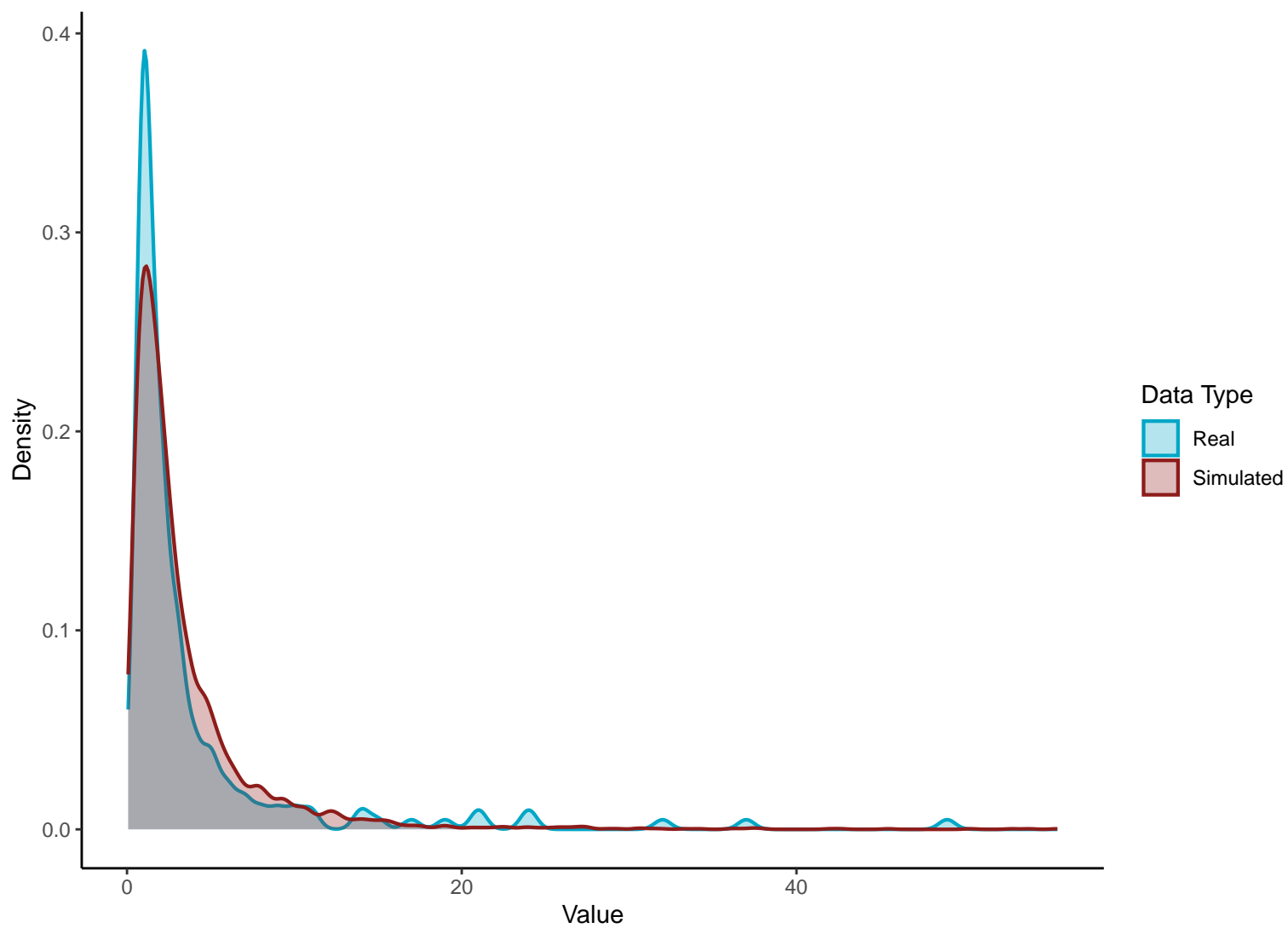
Catenisphaera



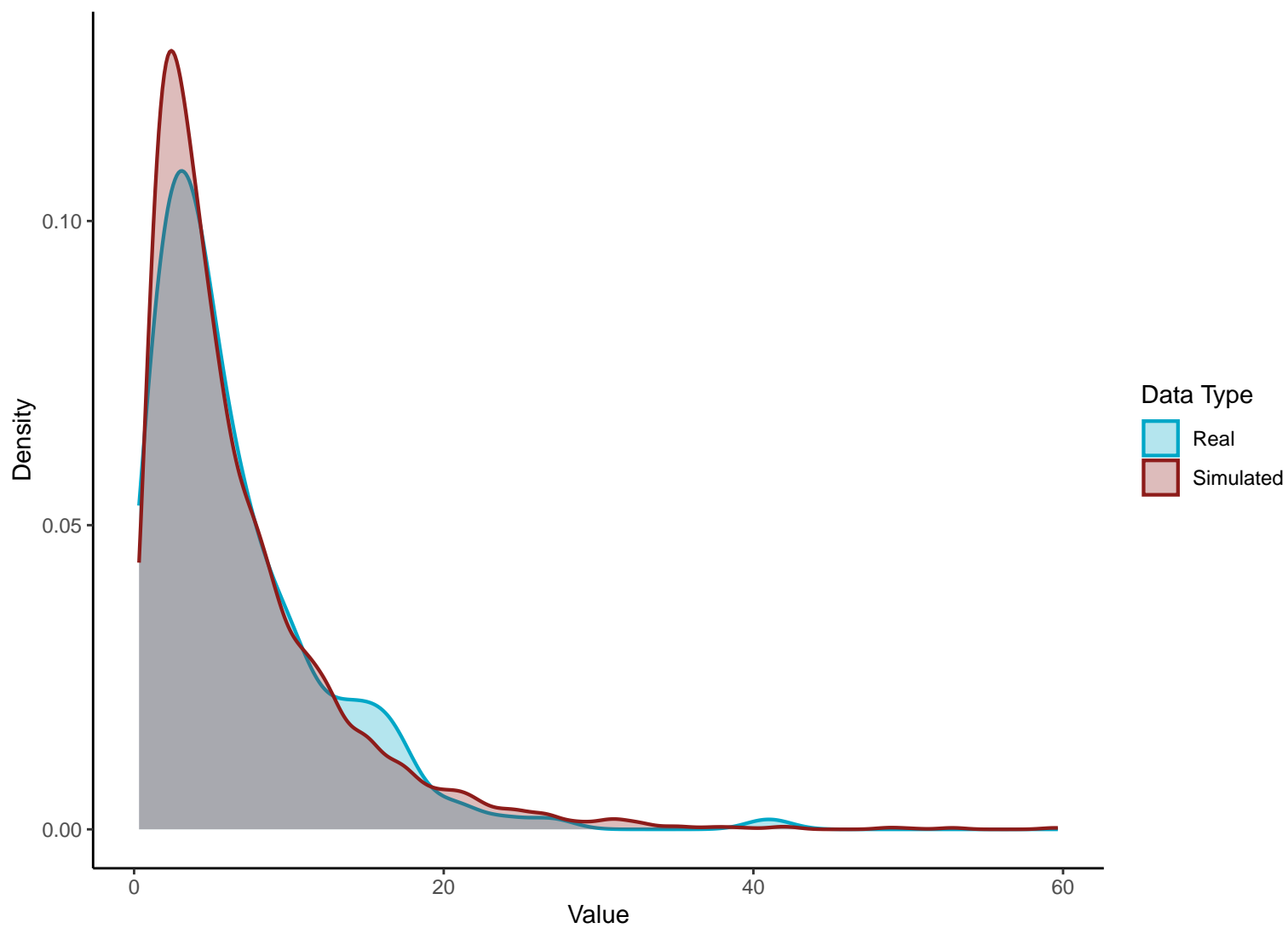
Prevotellaceae.UGC.004



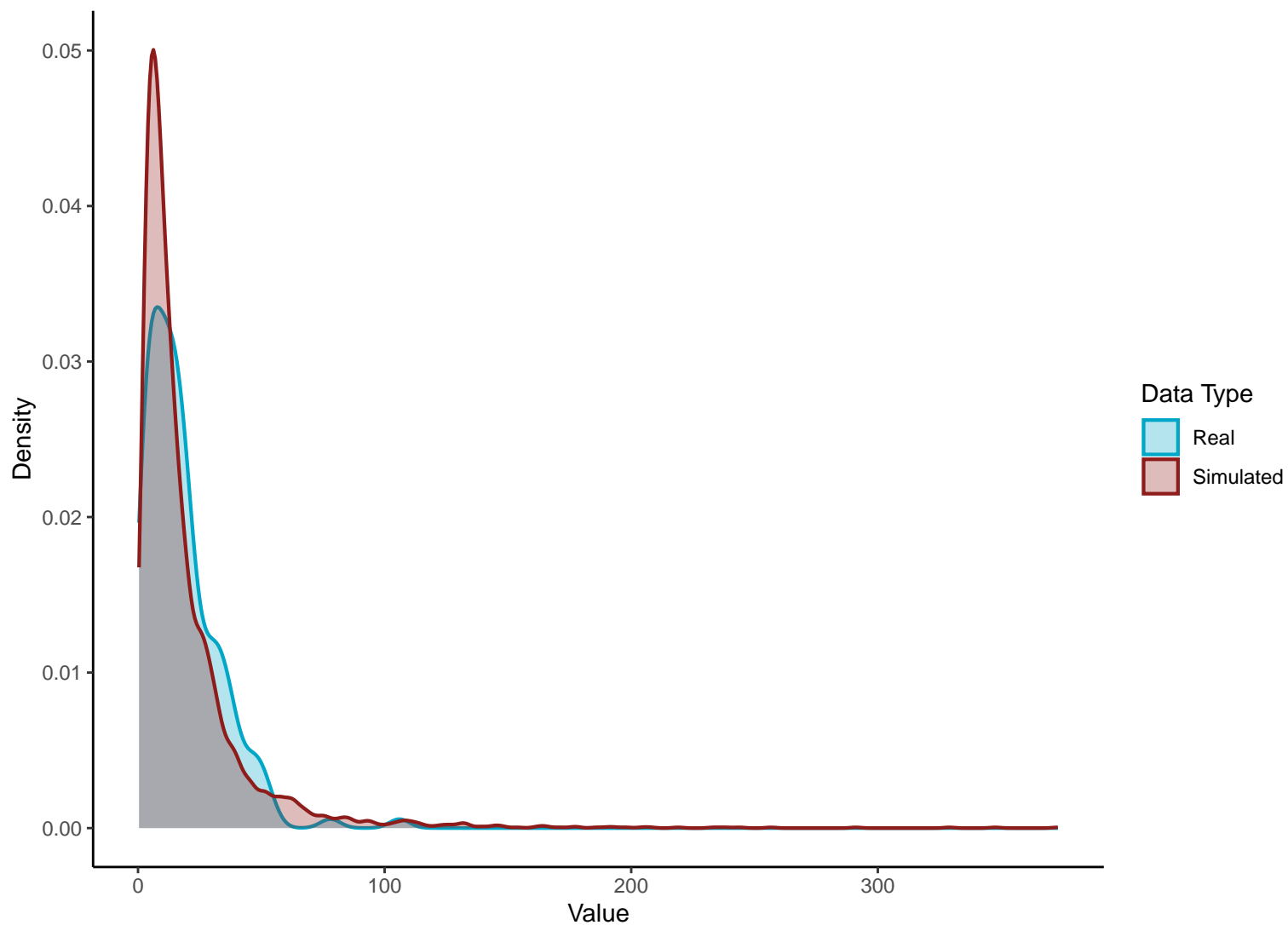
X.Eubacterium..brachy.group



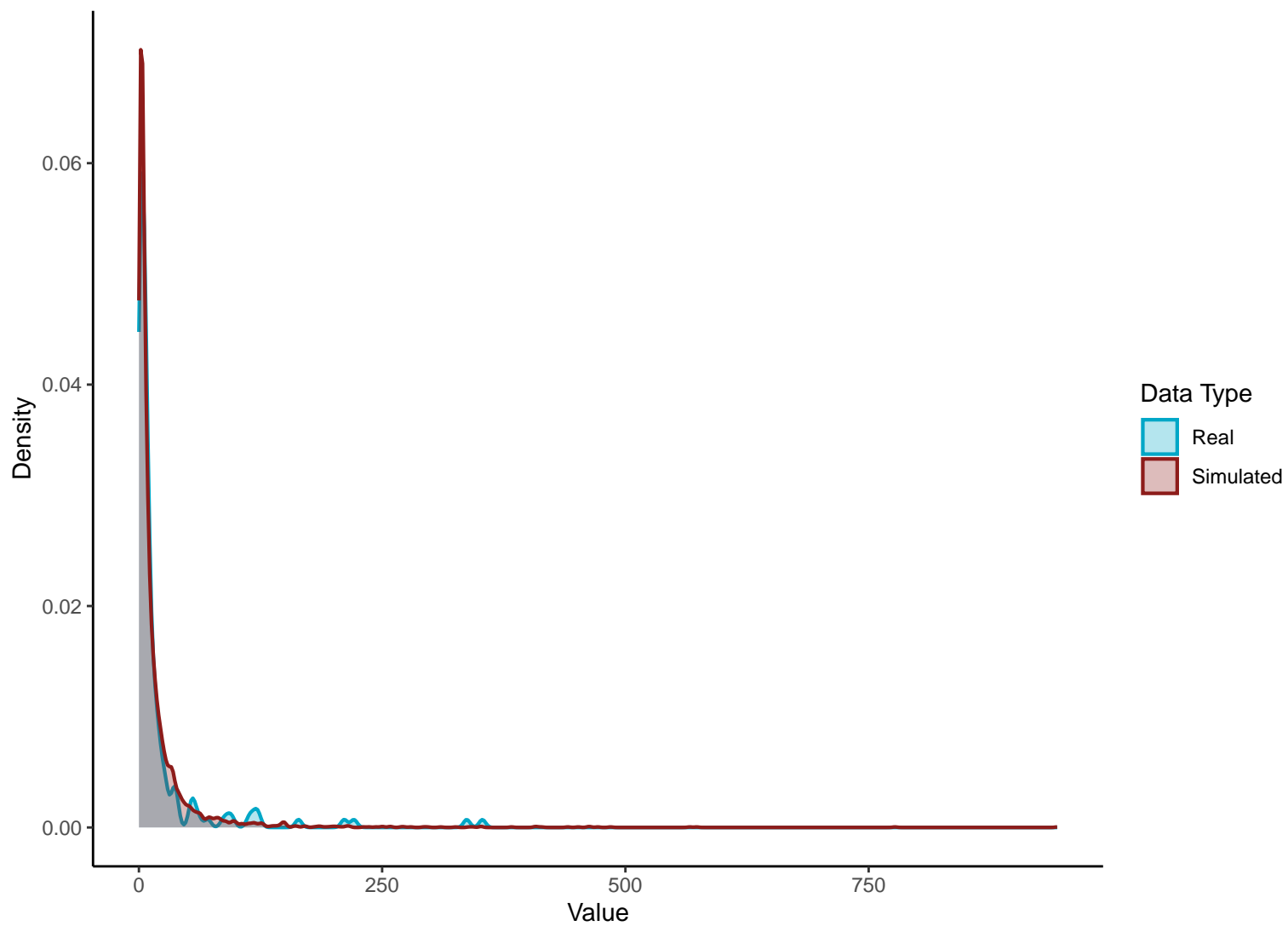
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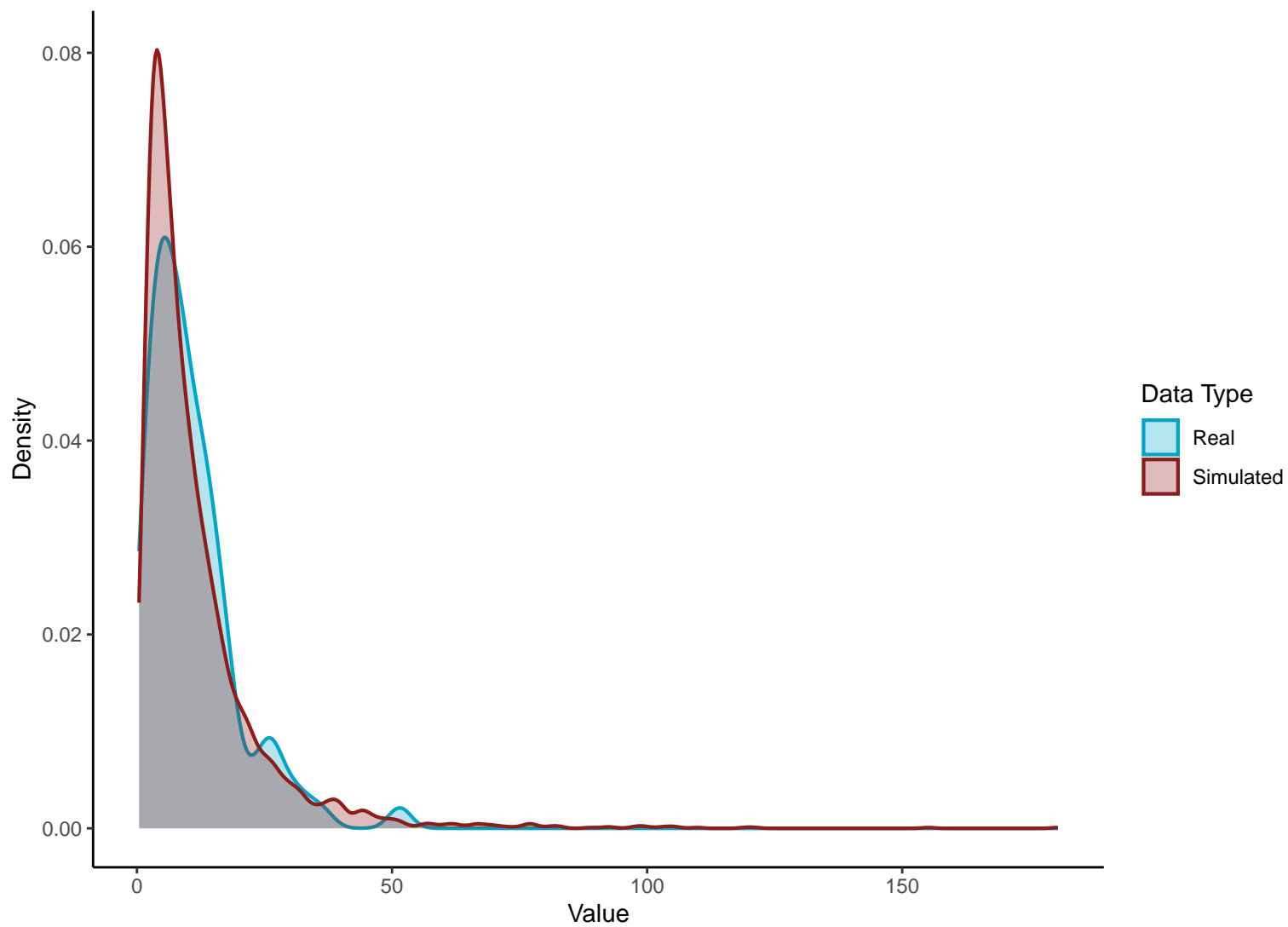
Lachnospiraceae.UCG.004



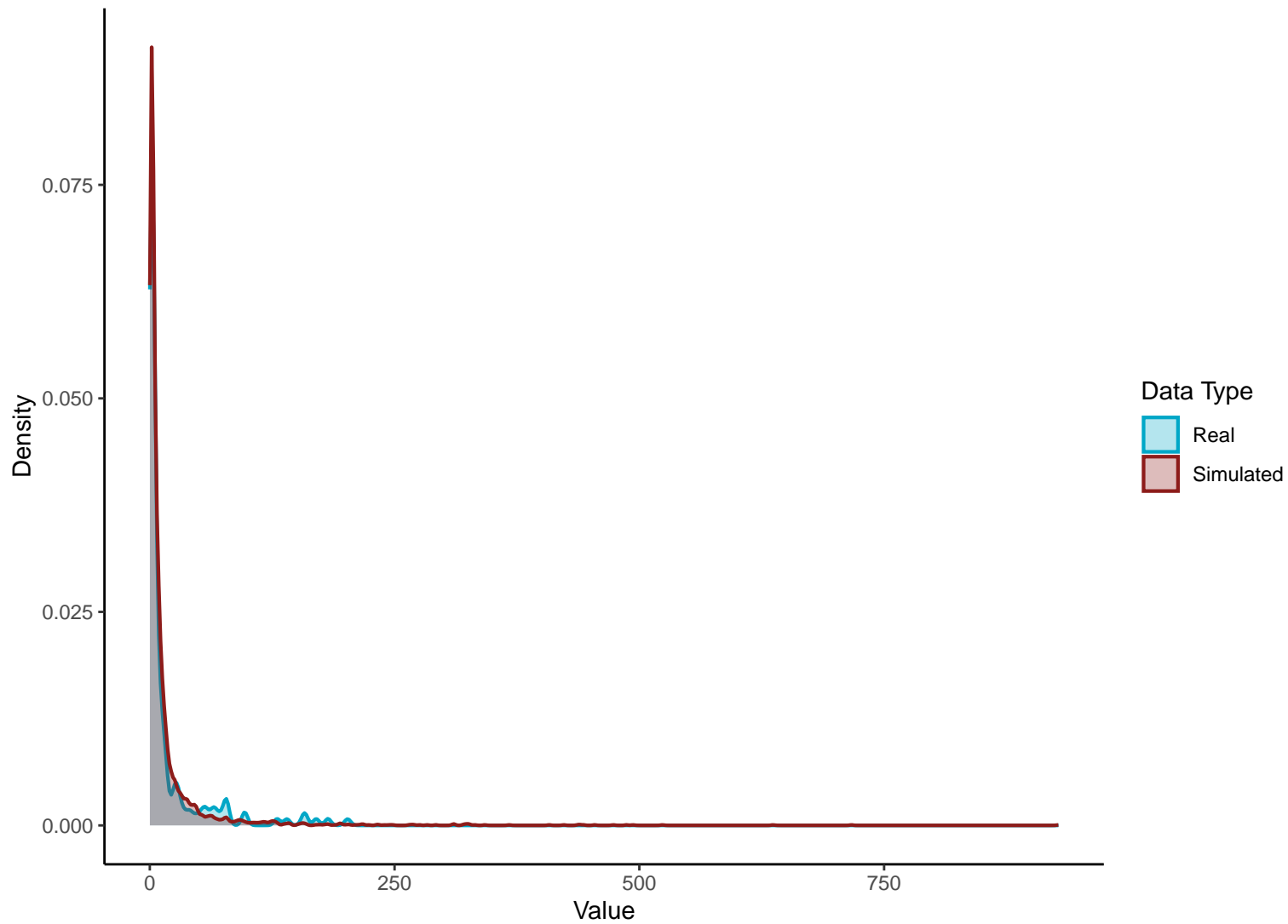
dgA.11.gut.group



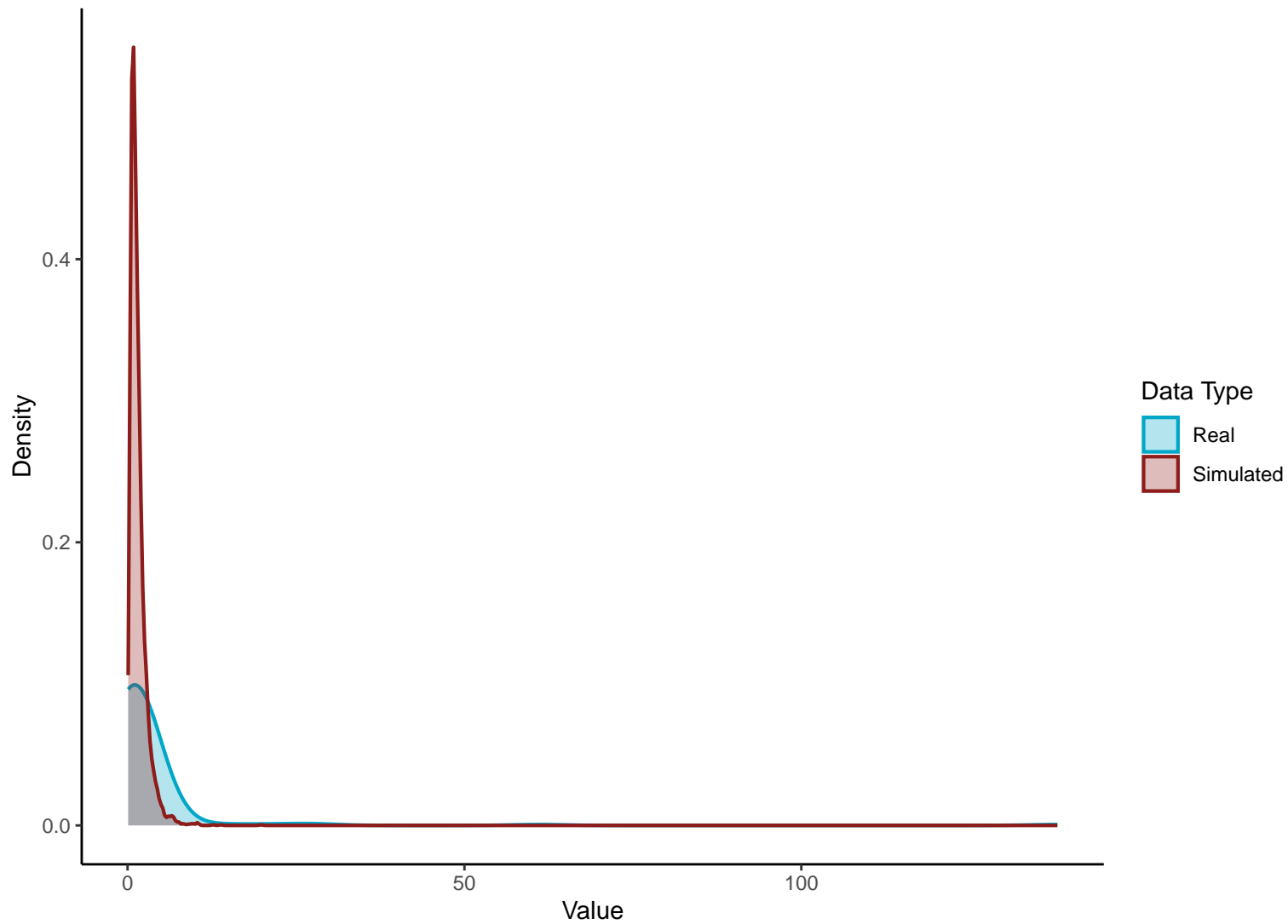
Erysipelotrichaceae.UGC.006



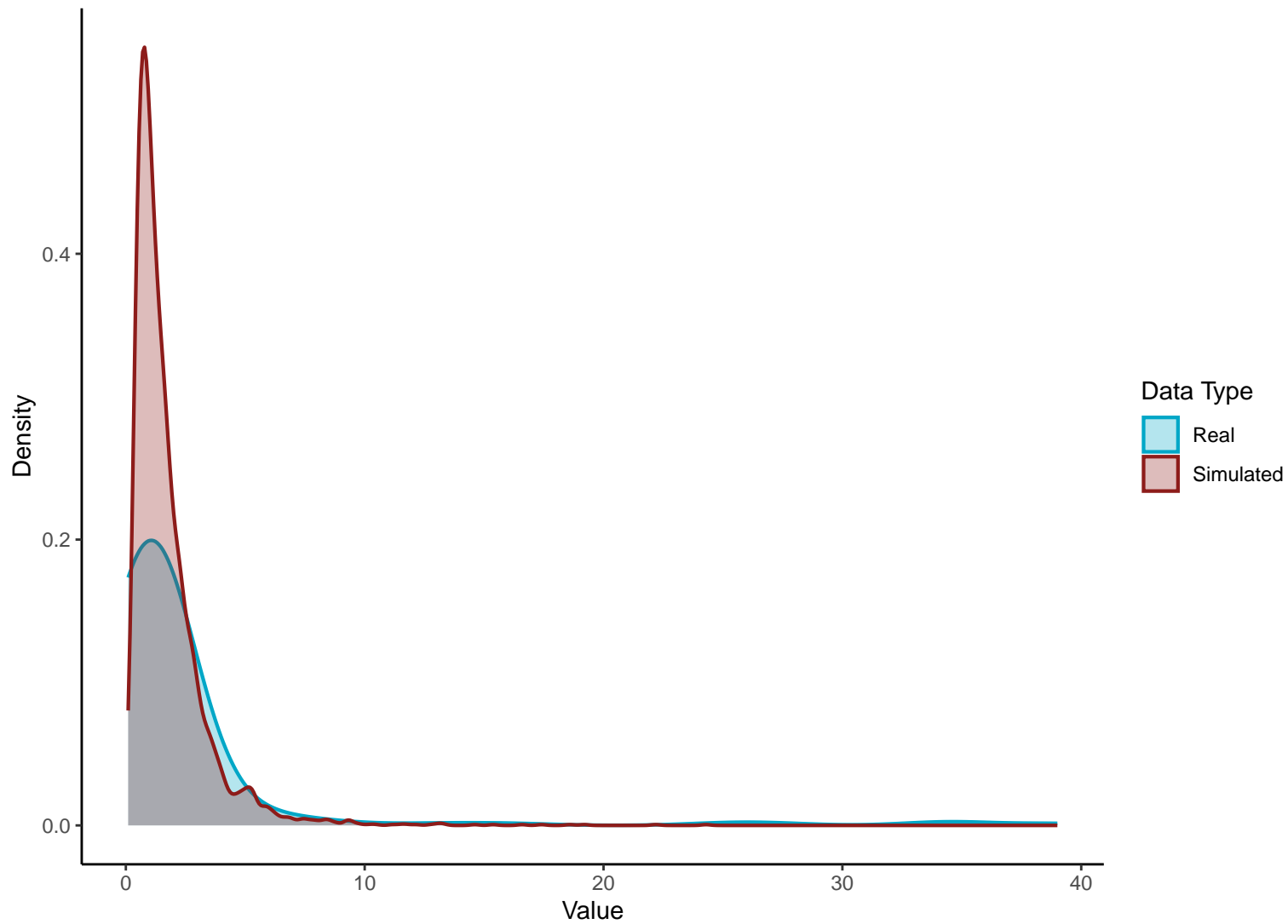
Erysipelotrichaceae.UCG.003



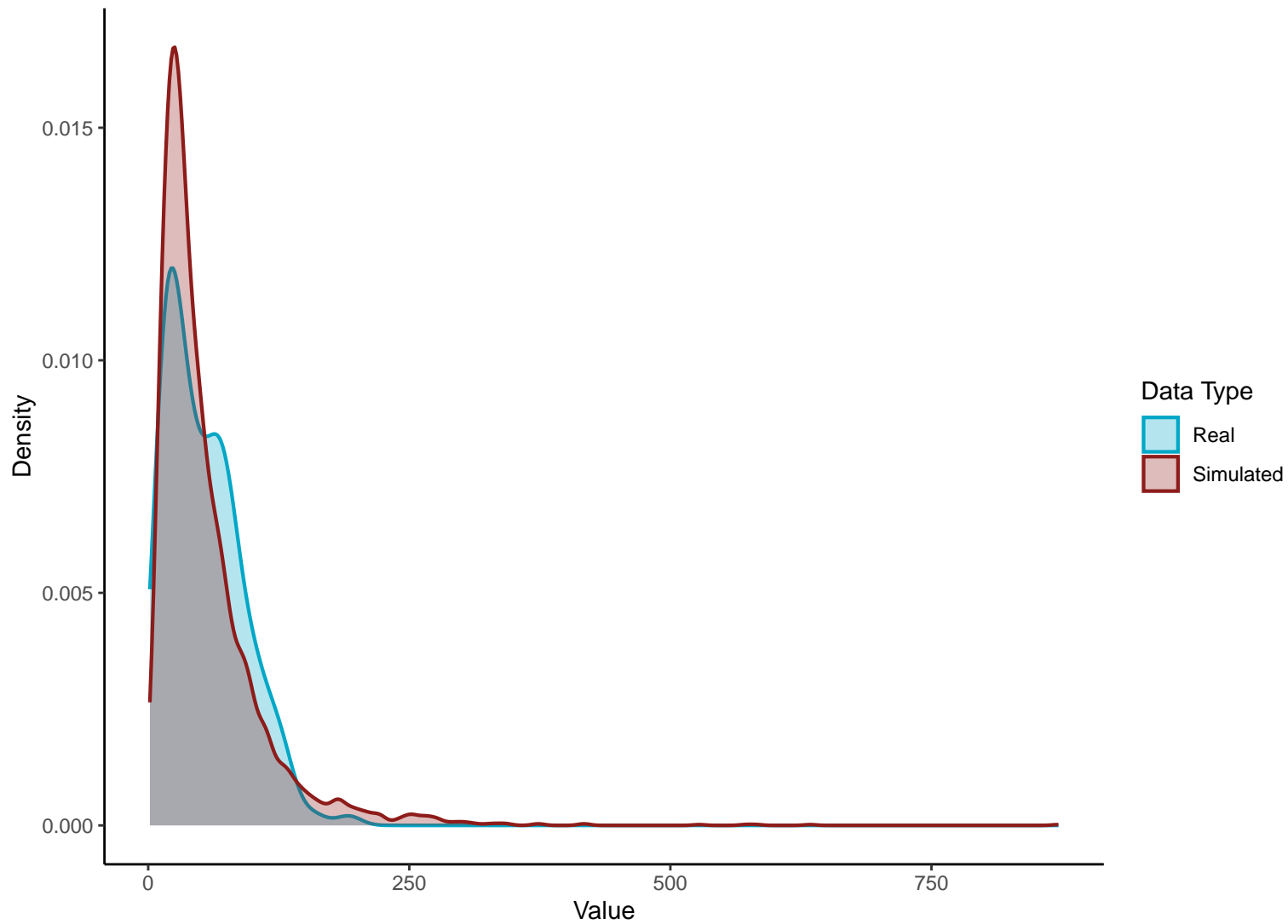
X.Eubacterium..saphenum.group



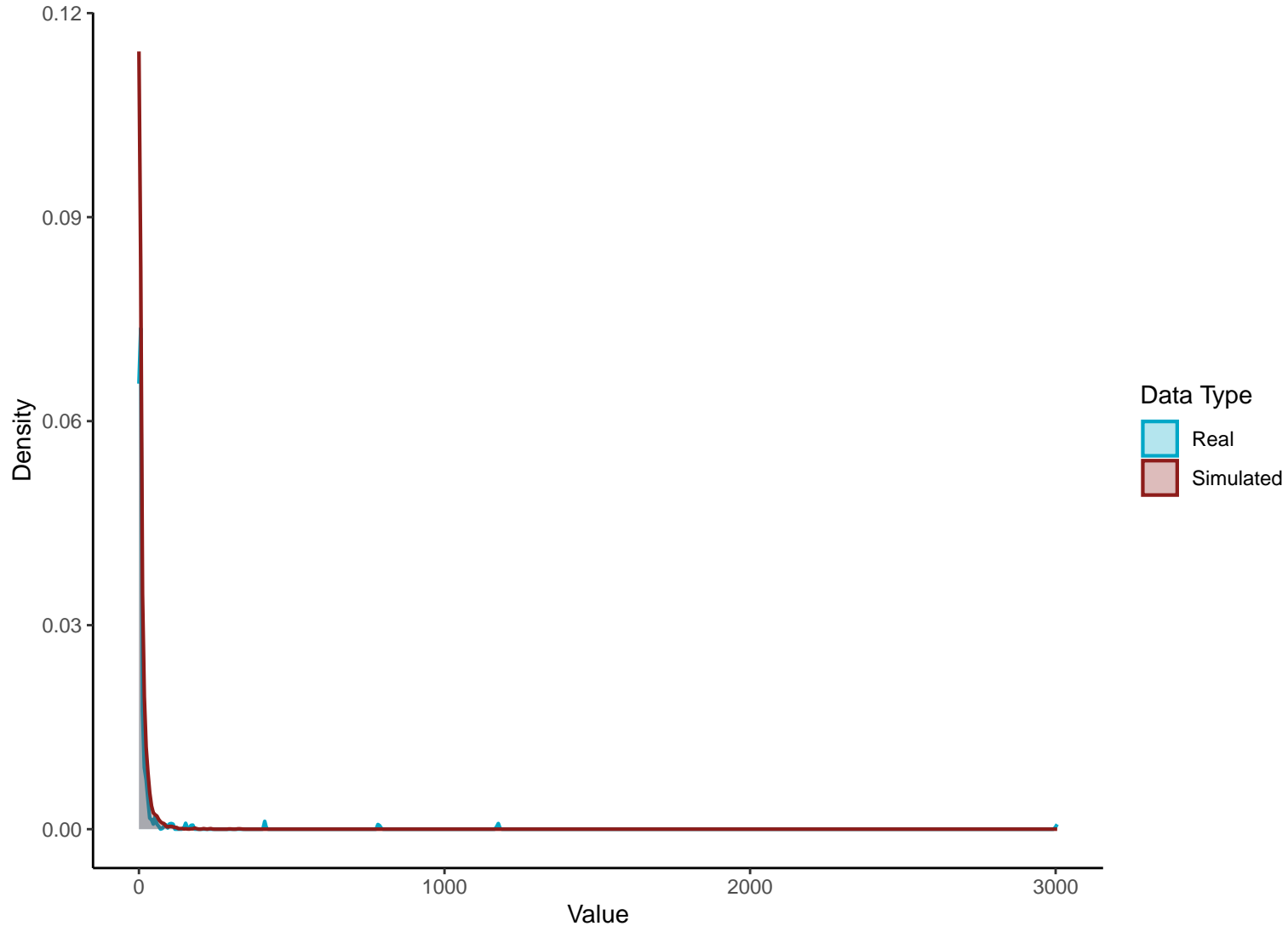
X.Ruminococcus..gnavus.group



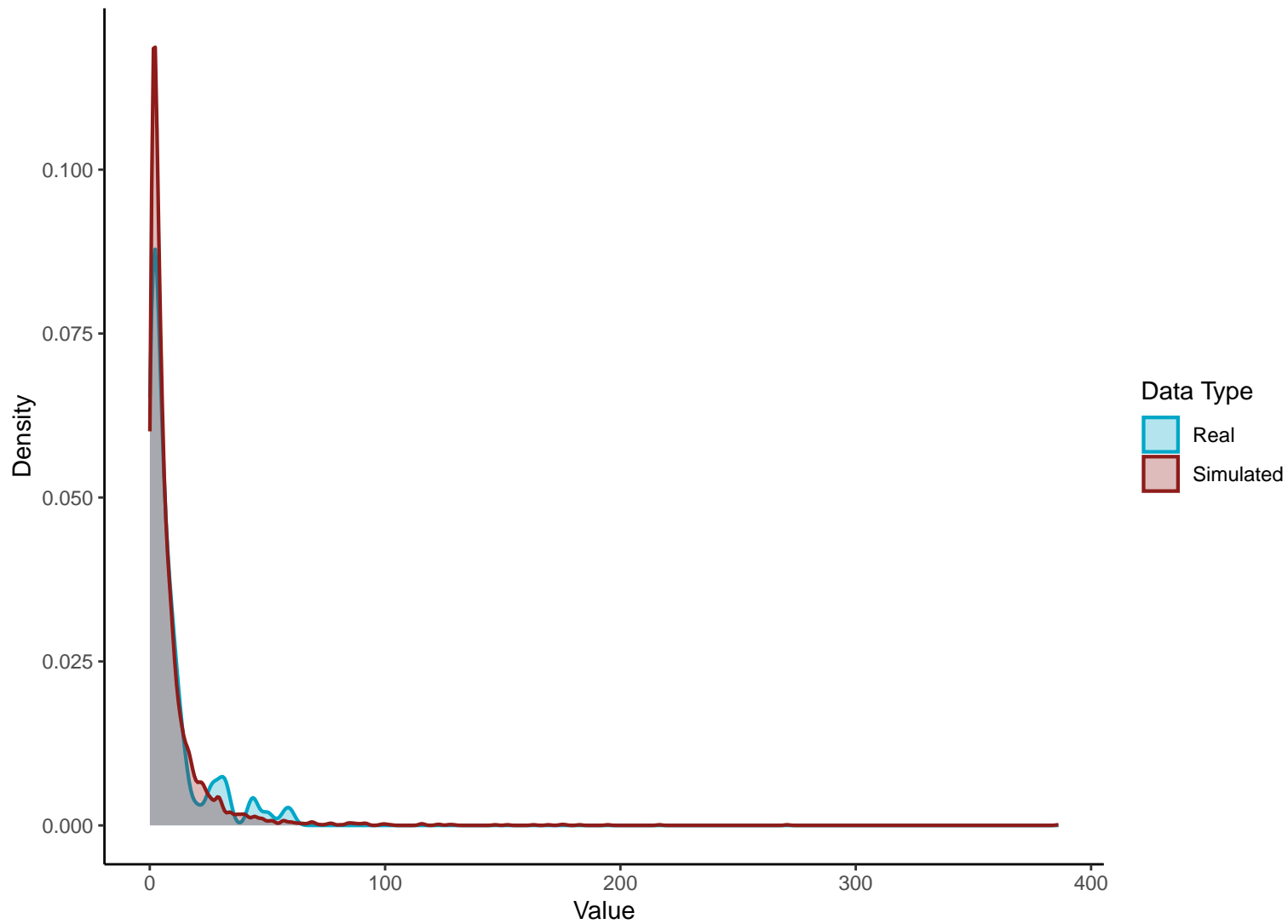
Fournierella



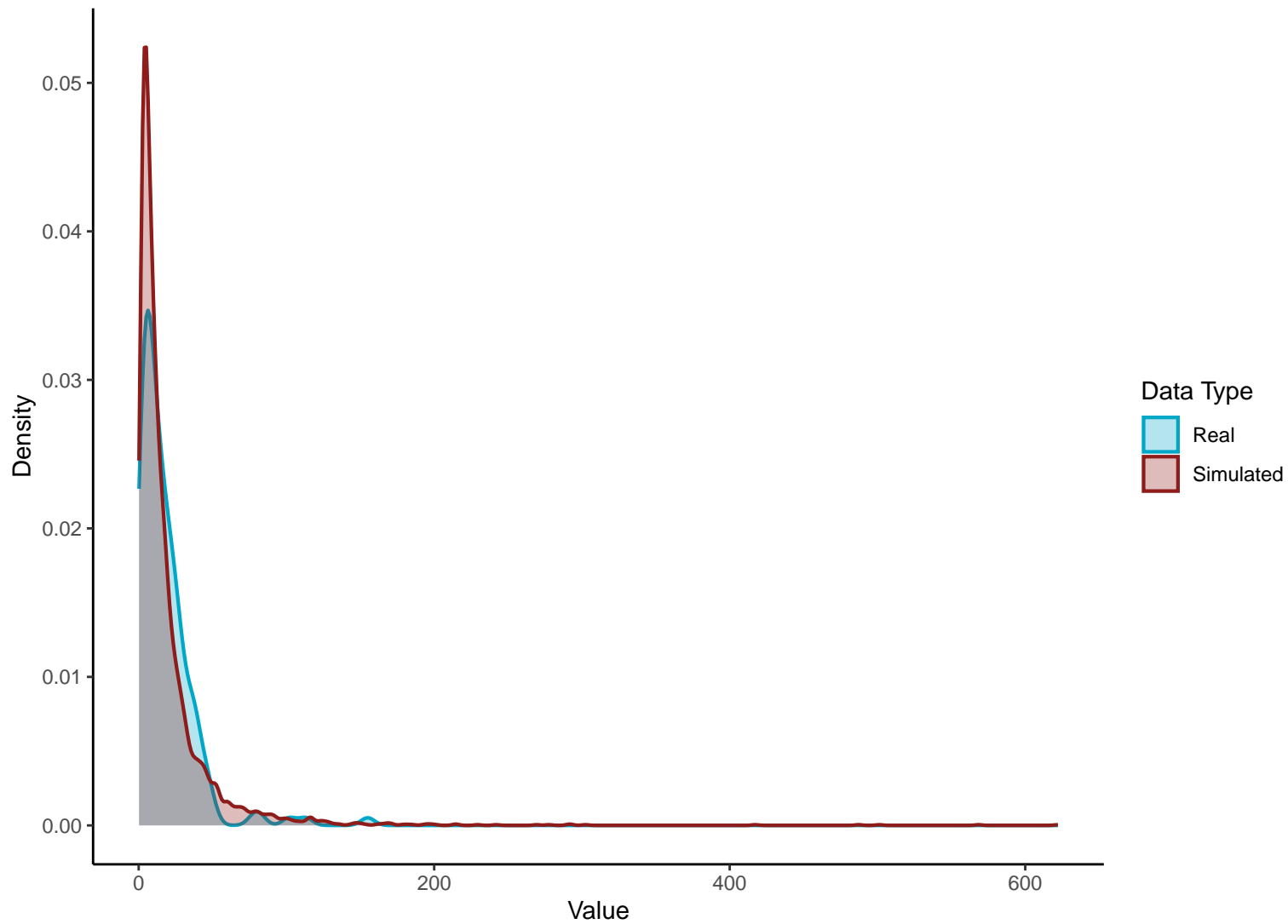
Escherichia.Shigella



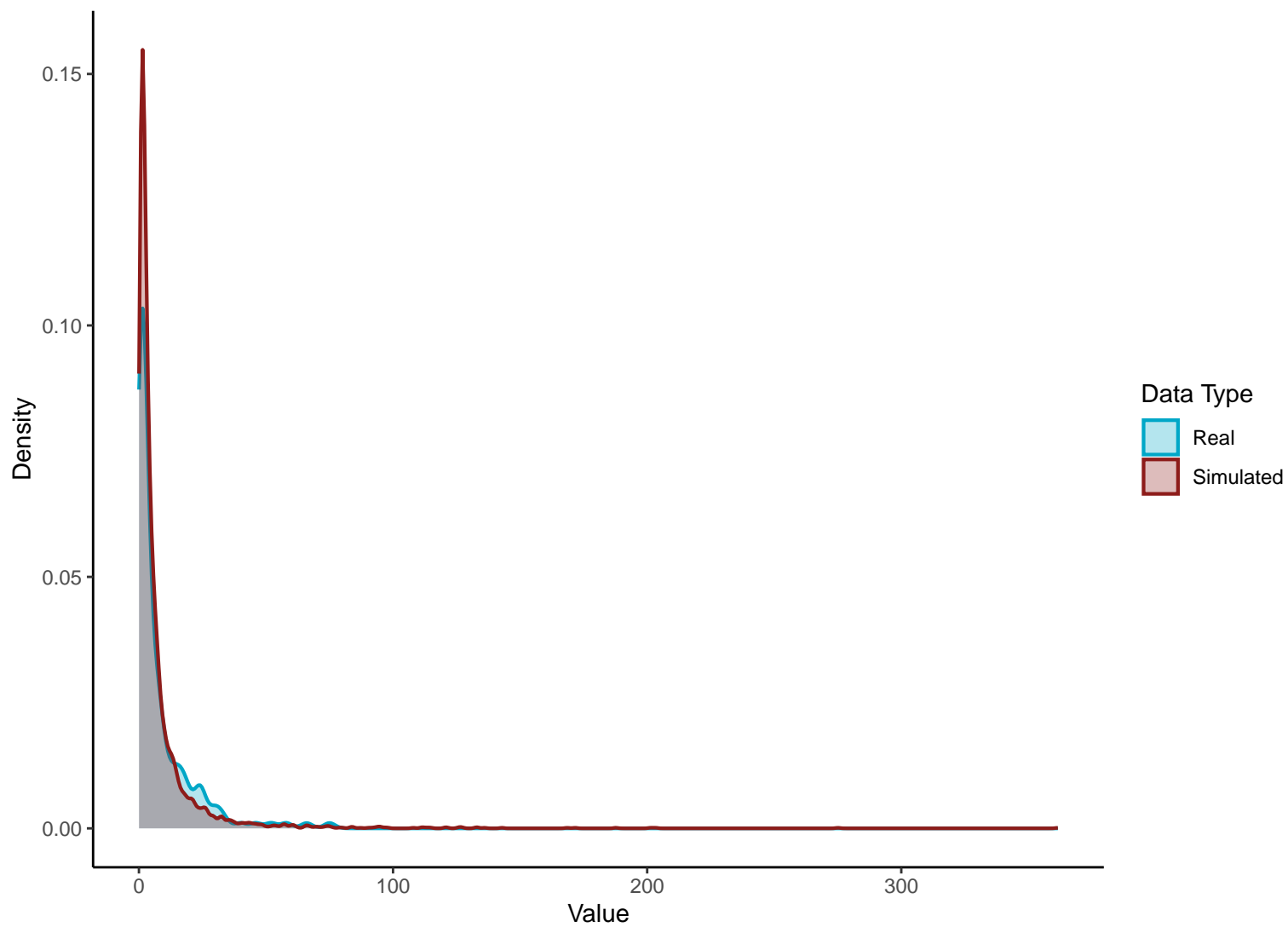
X.Eubacterium..fissicatena.group



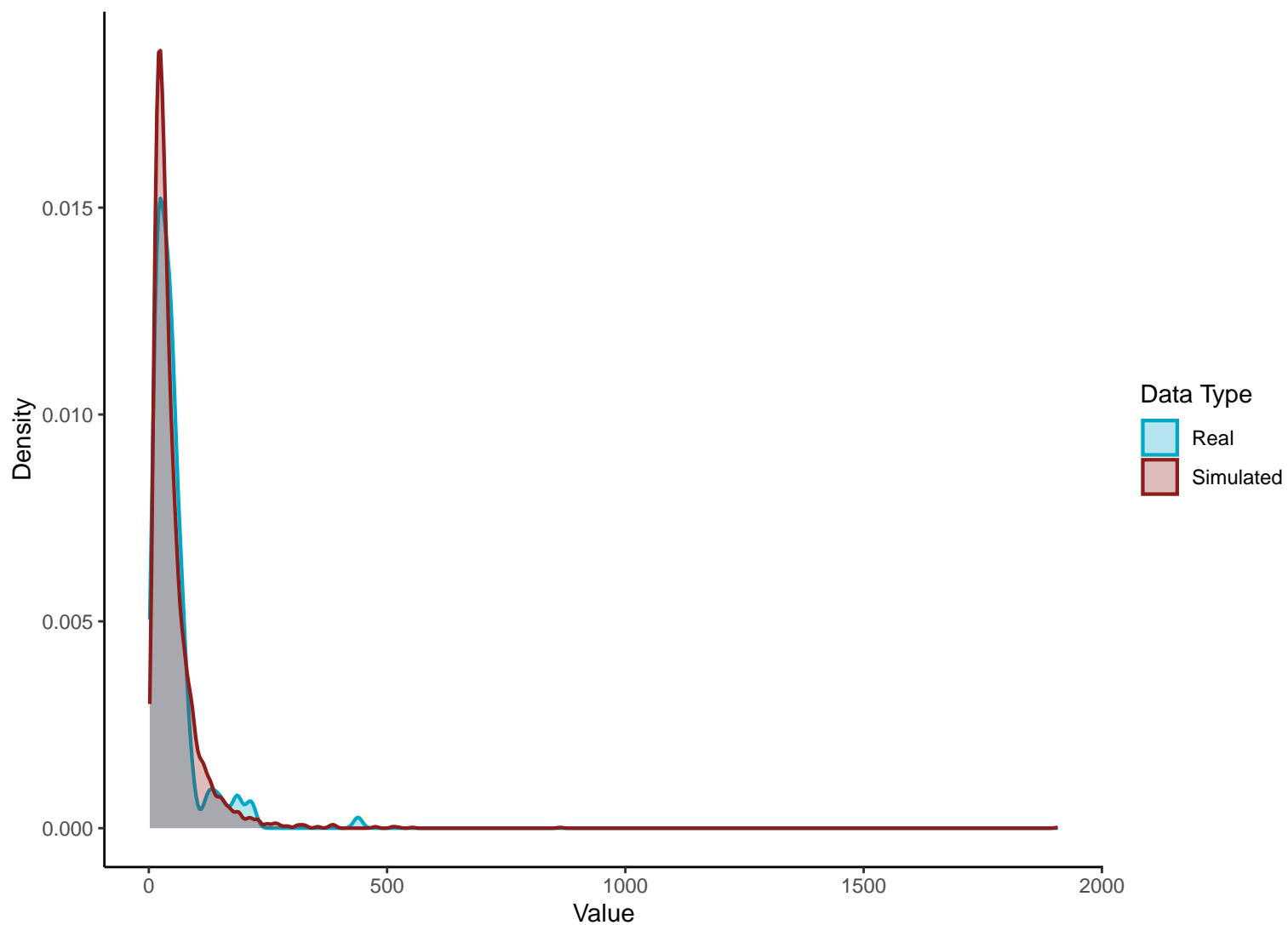
X.Anaerorhabdus..furcosa.group



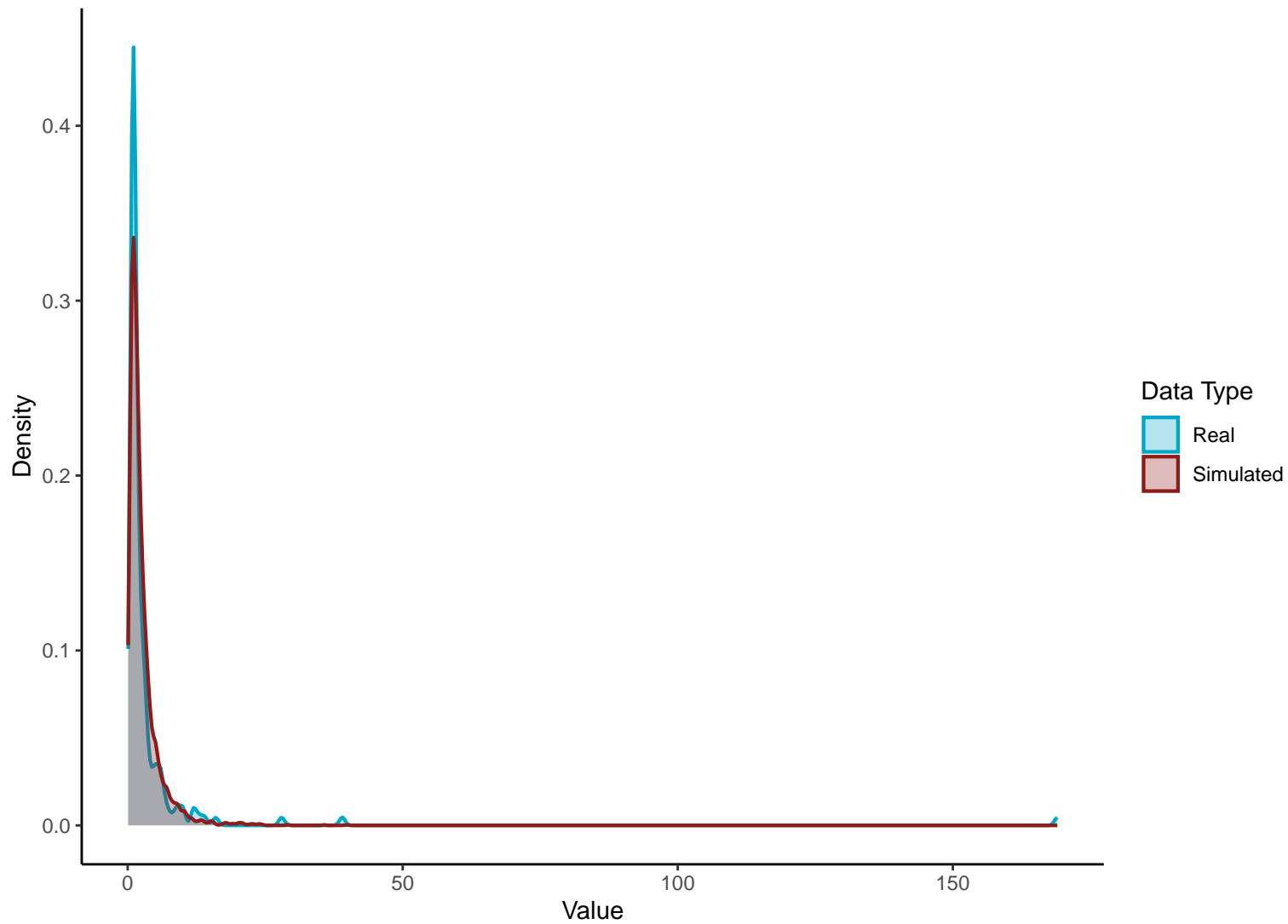
Lachnospiraceae.UGC.009



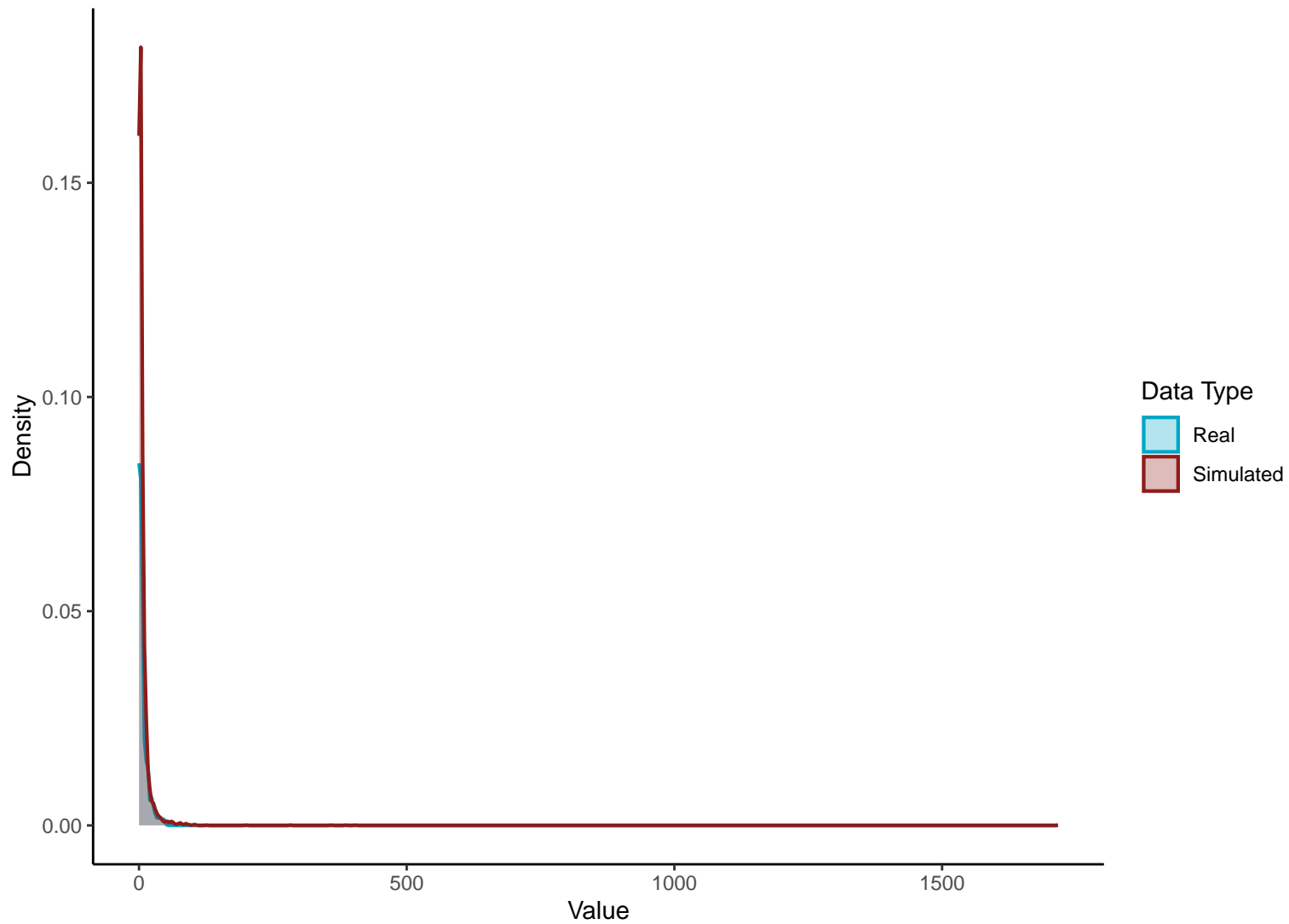
Paraeggerthella



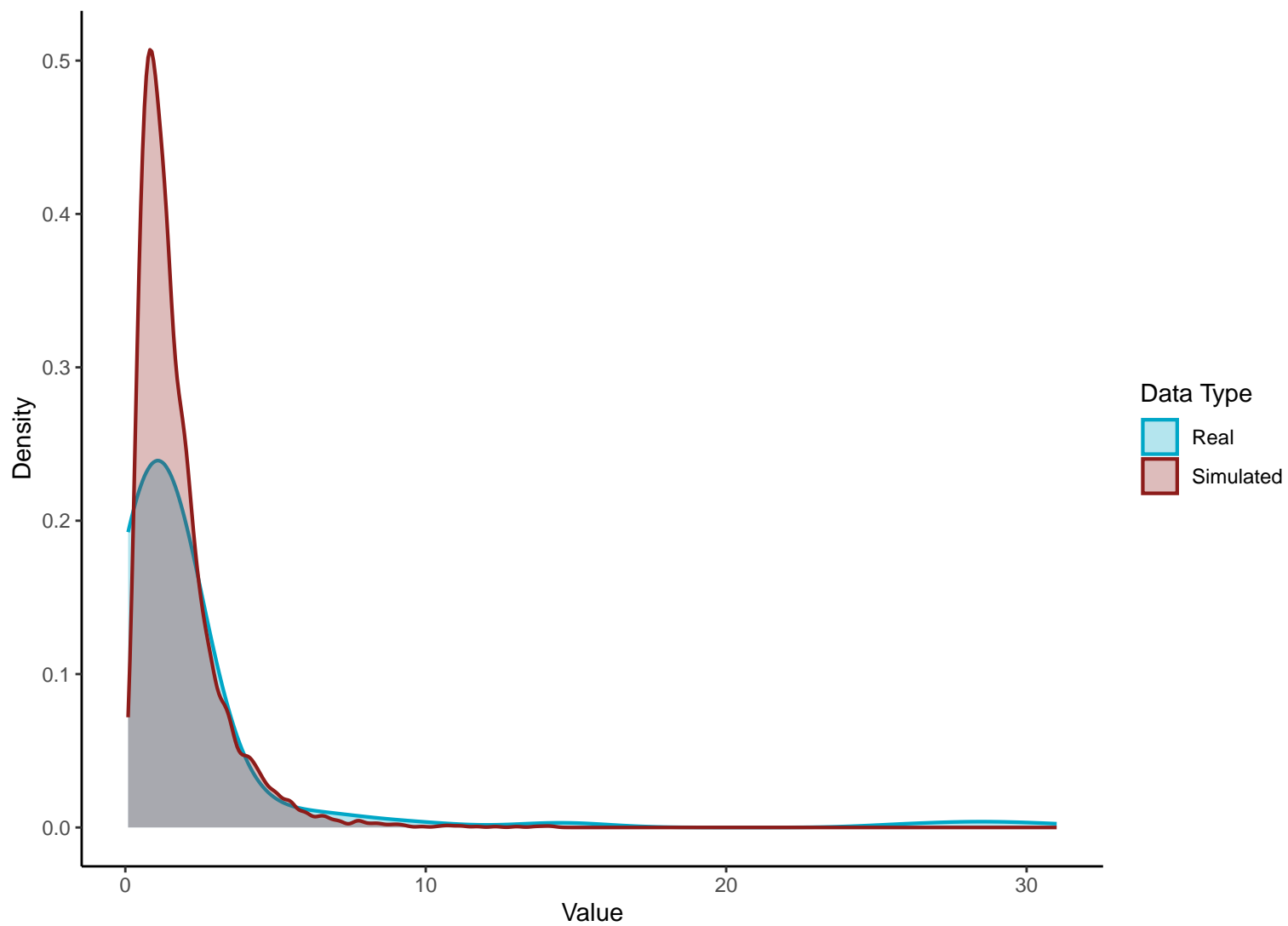
Selenomonas



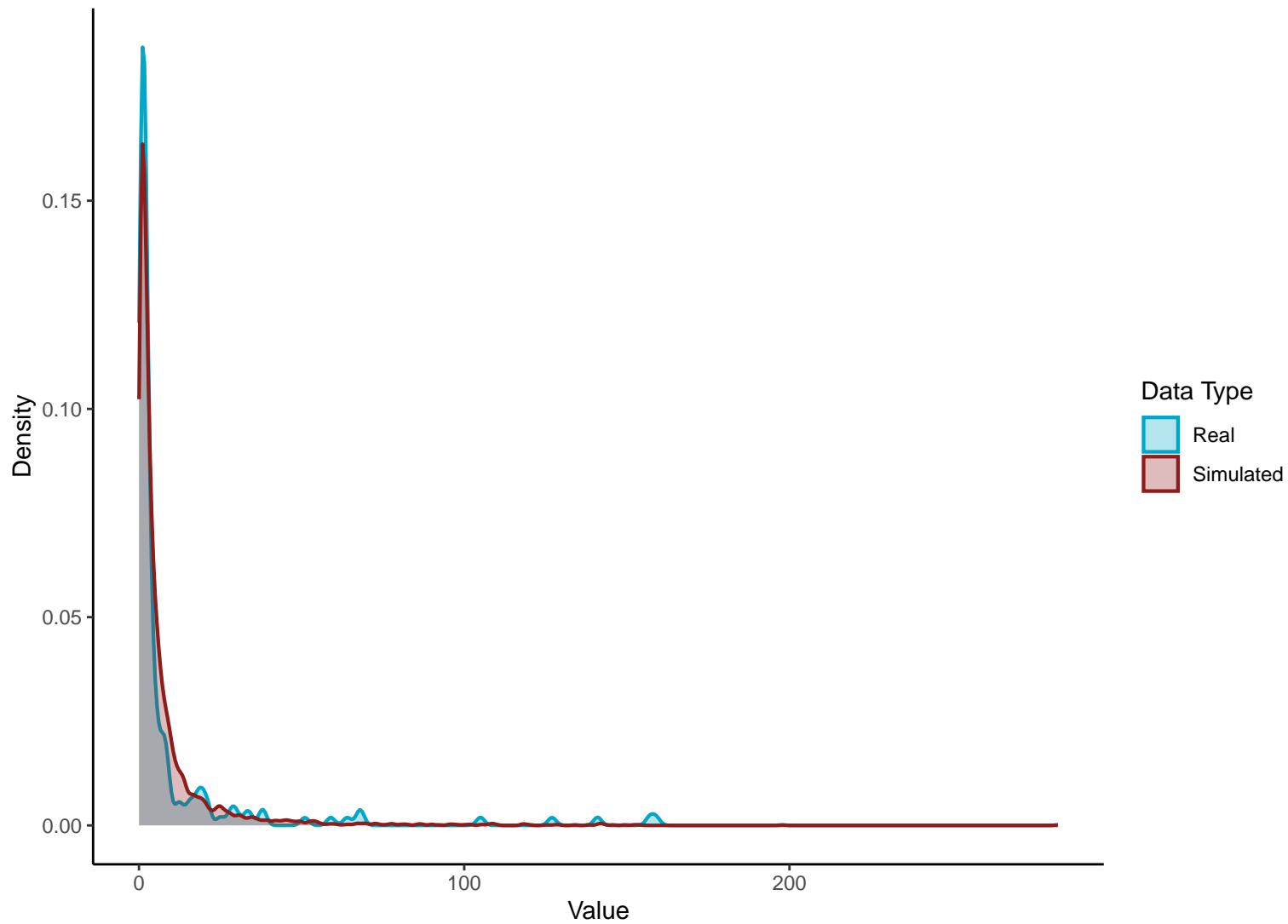
Senegalimassilia



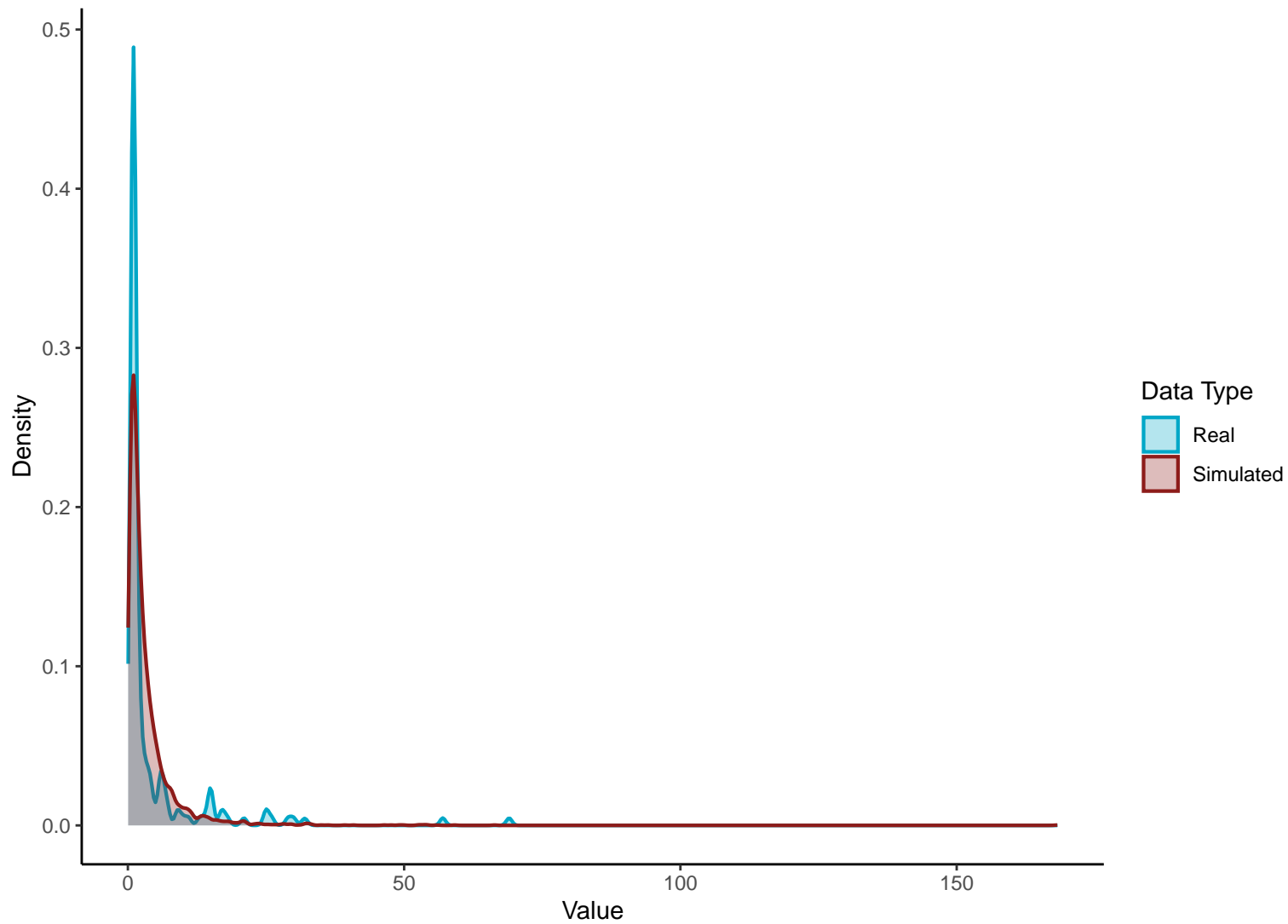
FD2005



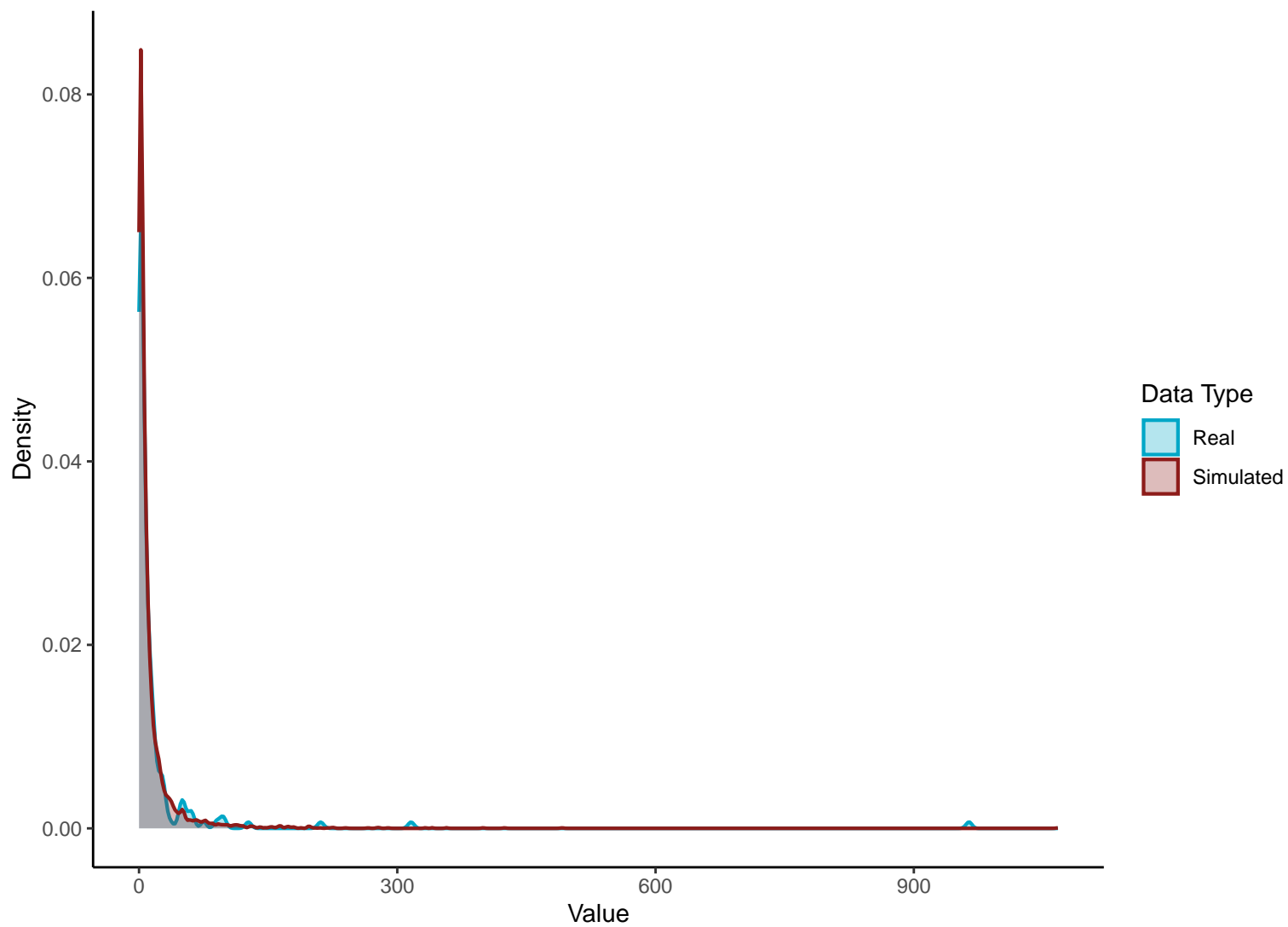
Veillonella



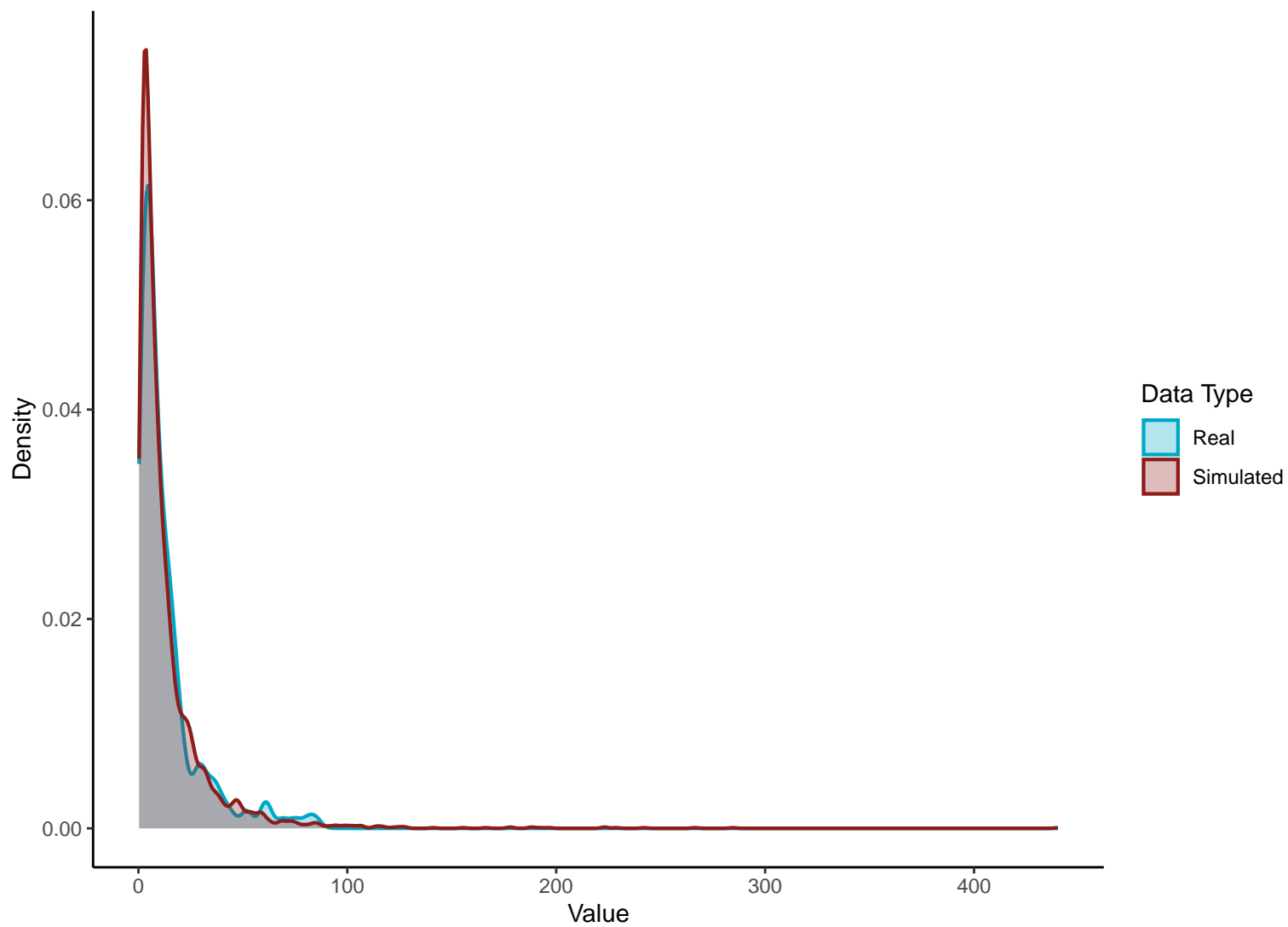
Clostridium.sensu.stricto.6



CAG.352



CAG.56



Candidatus.Stoquefichus

