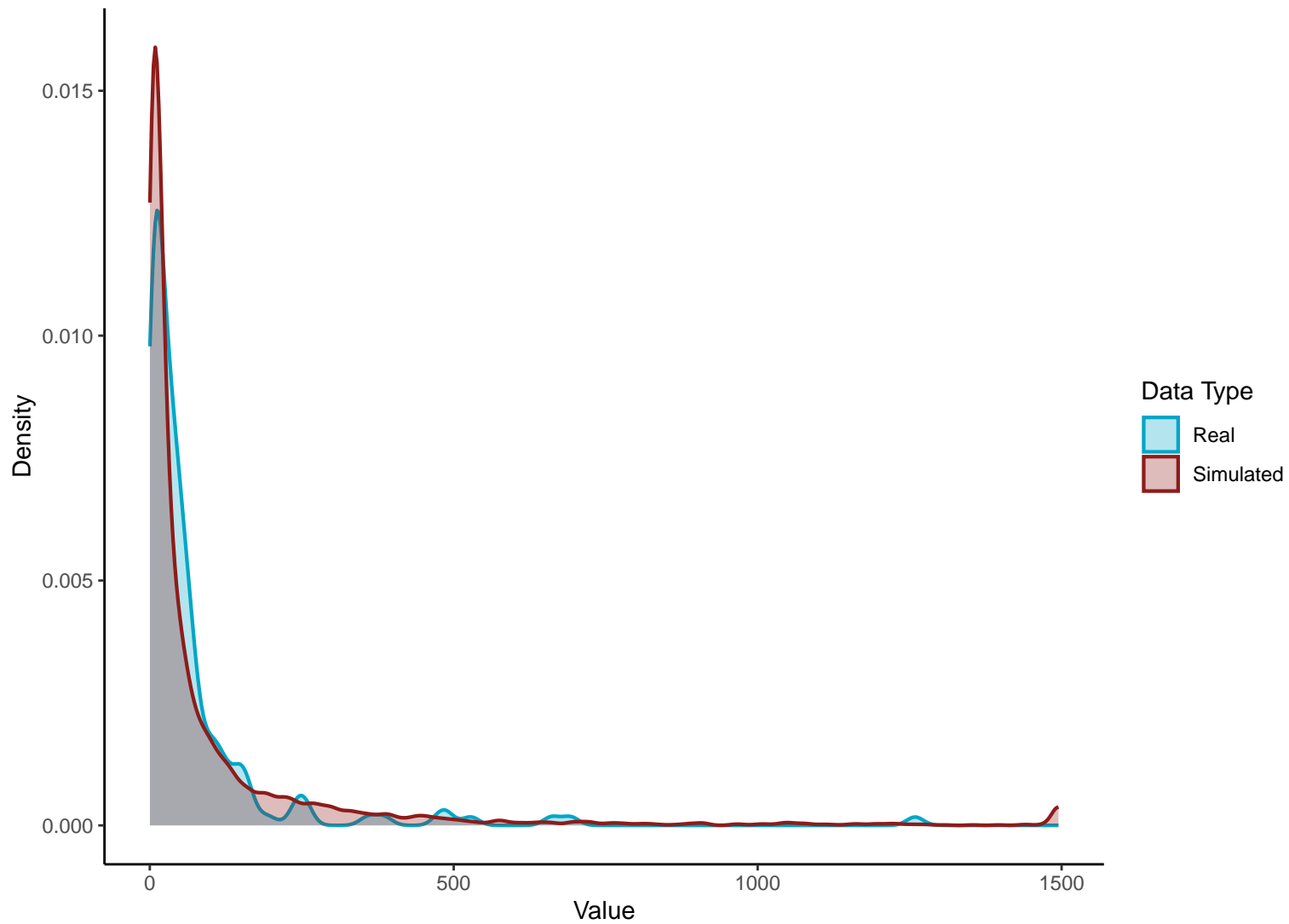
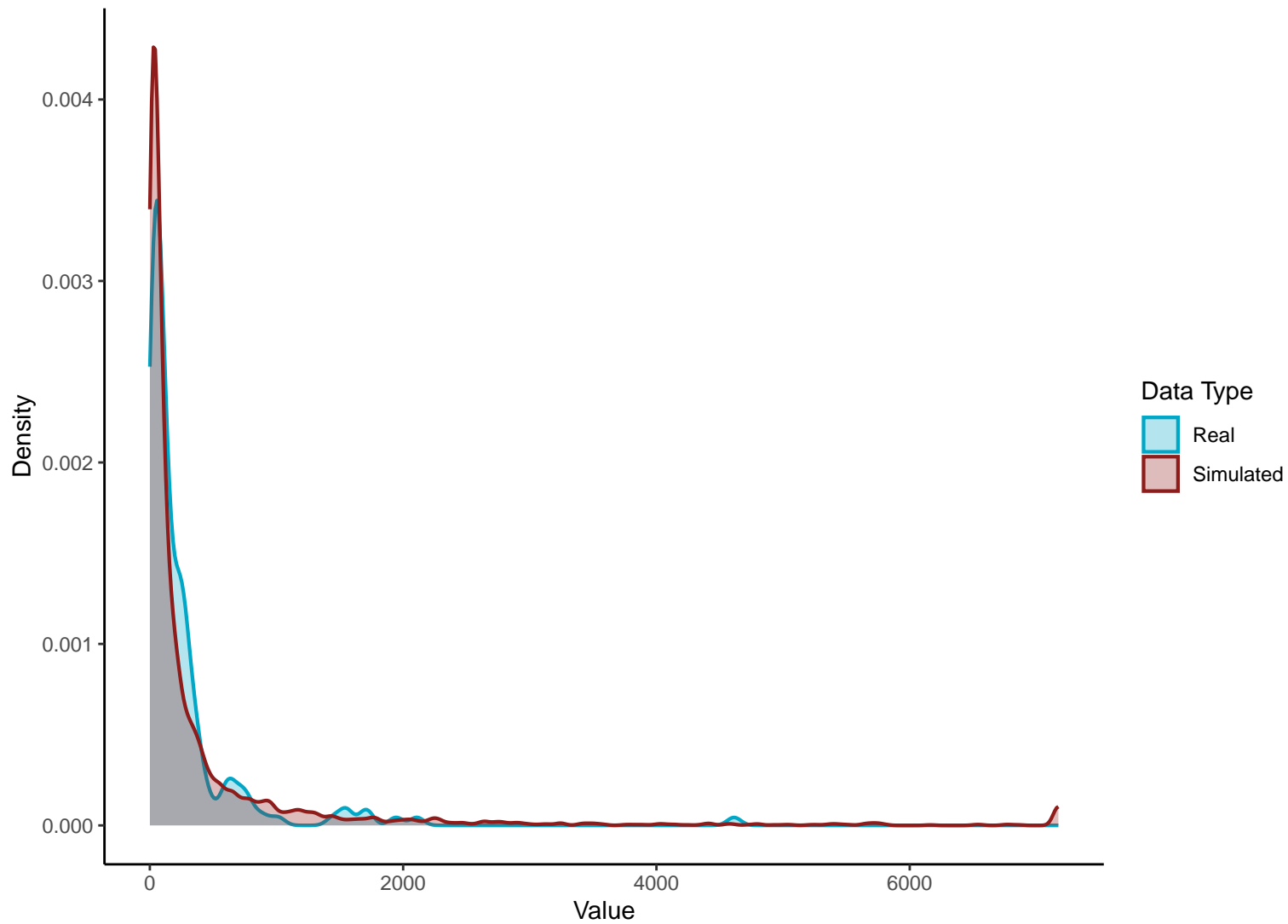


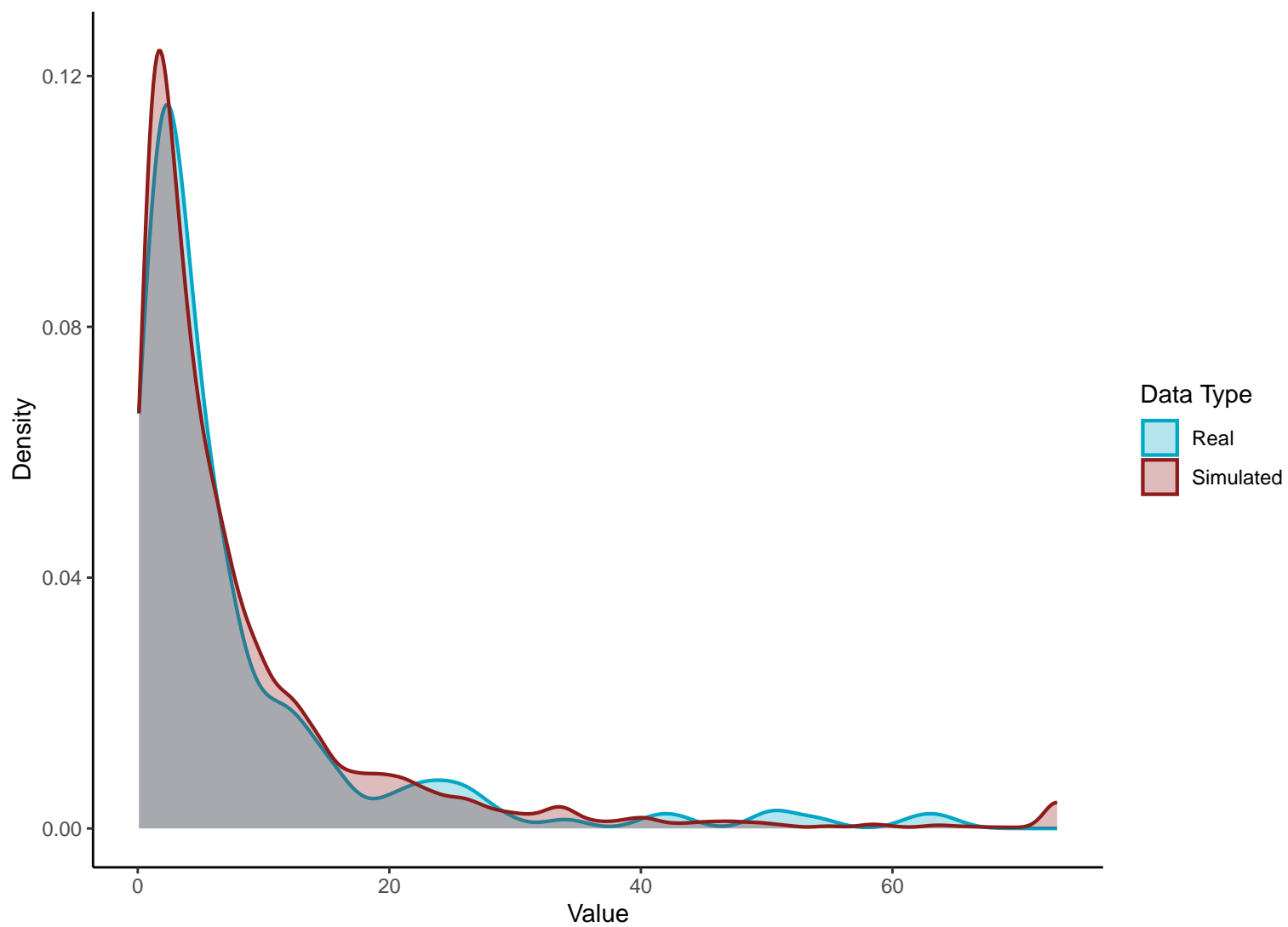
# Prevotellaceae.UGC.003



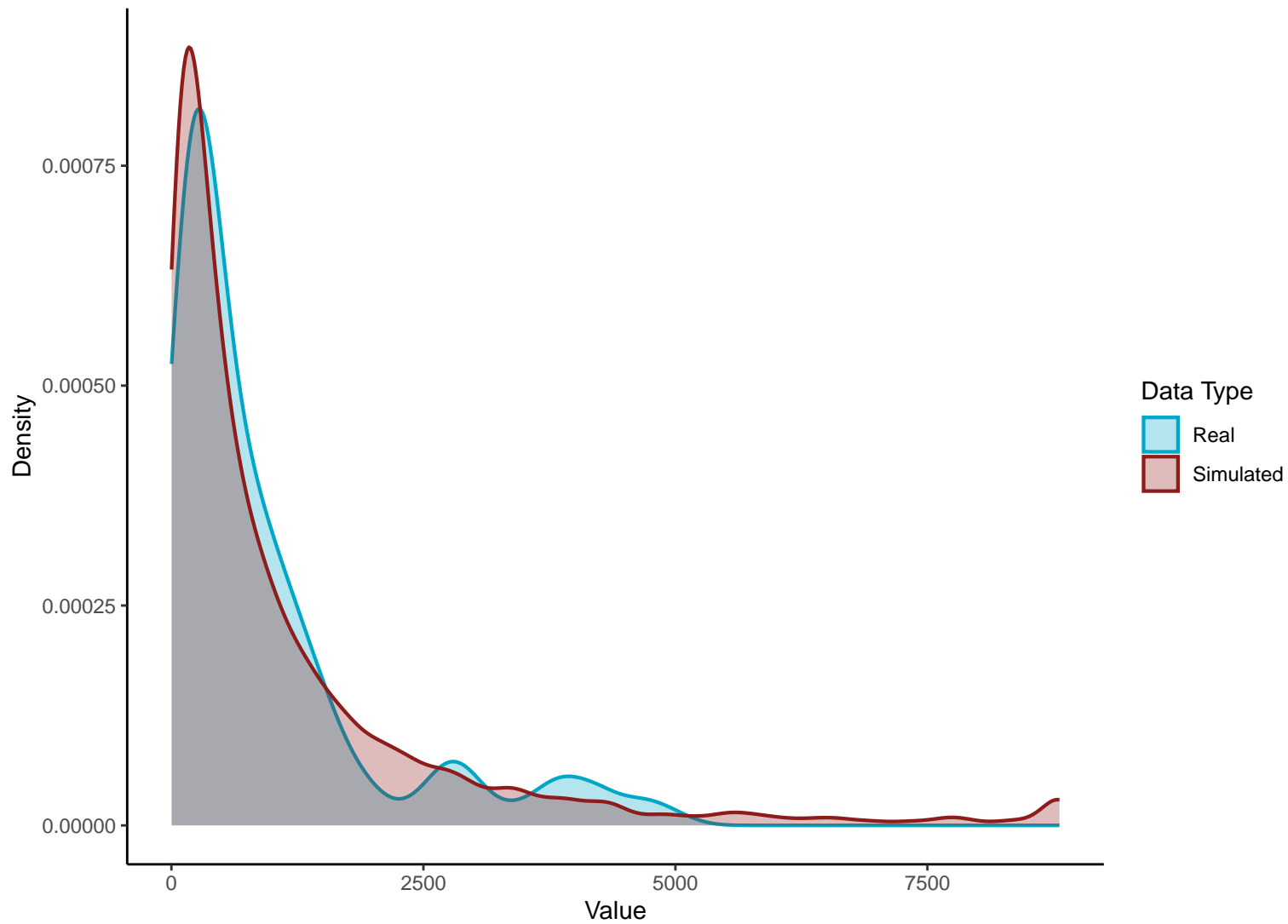
# Prevotellaceae.NK3B31.group



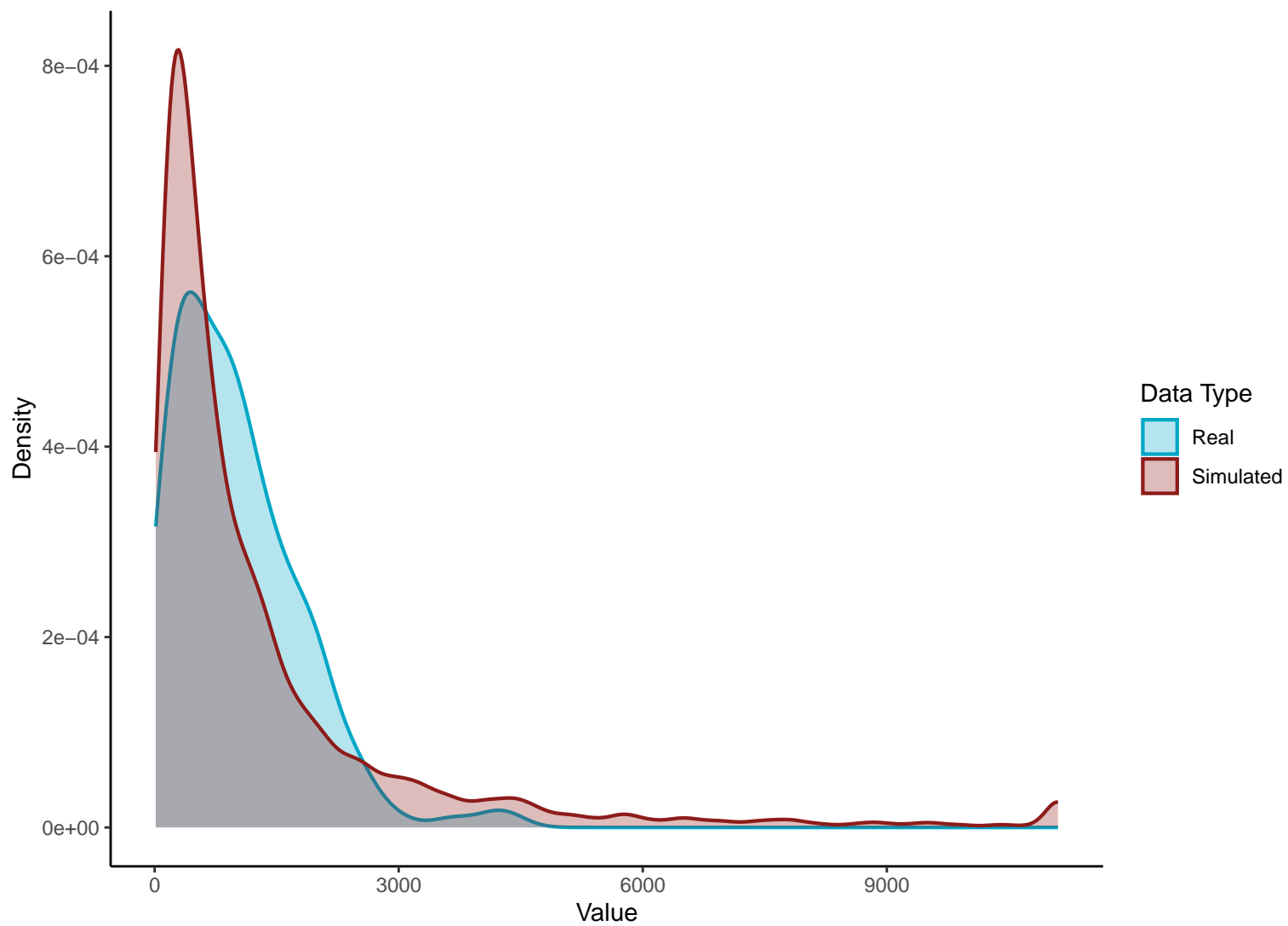
# Sutterella



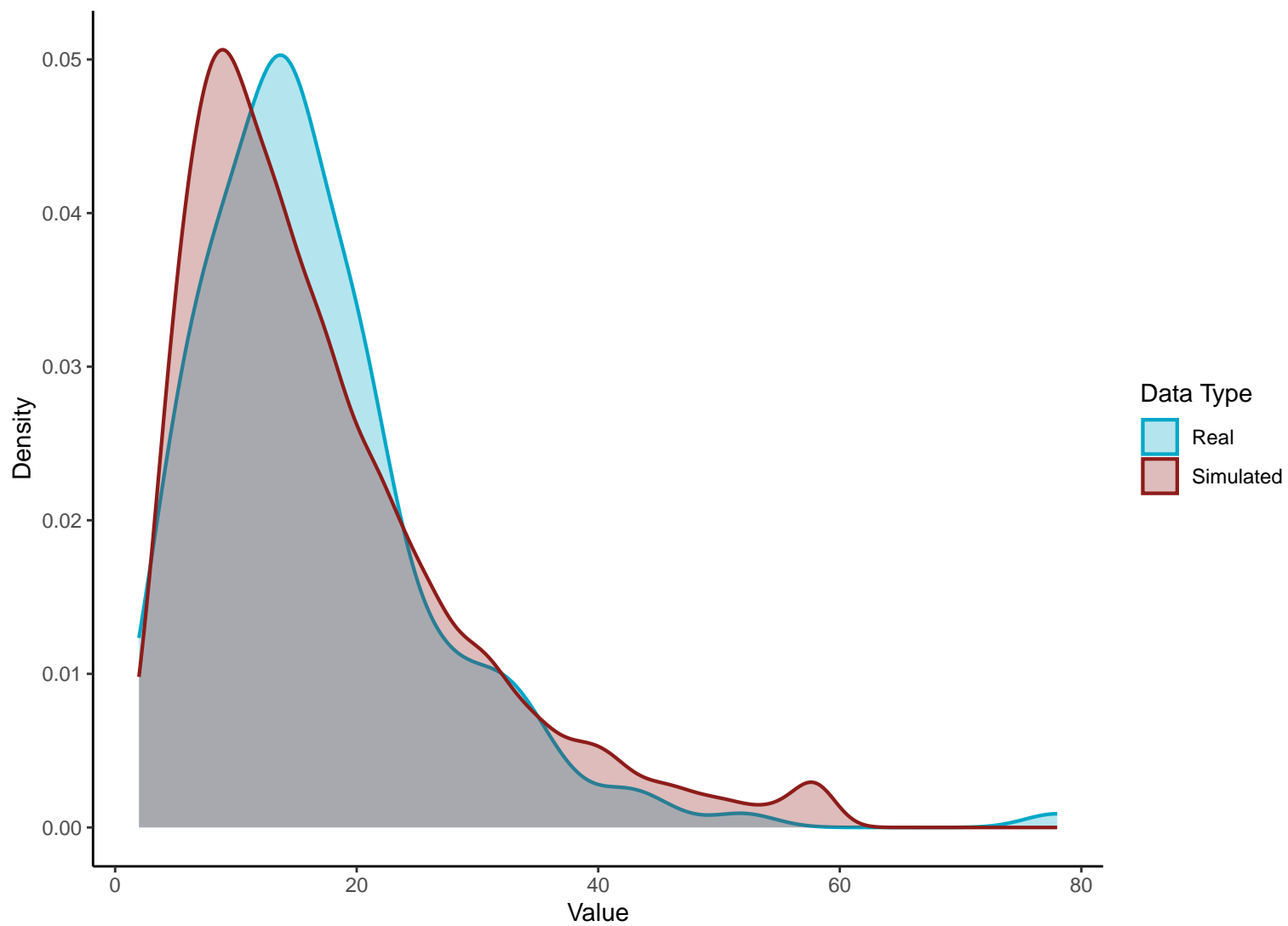
# Christensenellaceae.R.7.group



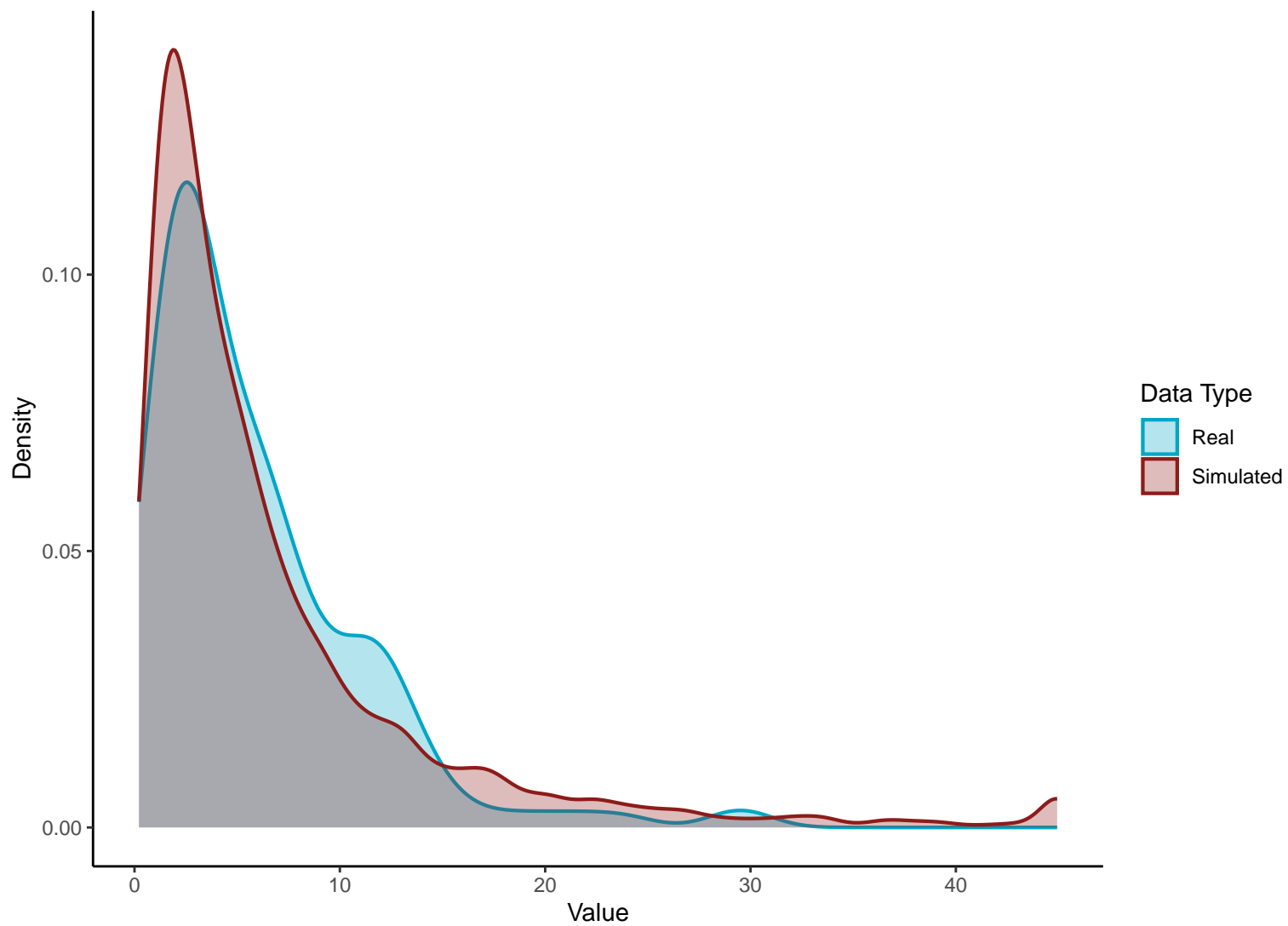
UCG.005



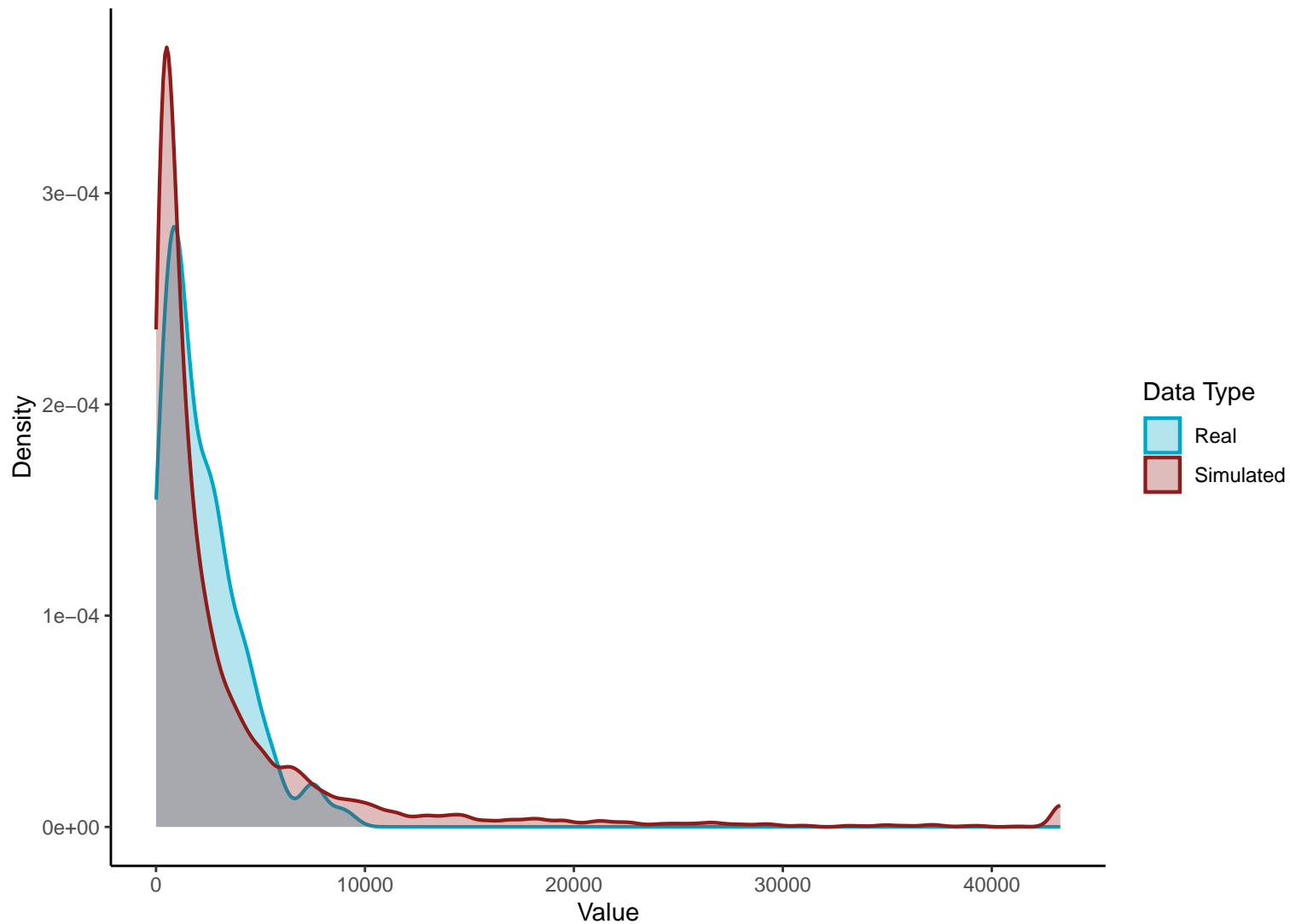
# Slackia



UCG.007

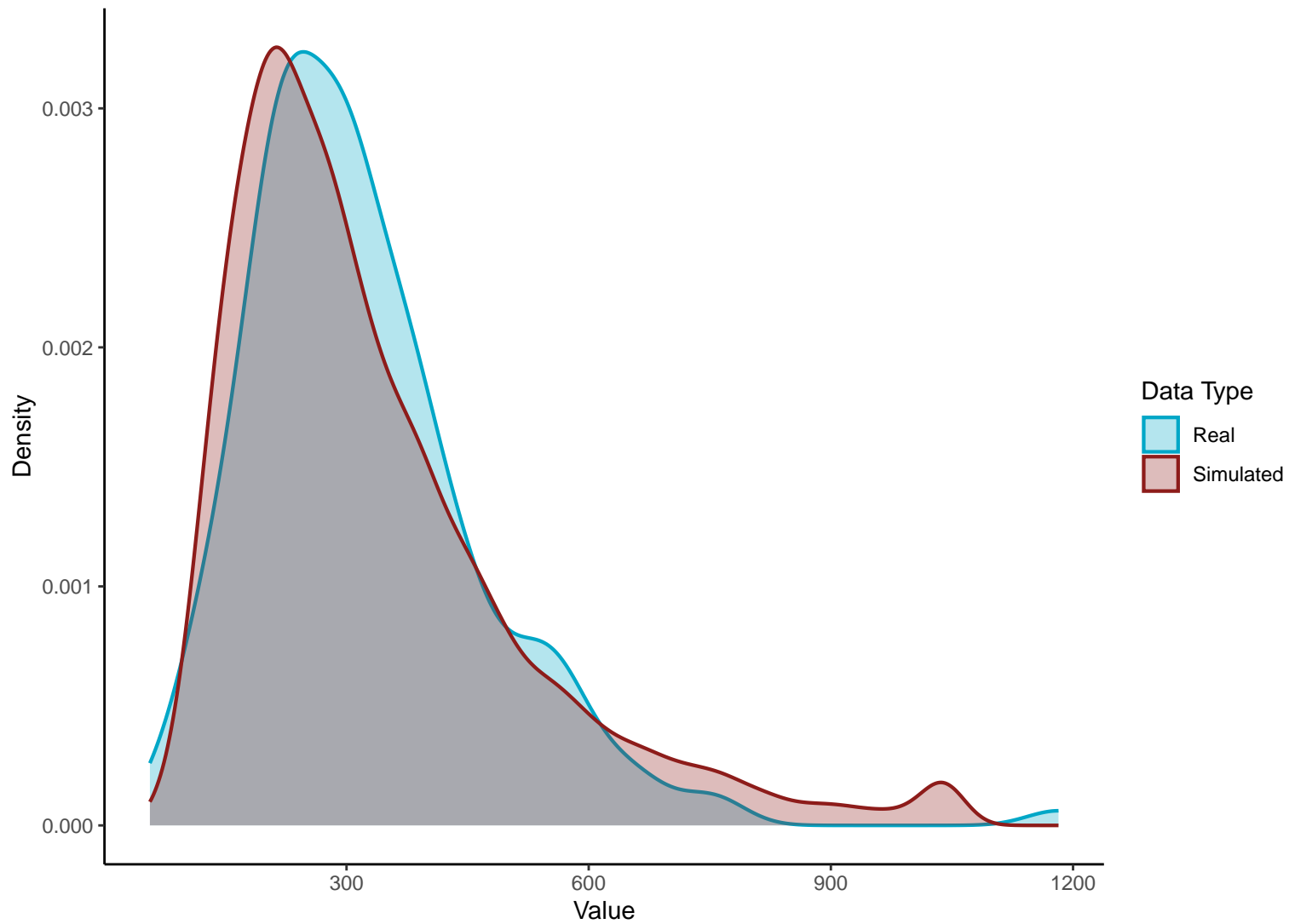


# Terrisporobacter

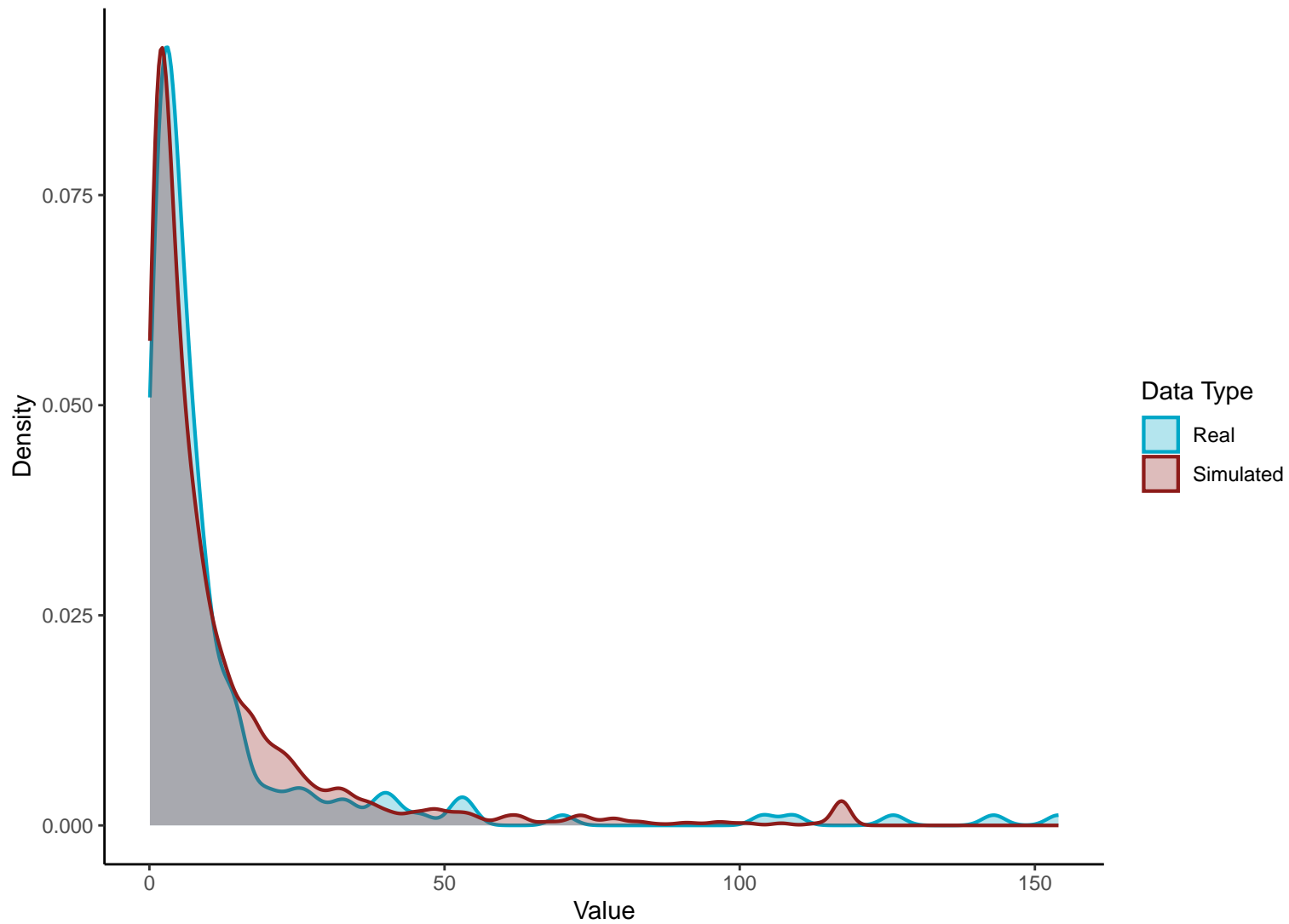




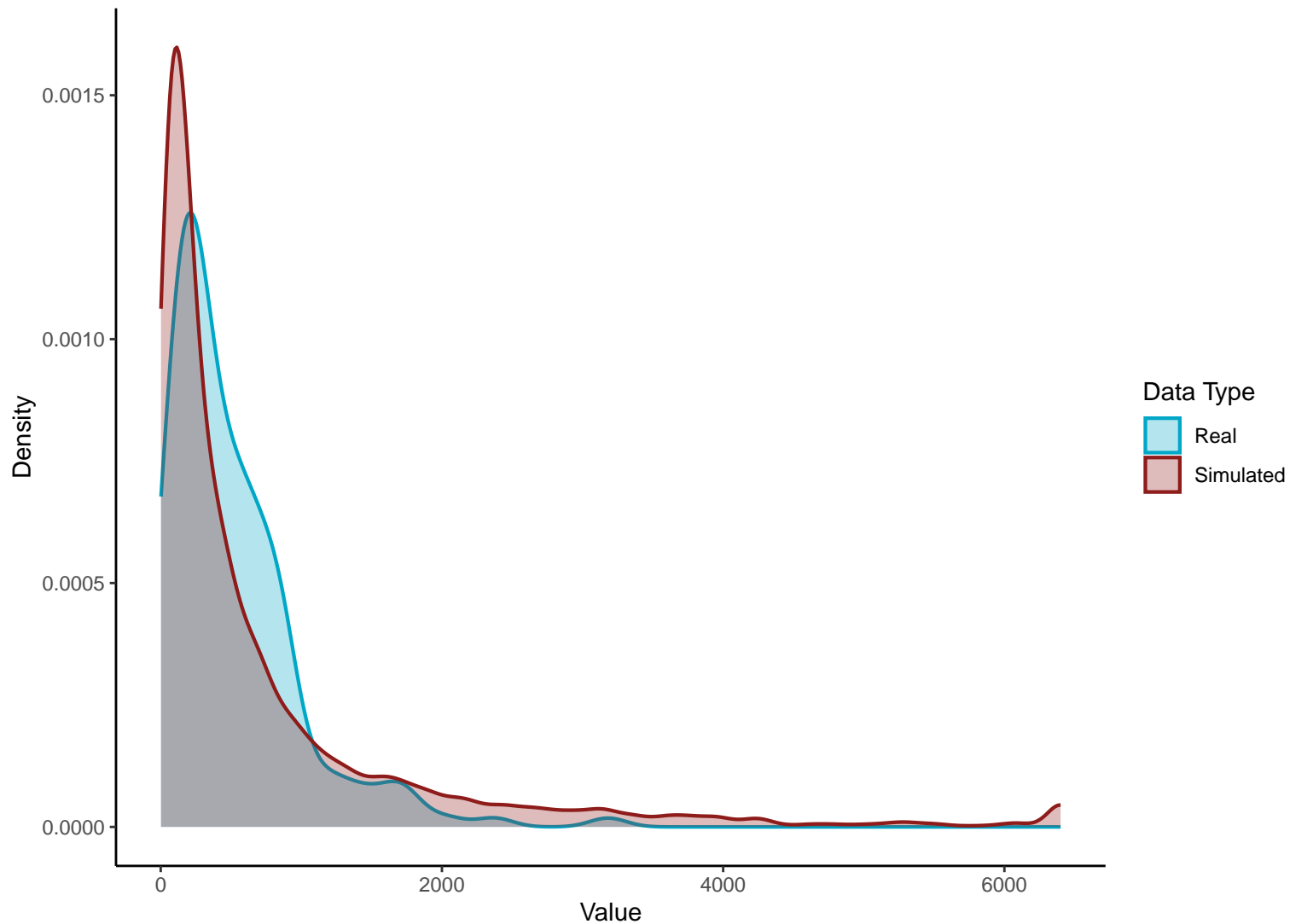
# X.Eubacterium..hallii.group



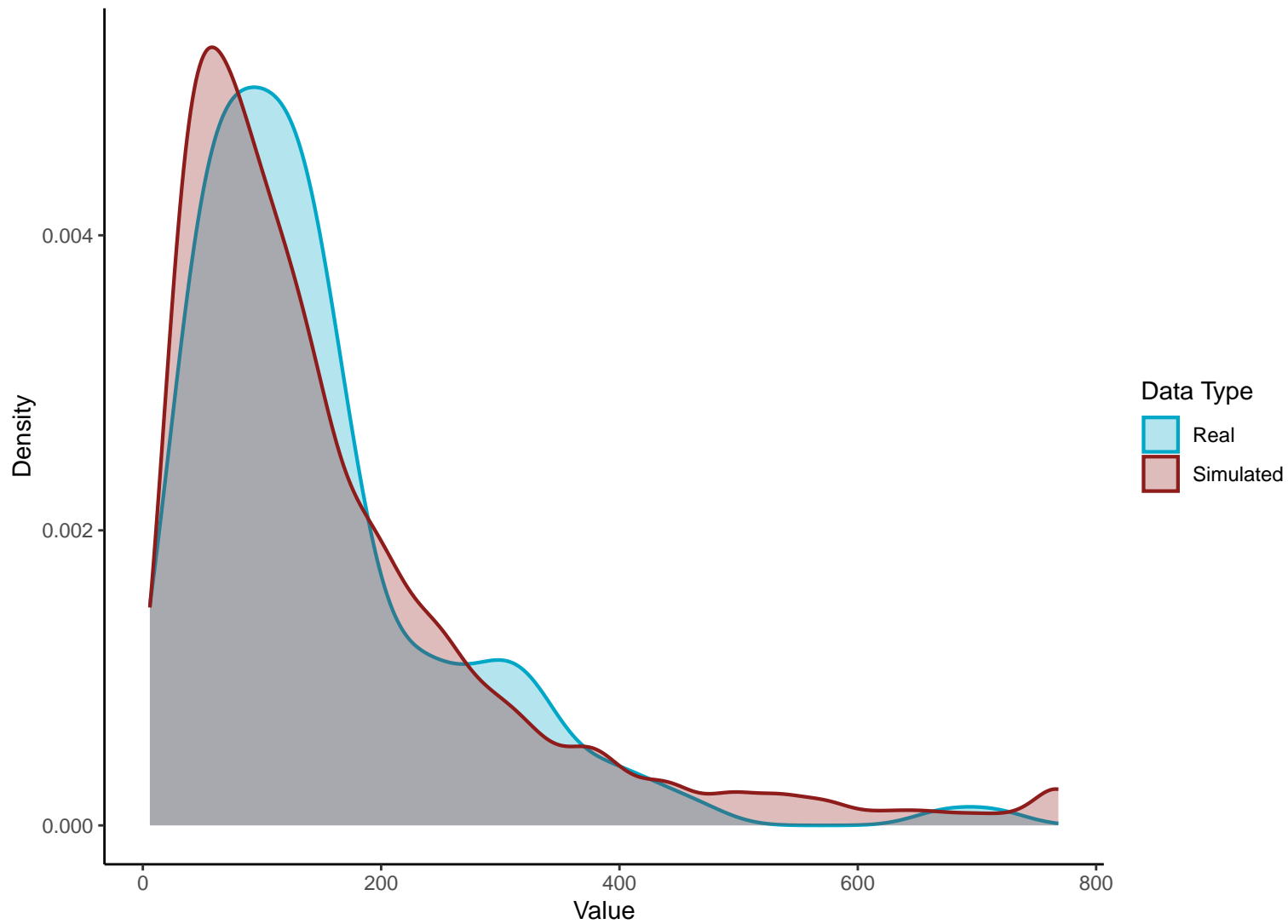
UCG.004



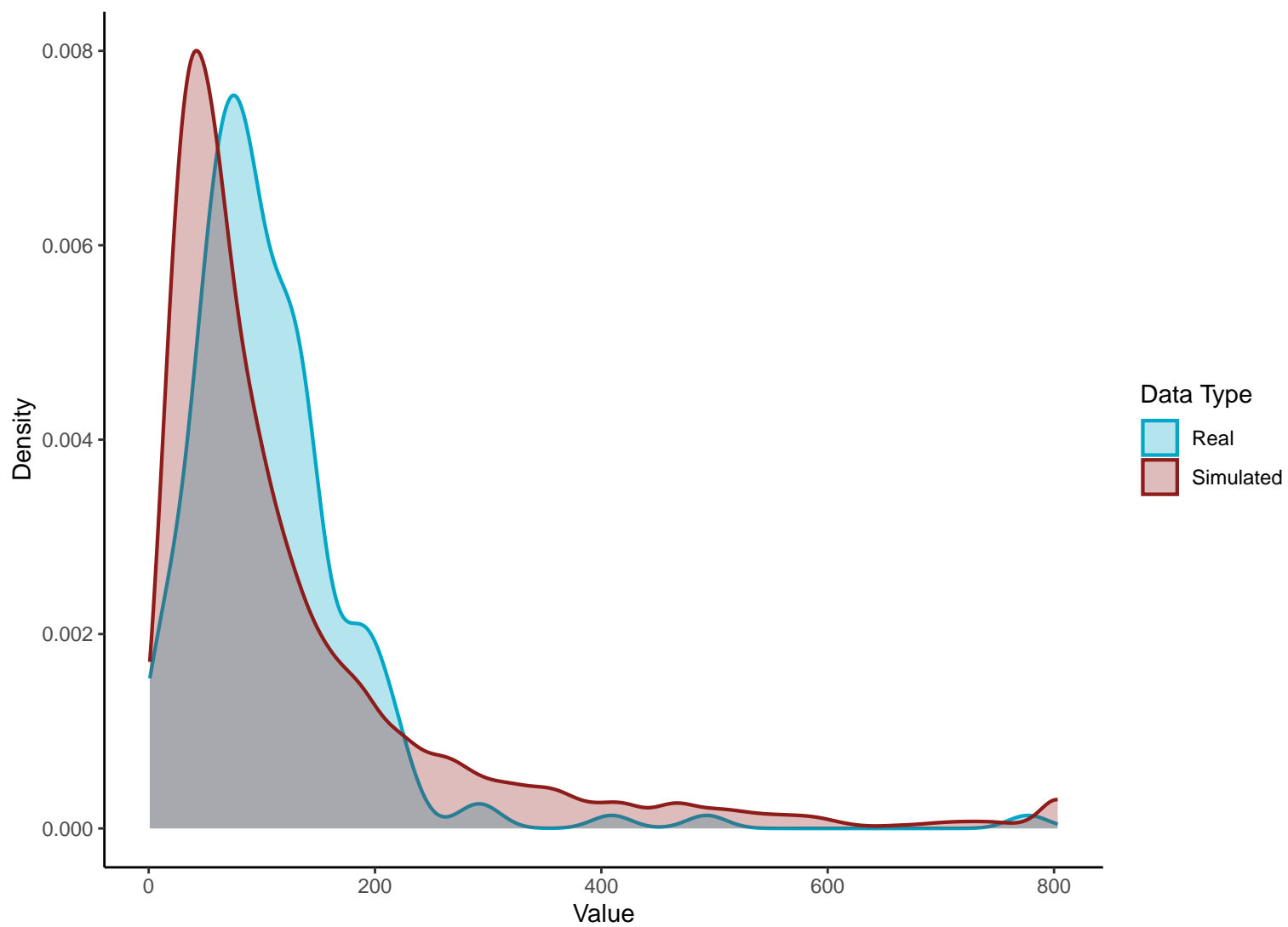
NK4A214.group



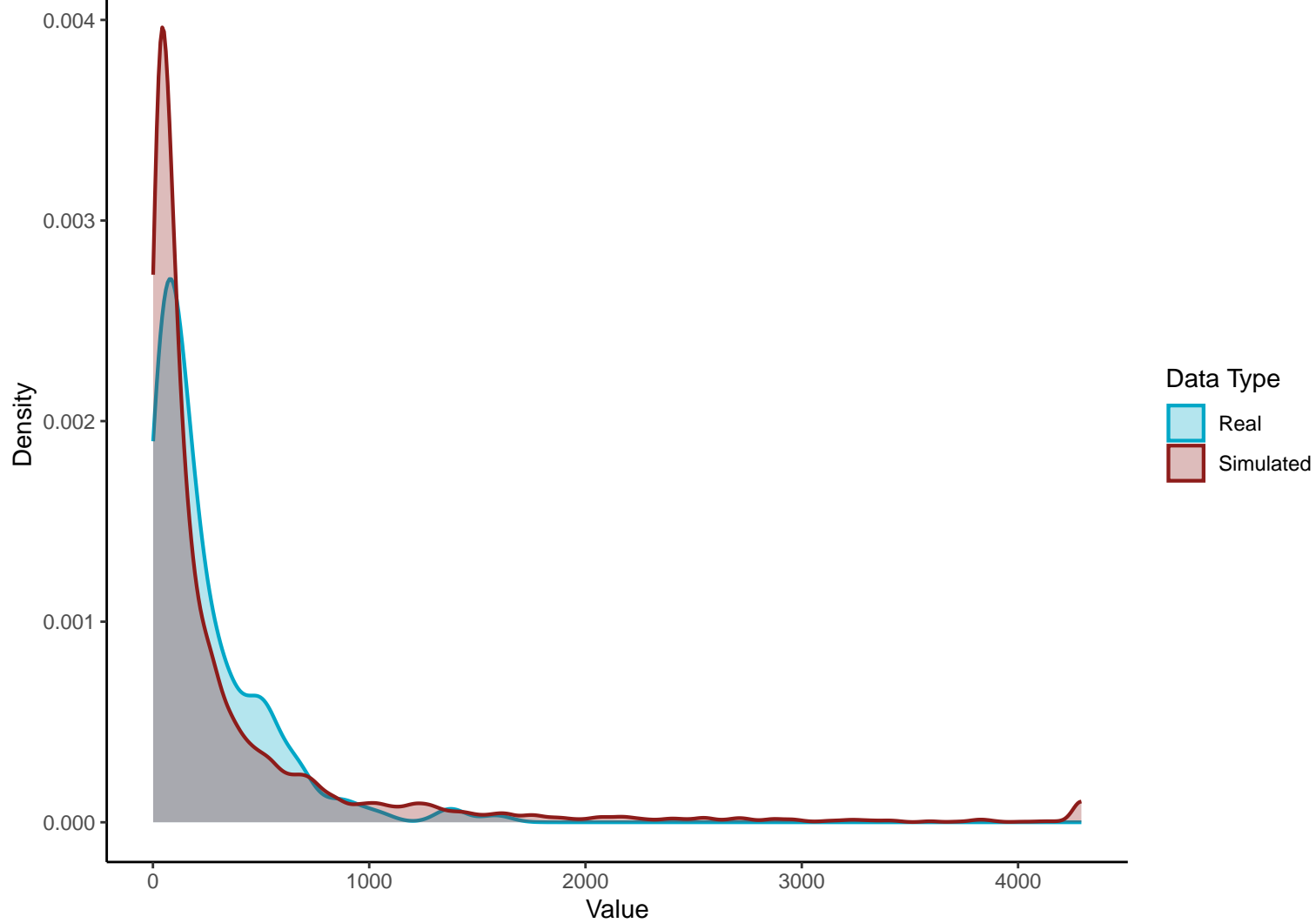
# Lachnospiraceae.NK4A136.group



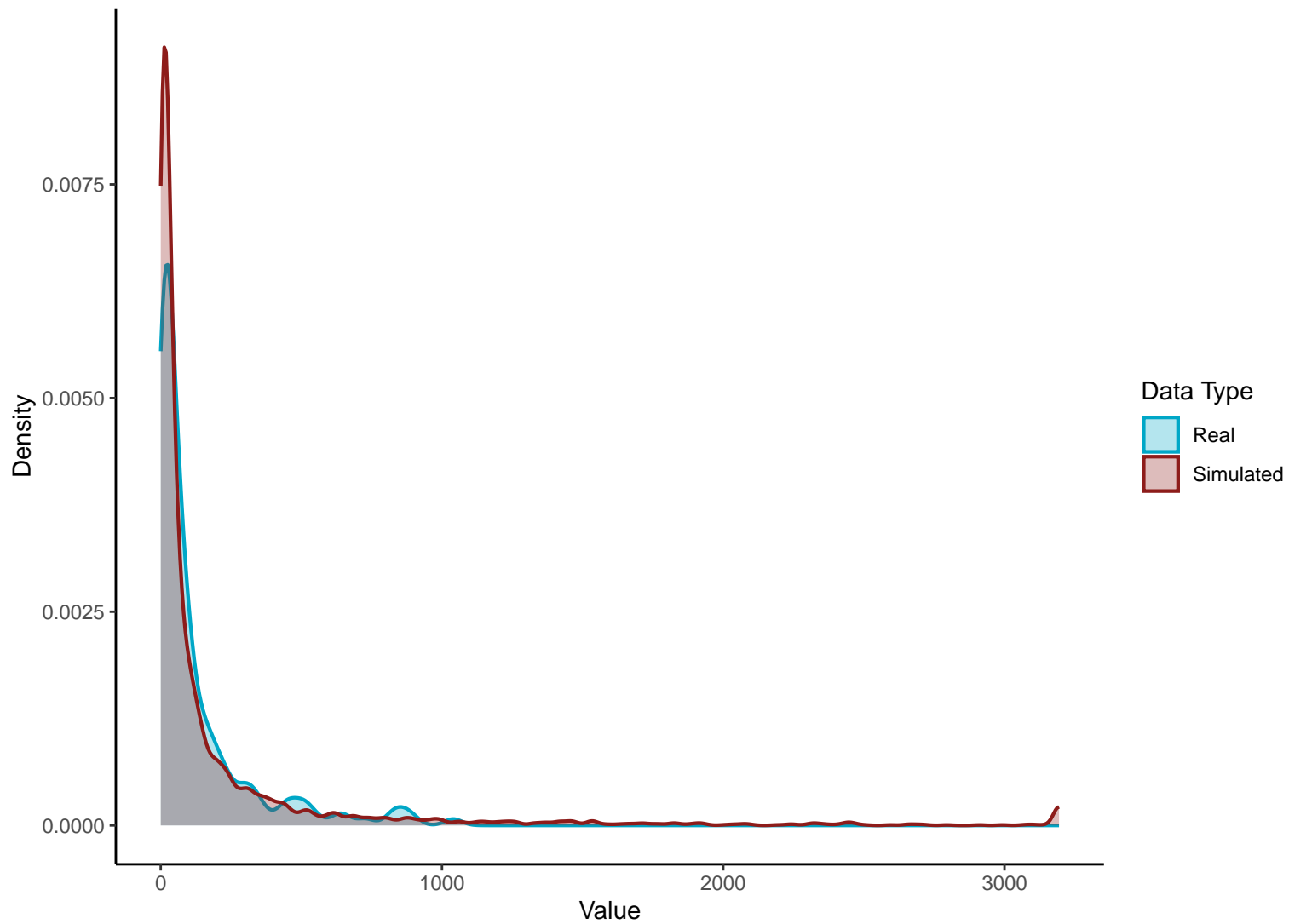
# Monoglobus



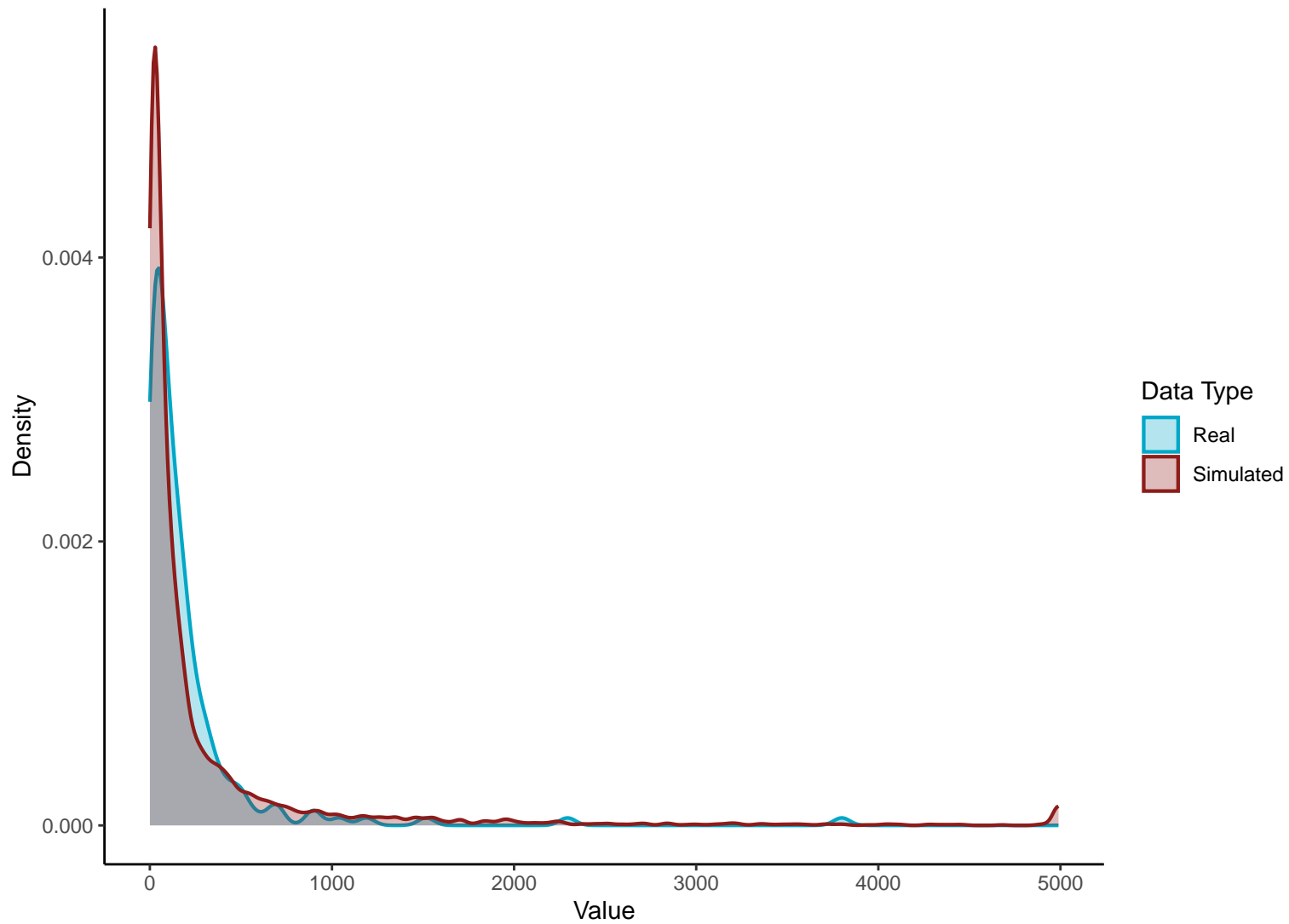
# Prevotella



# Treponema

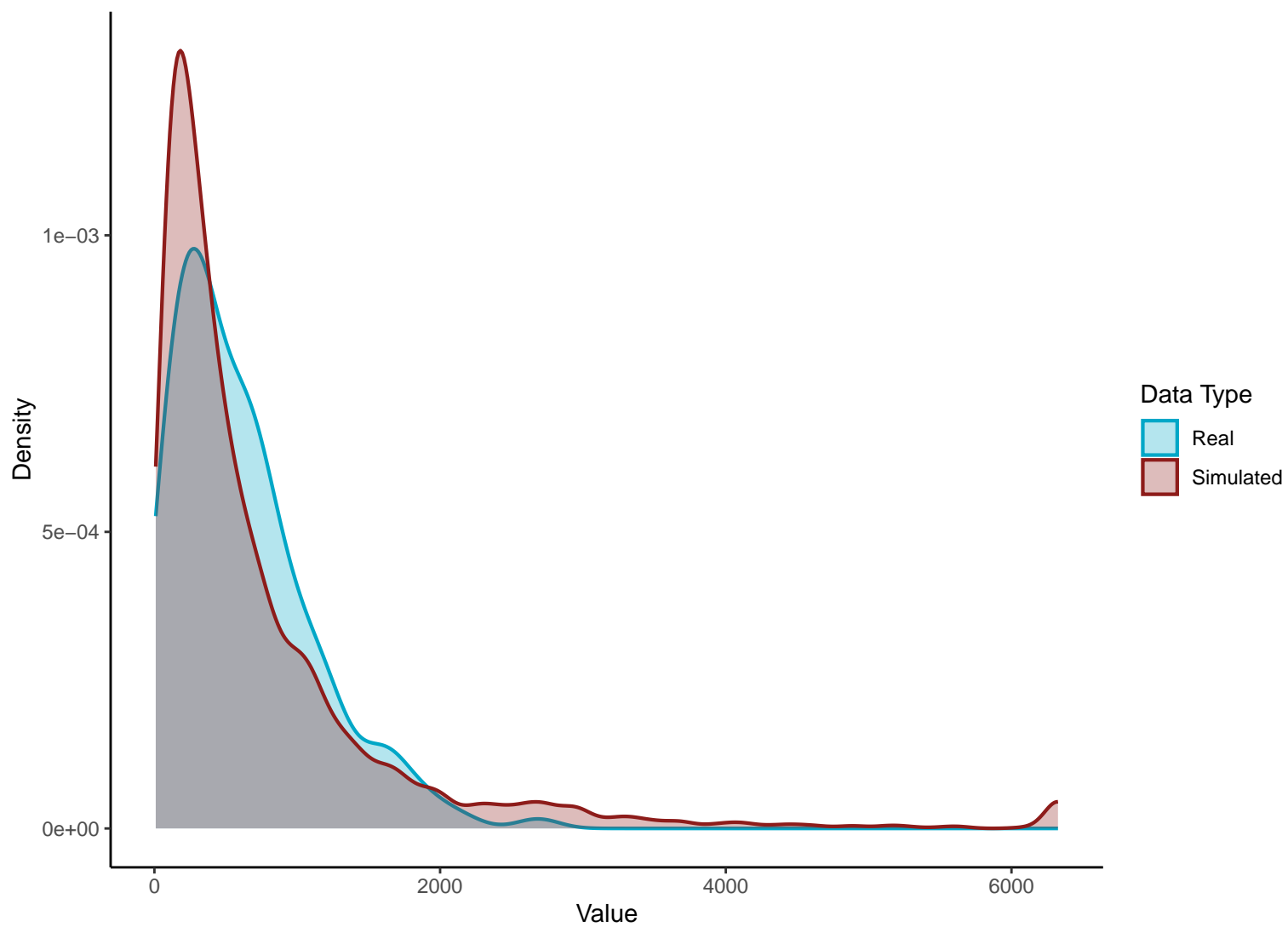


# Rikenellaceae.RC9.gut.group

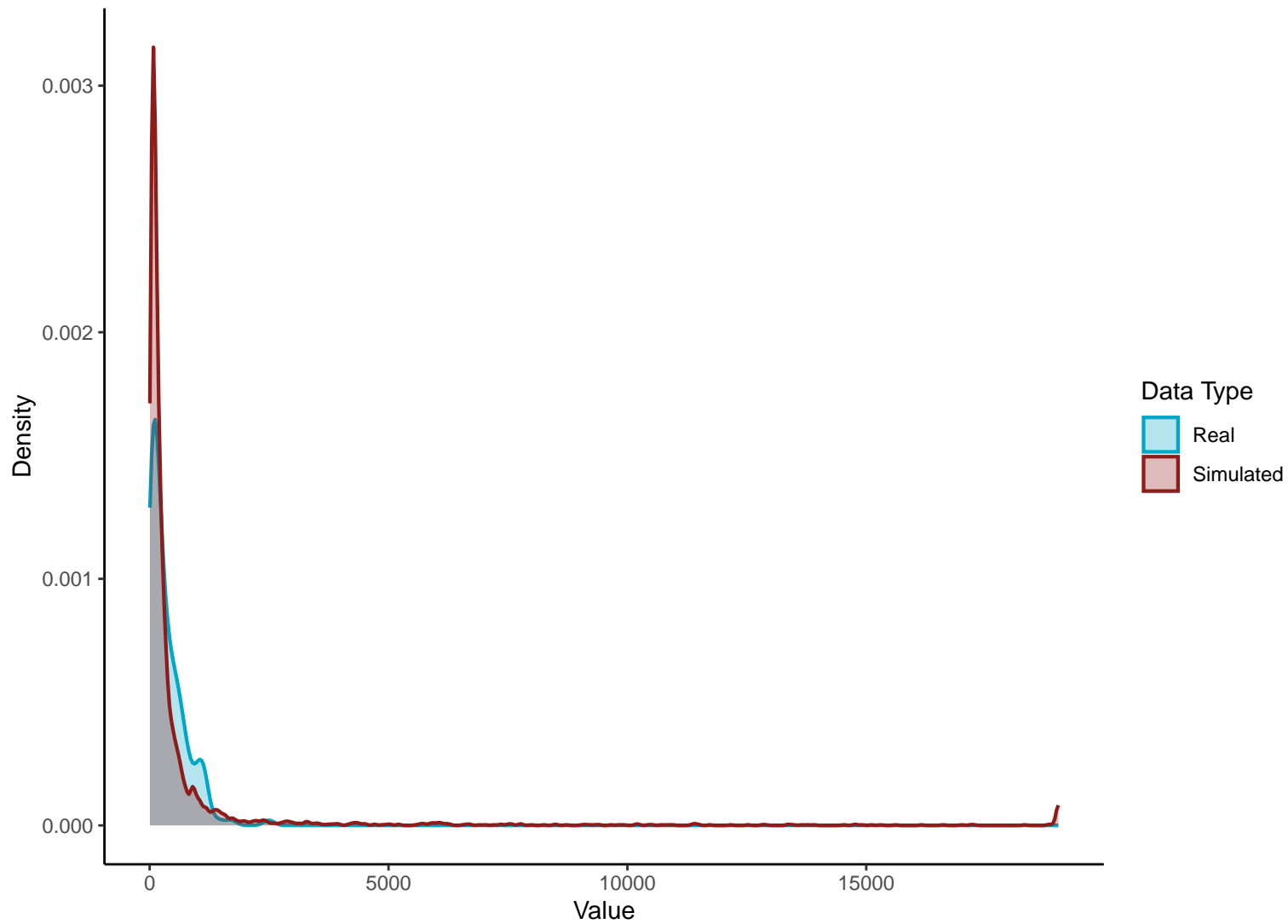




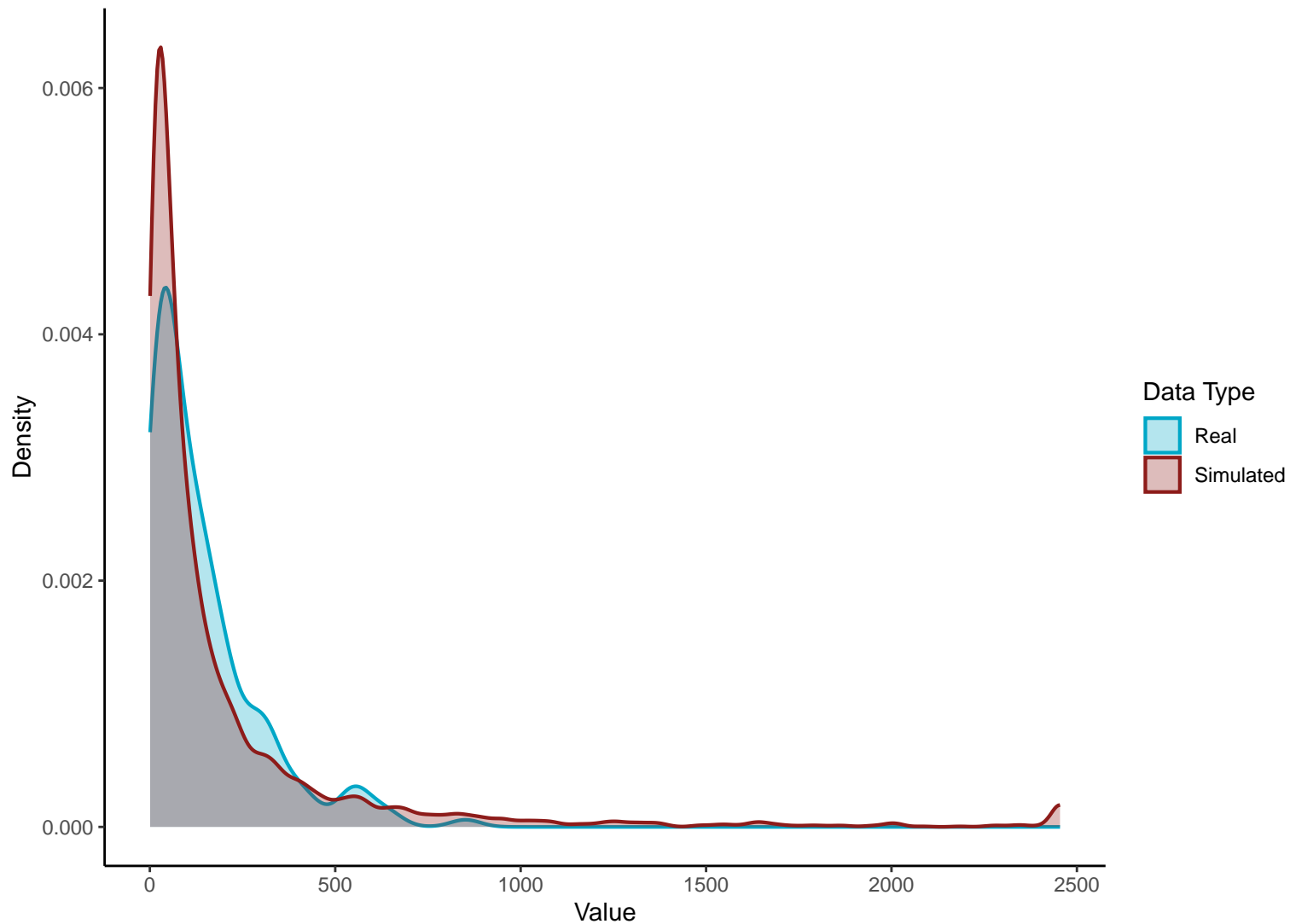
# Faecalibacterium



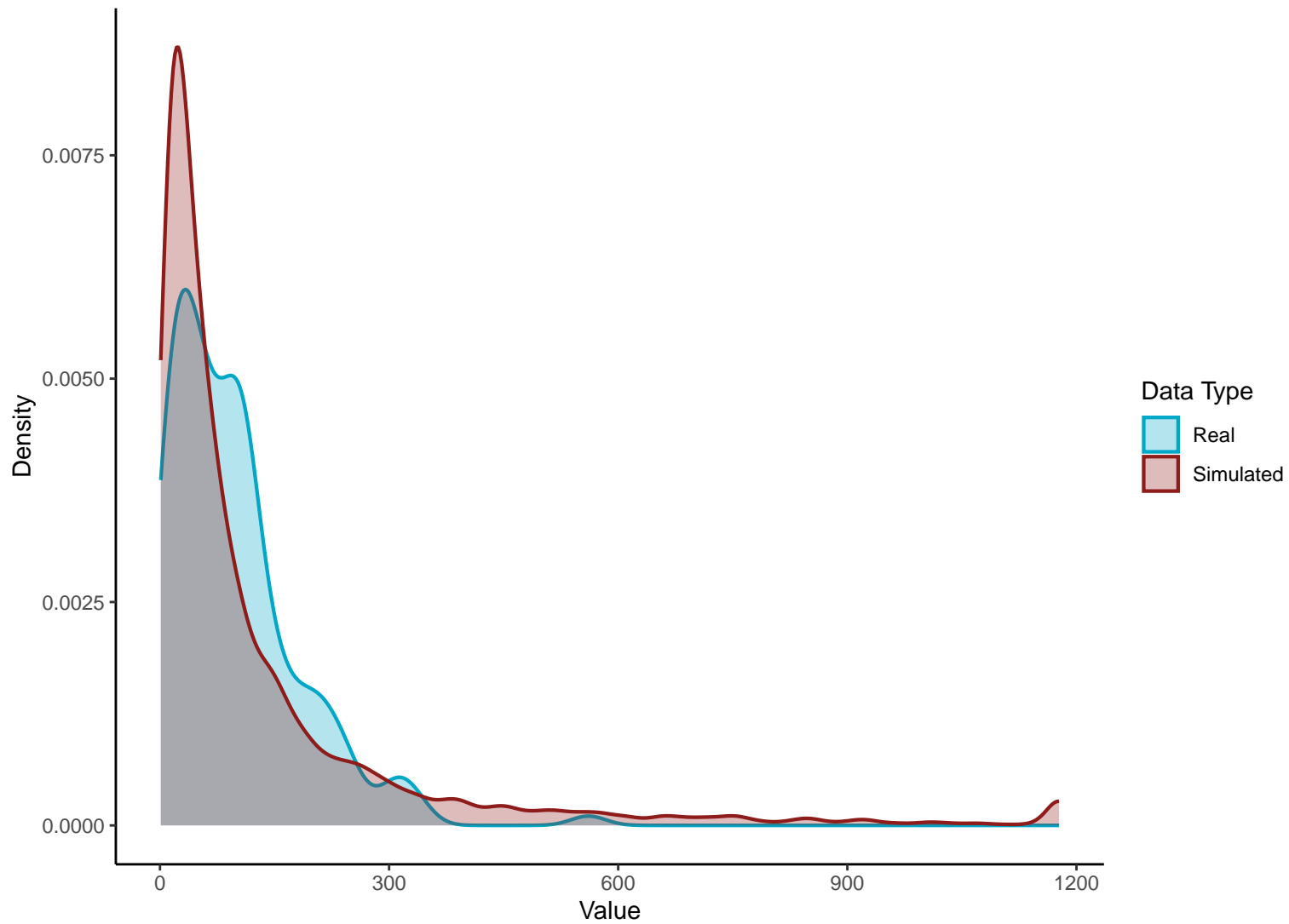
# Anaerovibrio



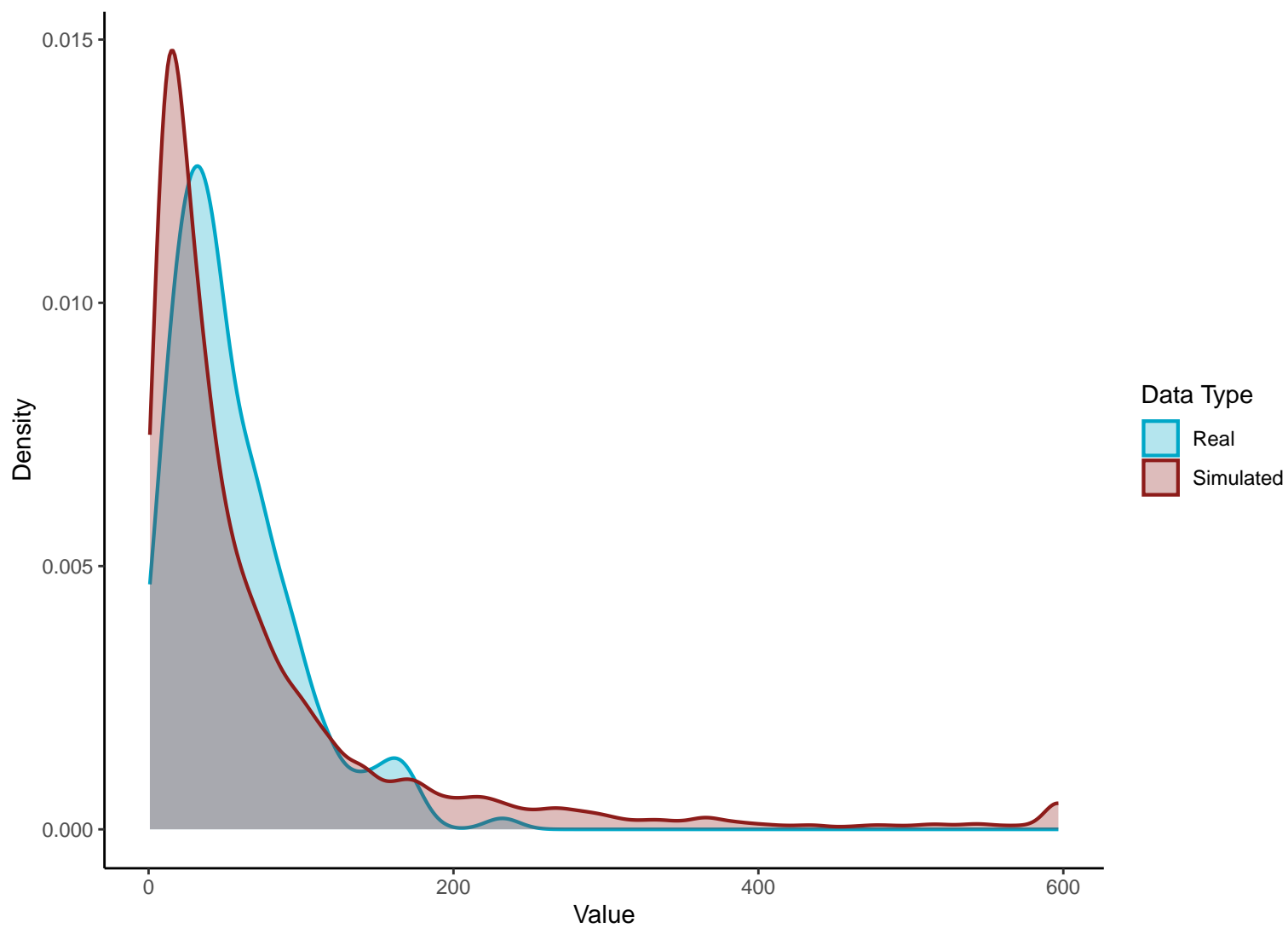
# X.Eubacterium..xylanophilum.group



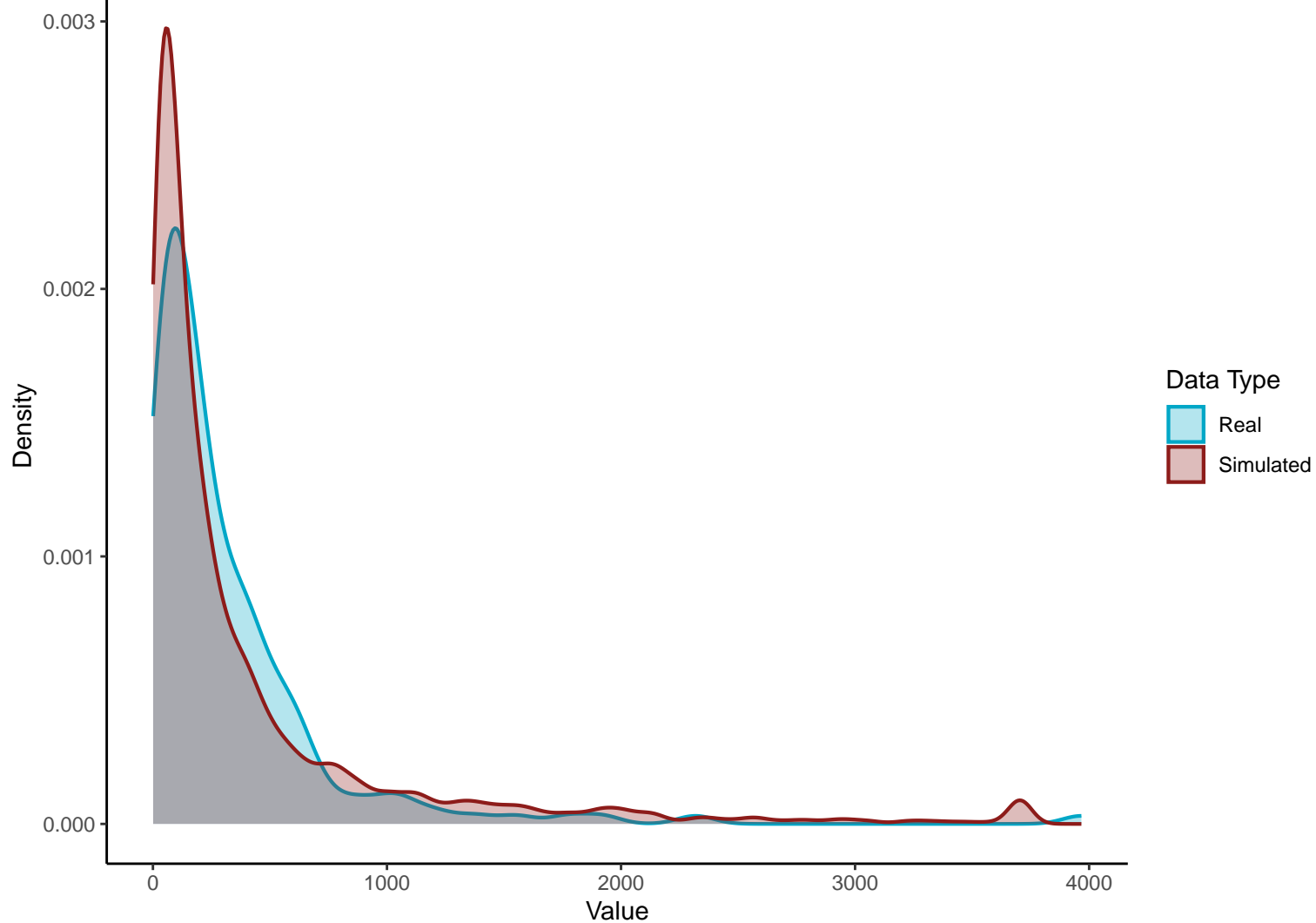
# X.Ruminococcus..torques.group



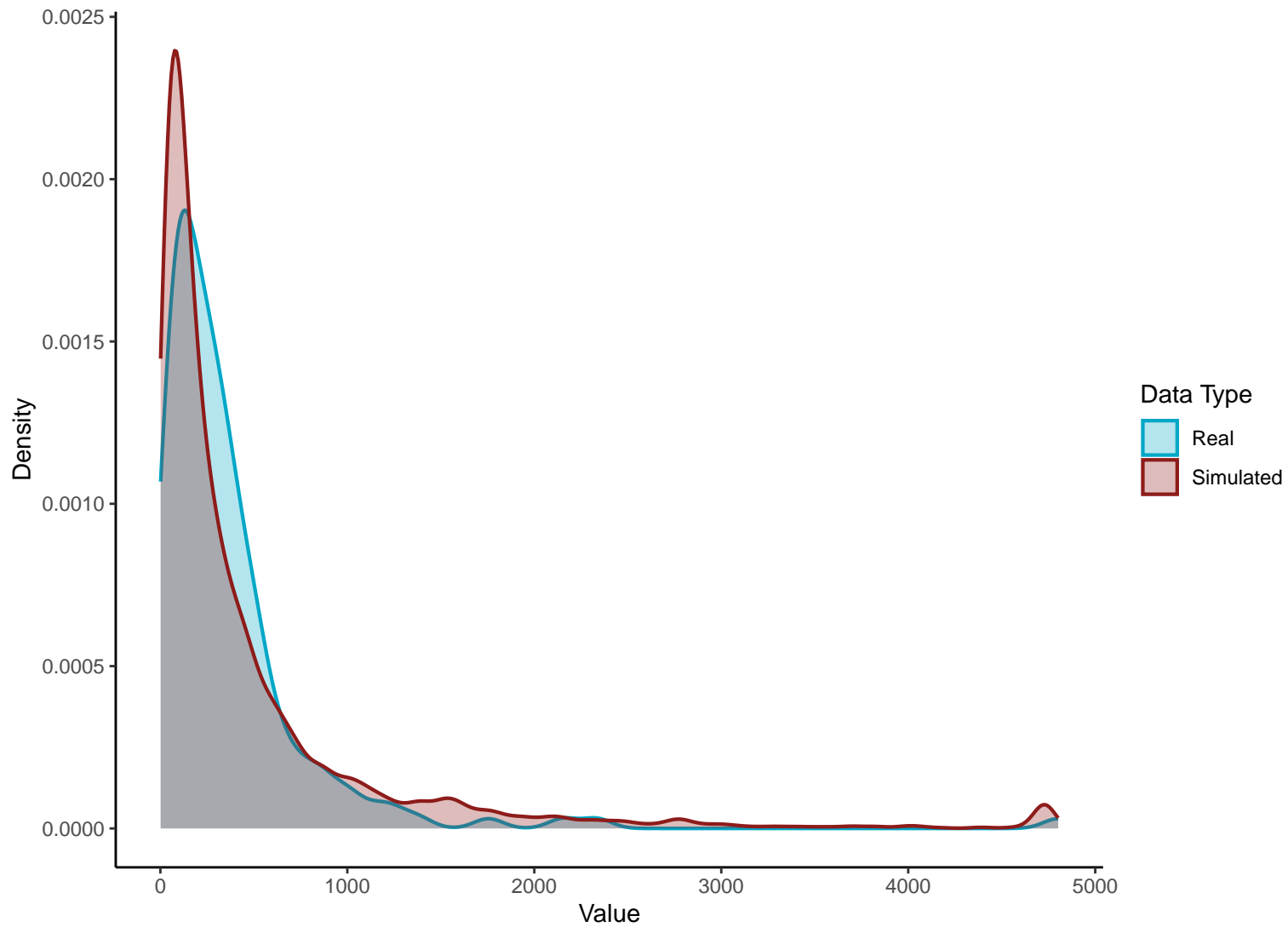
# X.Eubacterium..siraeum.group



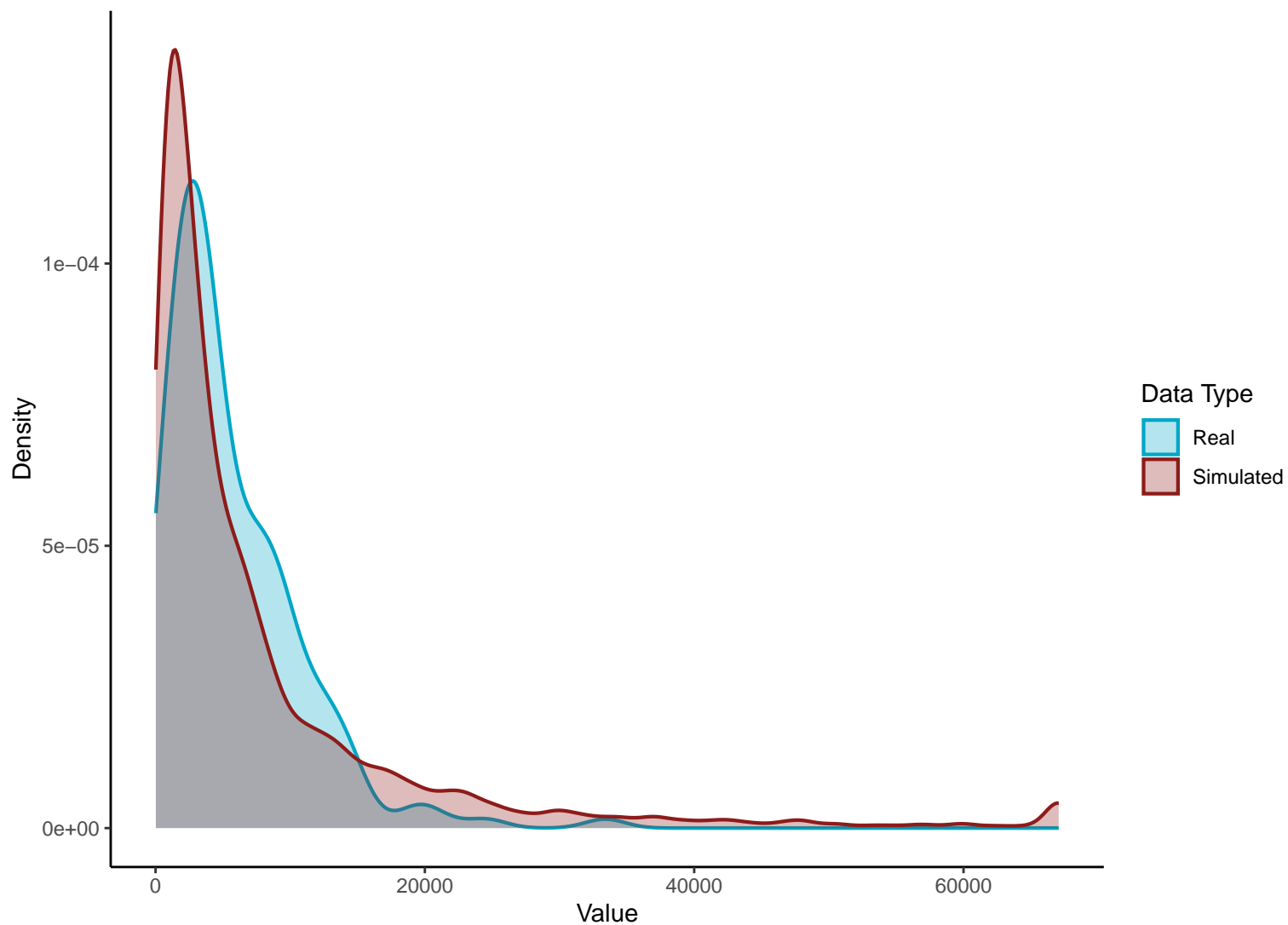
# Alloprevotella



# Catenibacterium

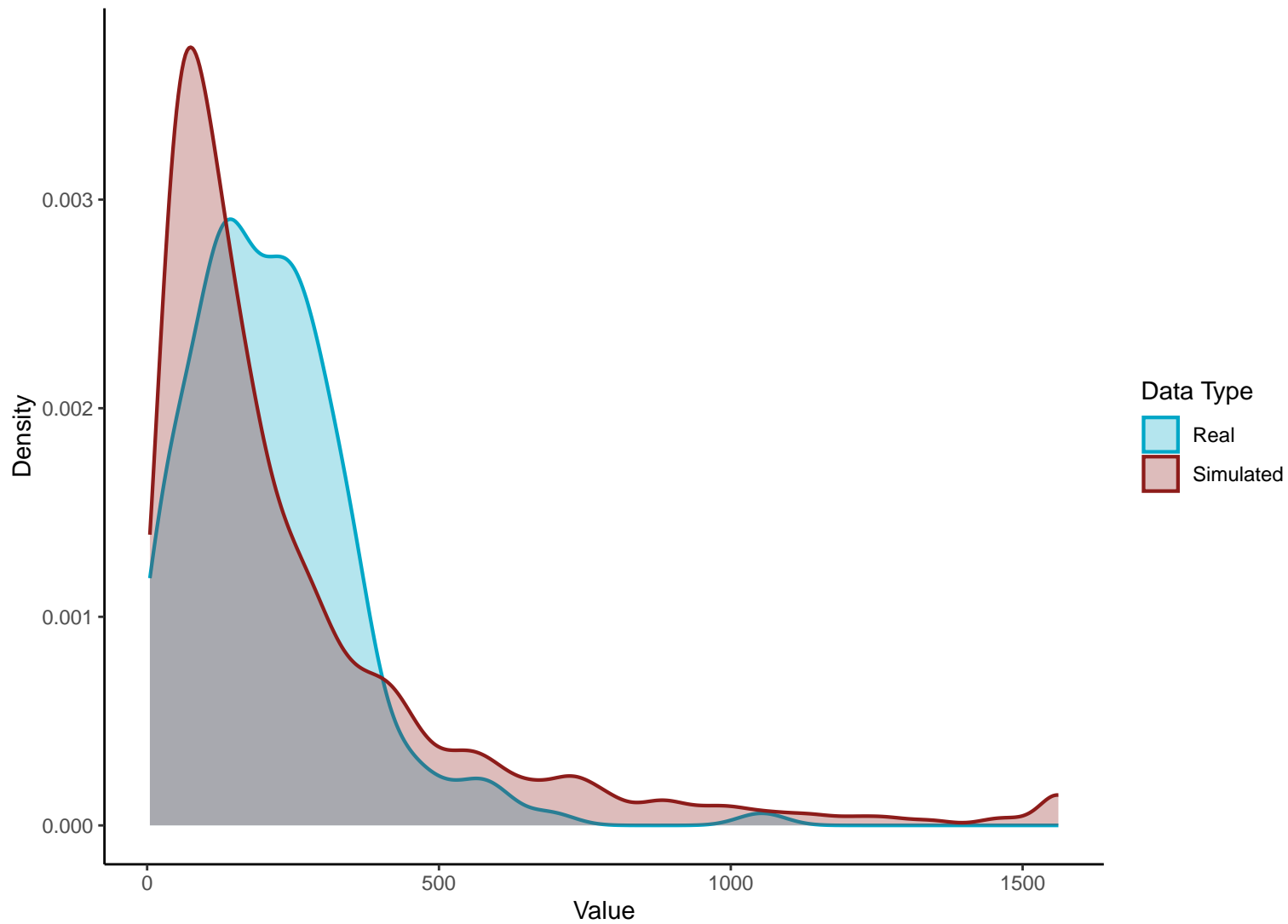


# Clostridium.sensu.stricto.1

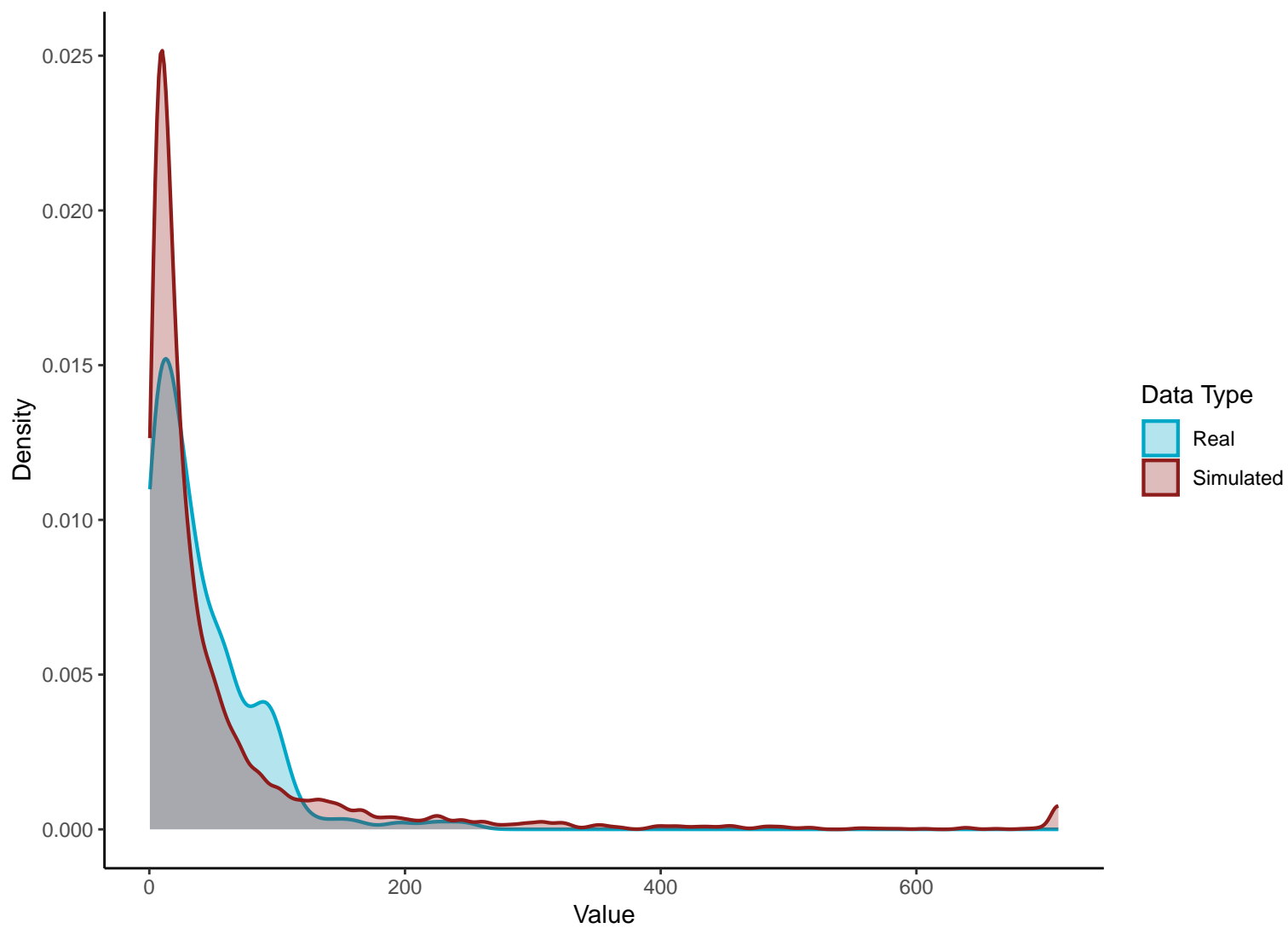




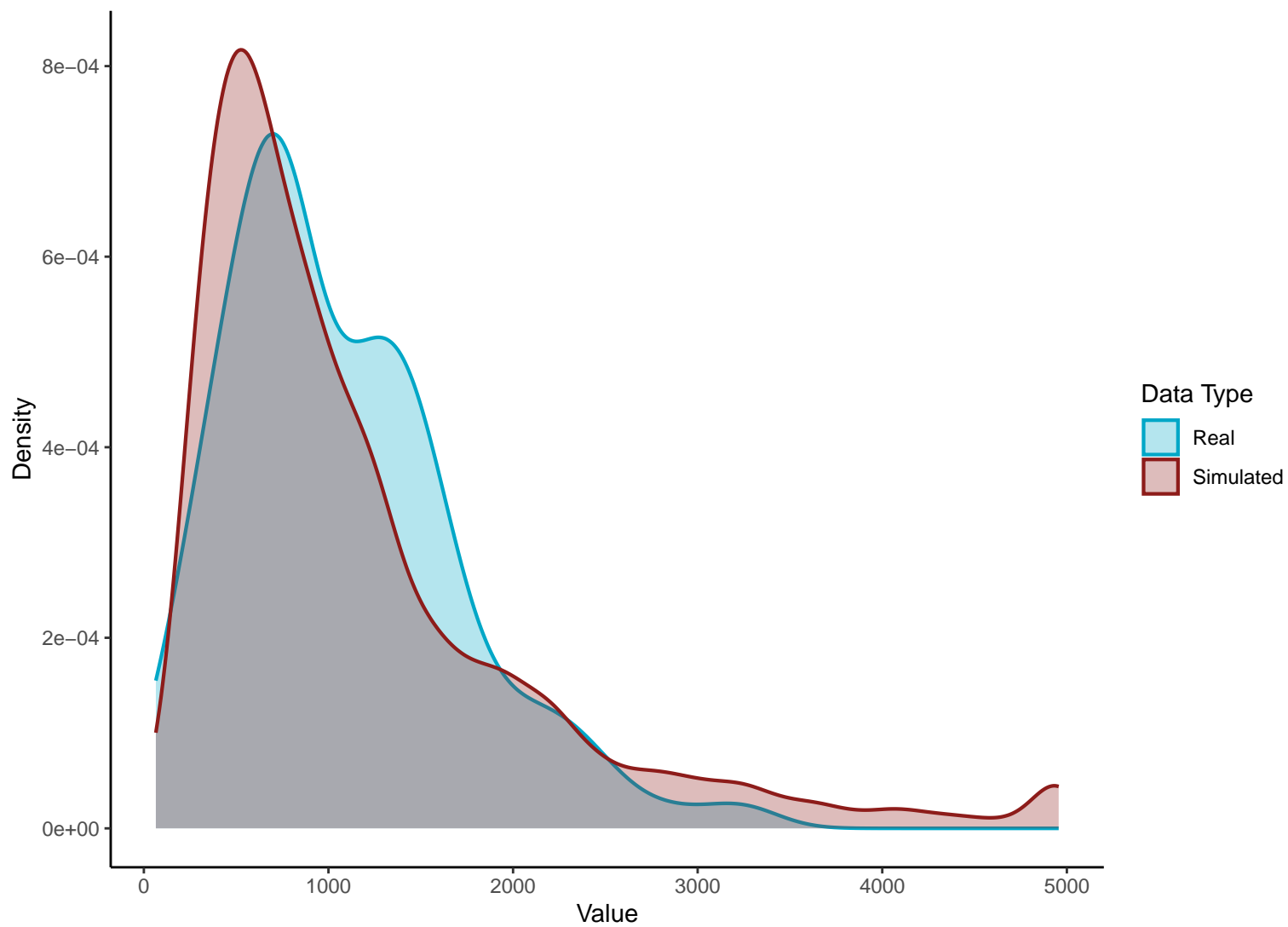
# Butyricicoccus



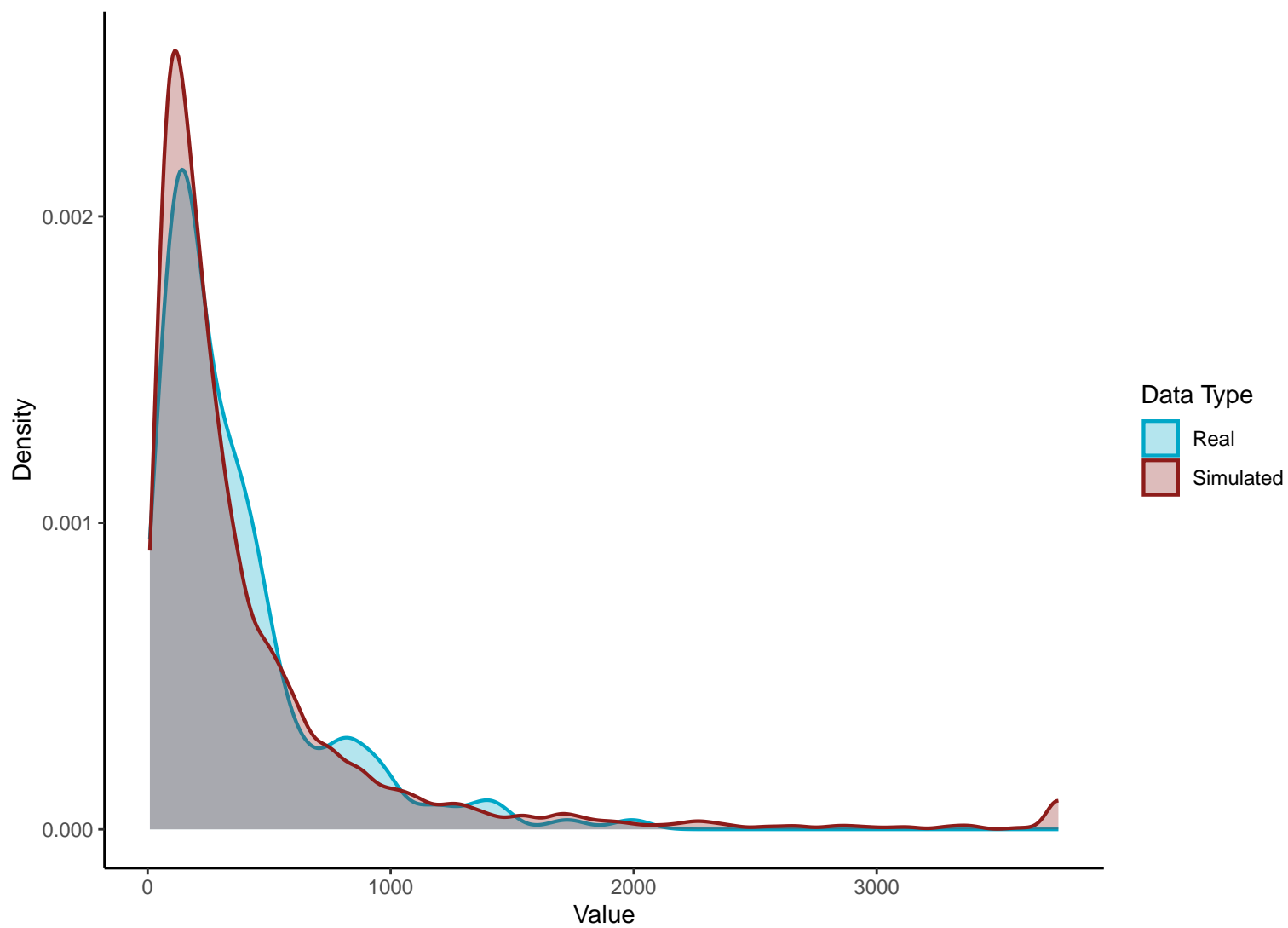
# Intestinimonas



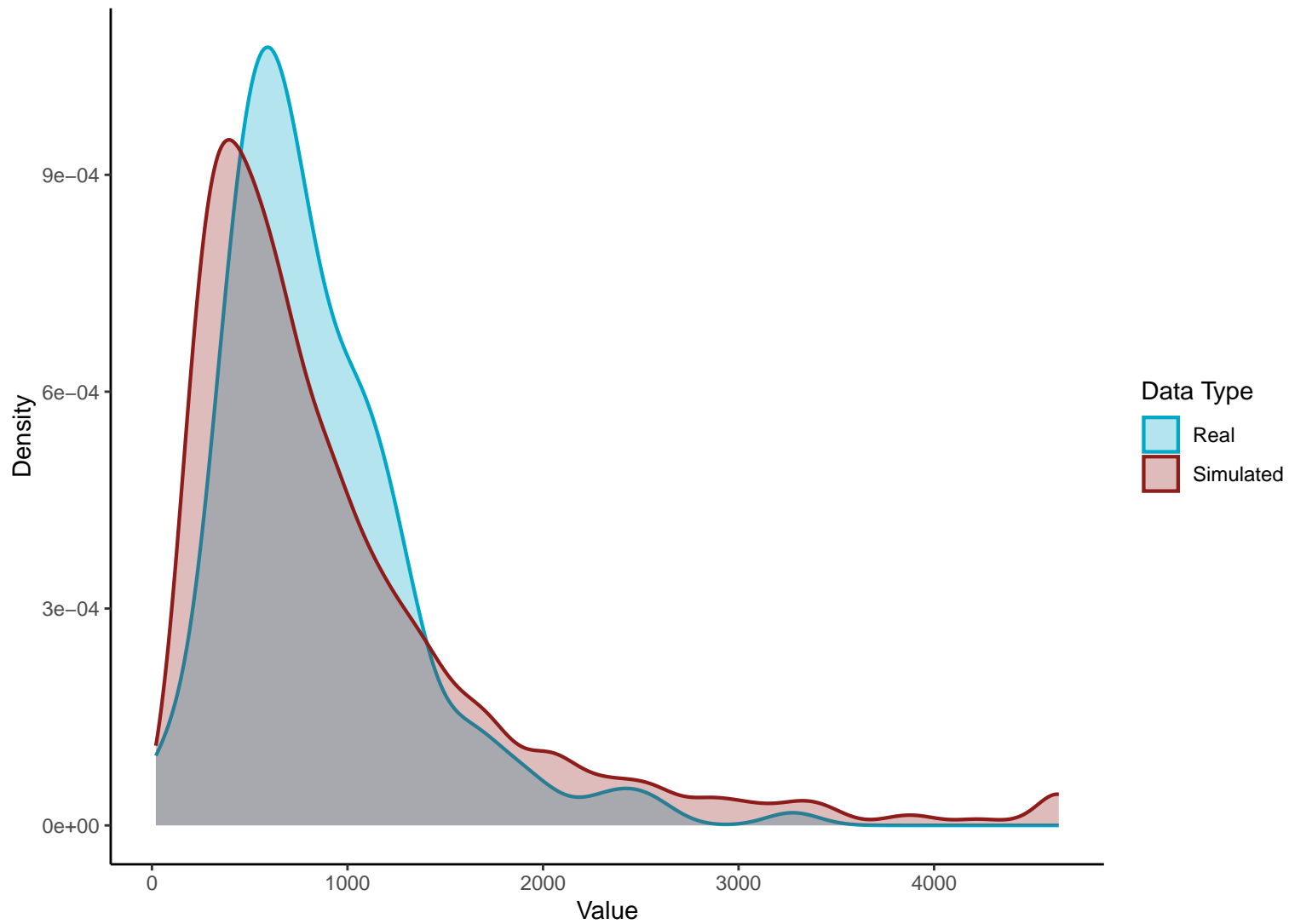
# Subdoligranulum



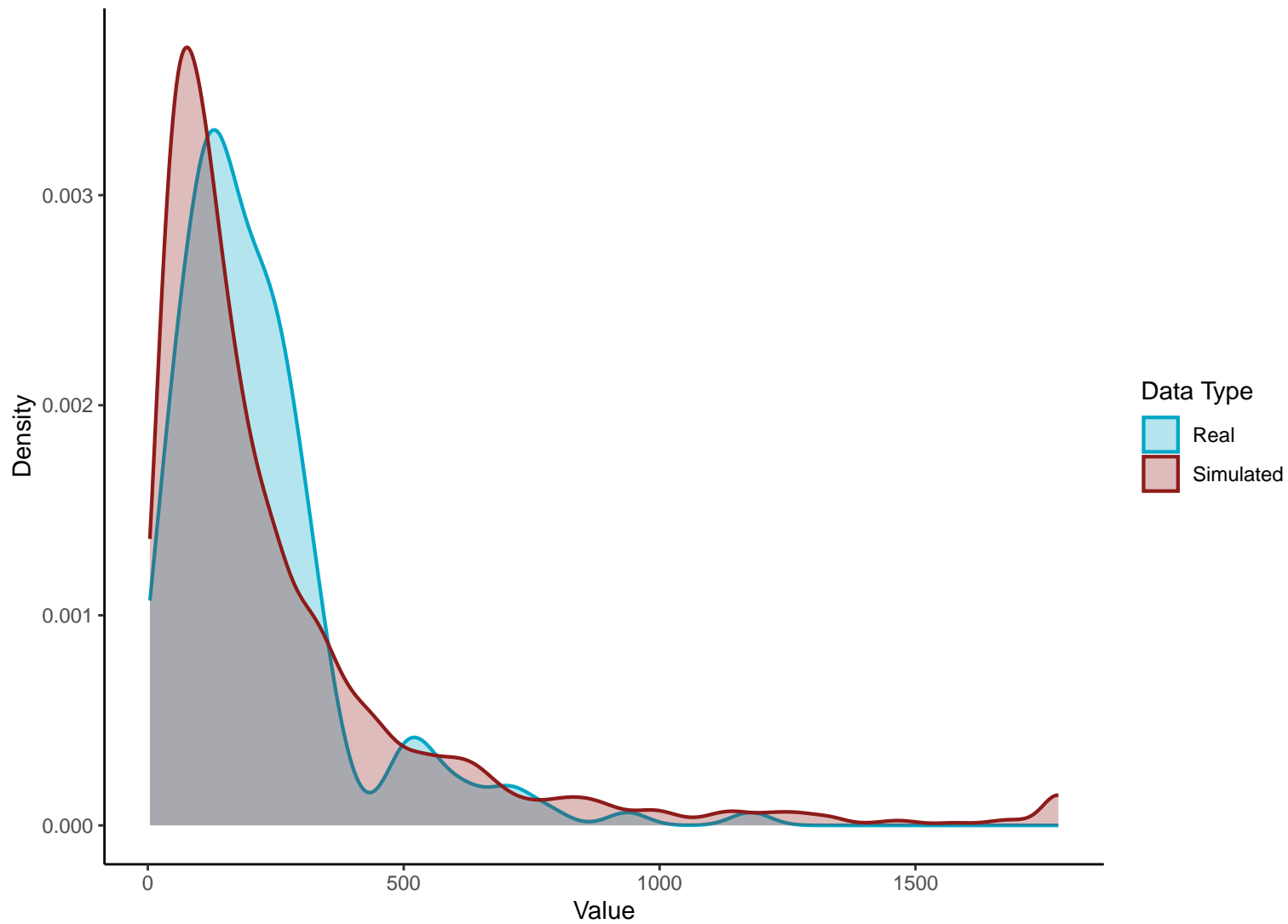
# Roseburia



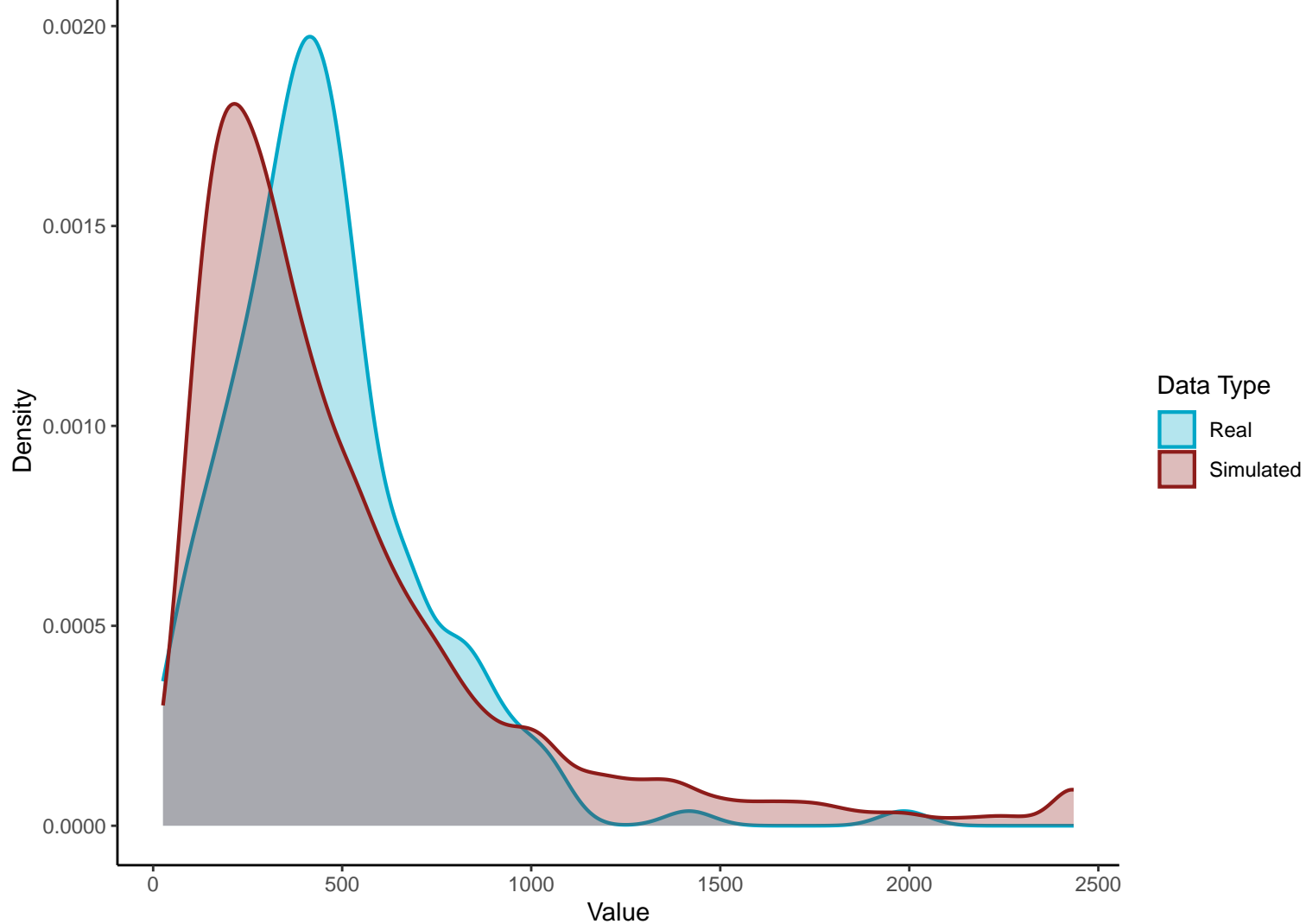
# Ruminococcus



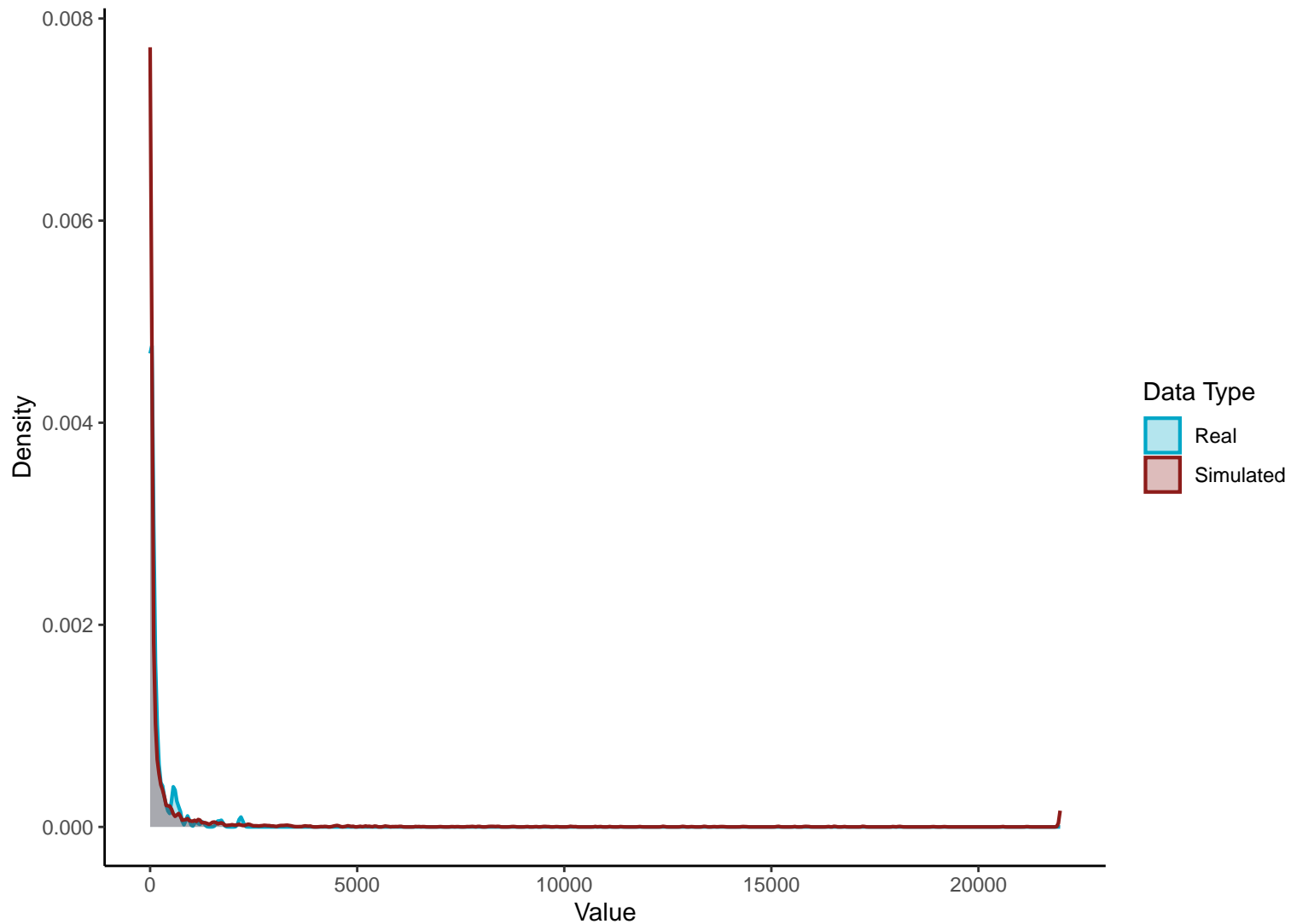
Family.XIII.AD3011.group



# Solobacterium

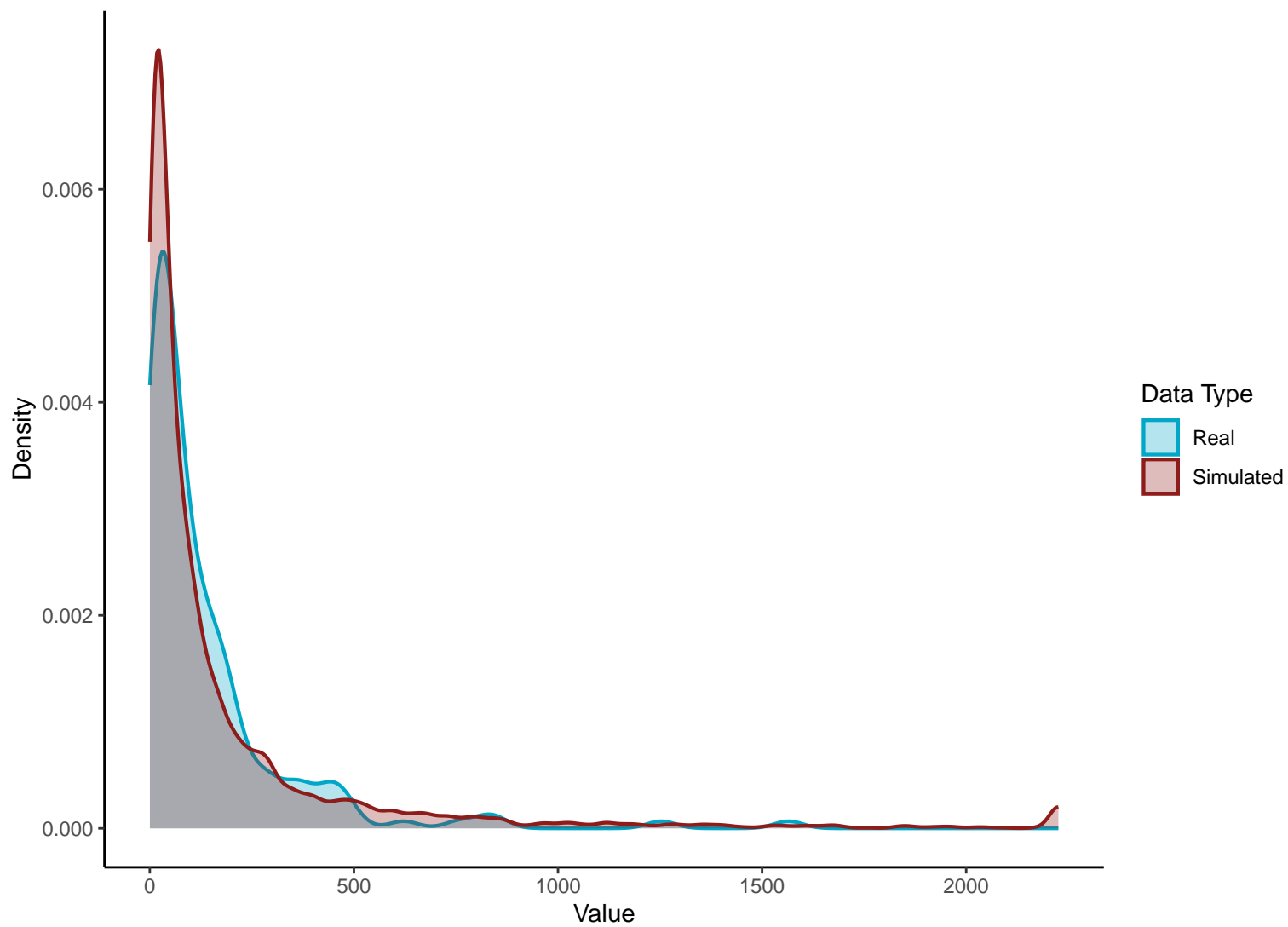


Lachnospiraceae.XPB1014.group

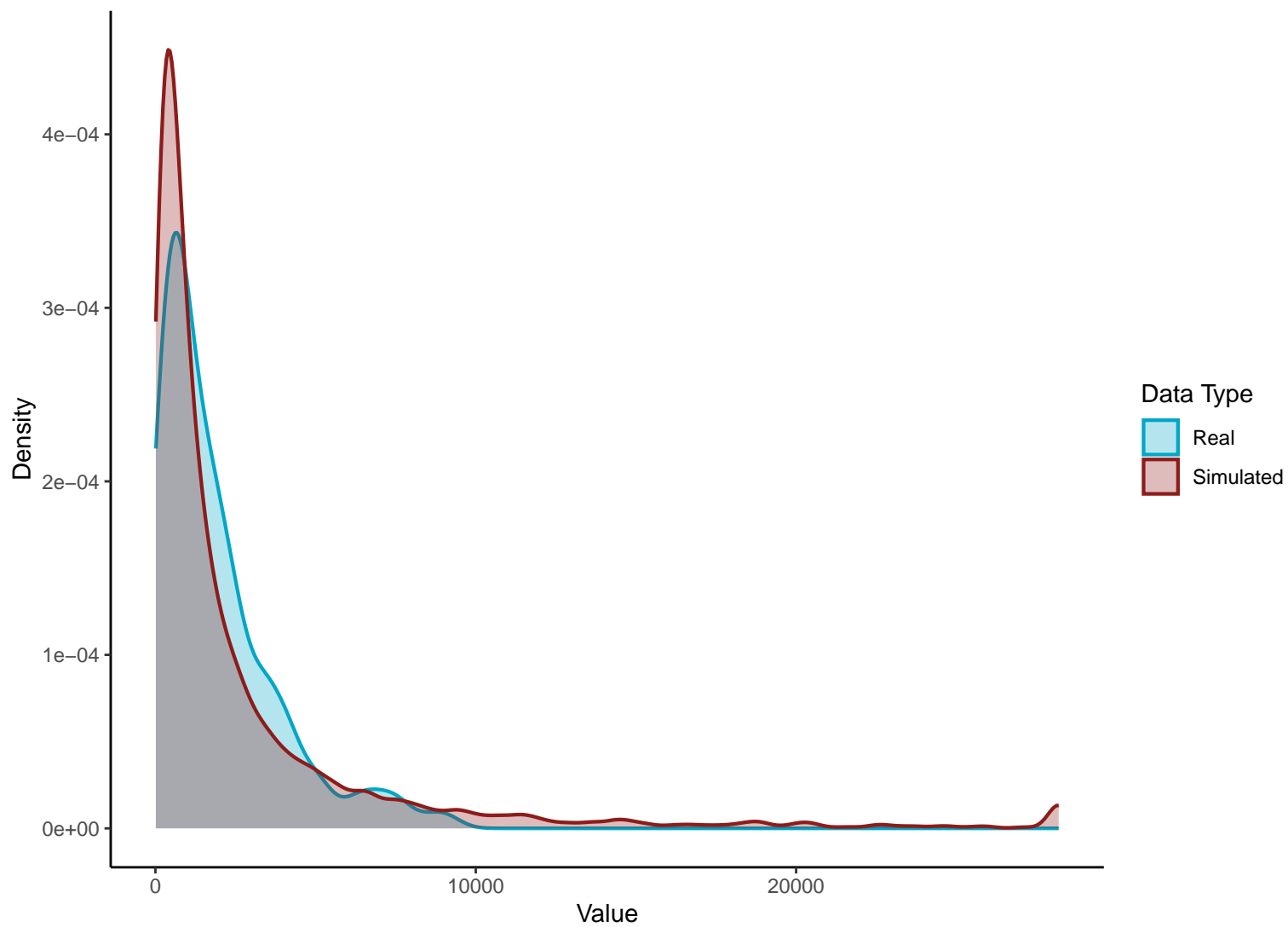




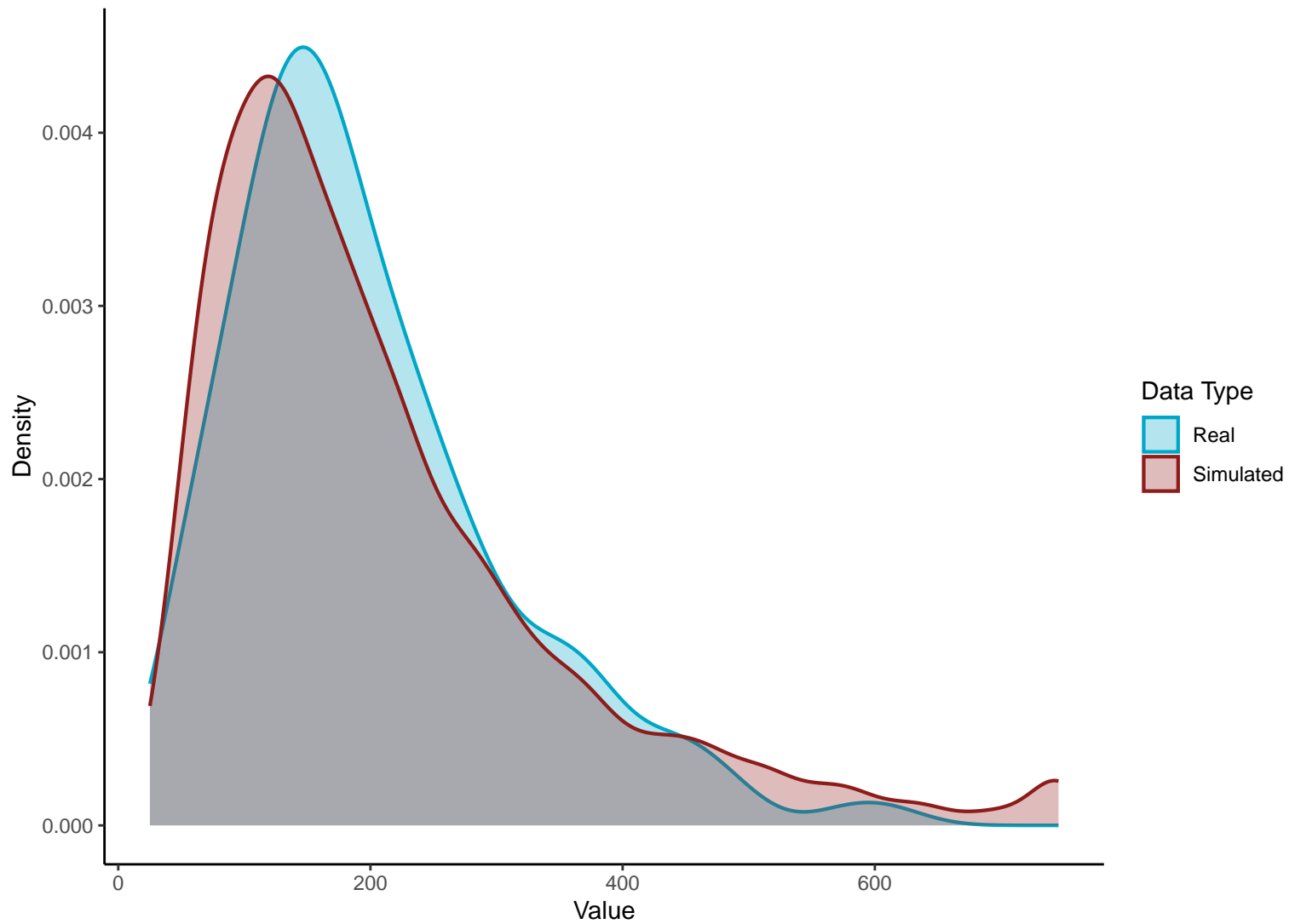
Prevotella\_7



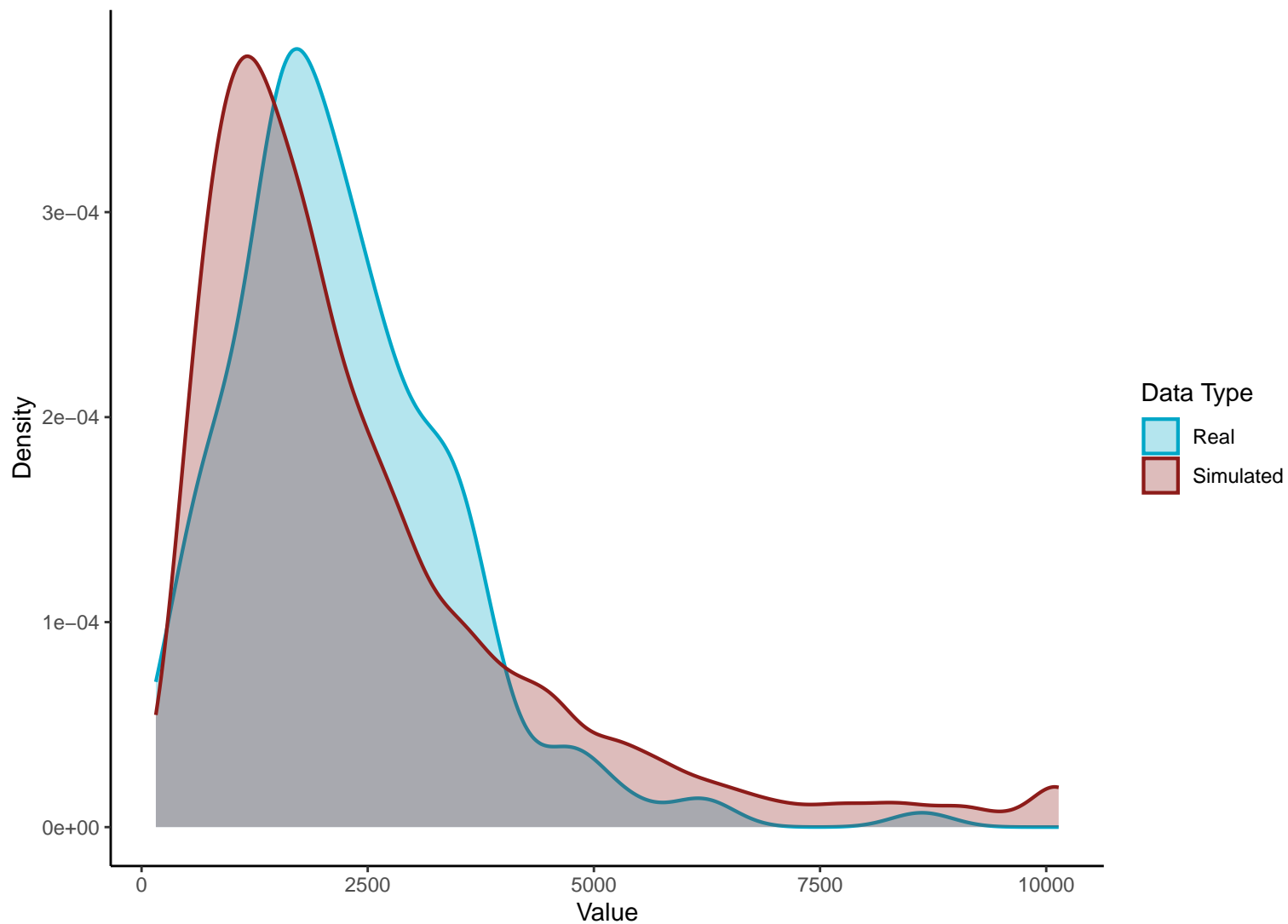
Prevotella\_9



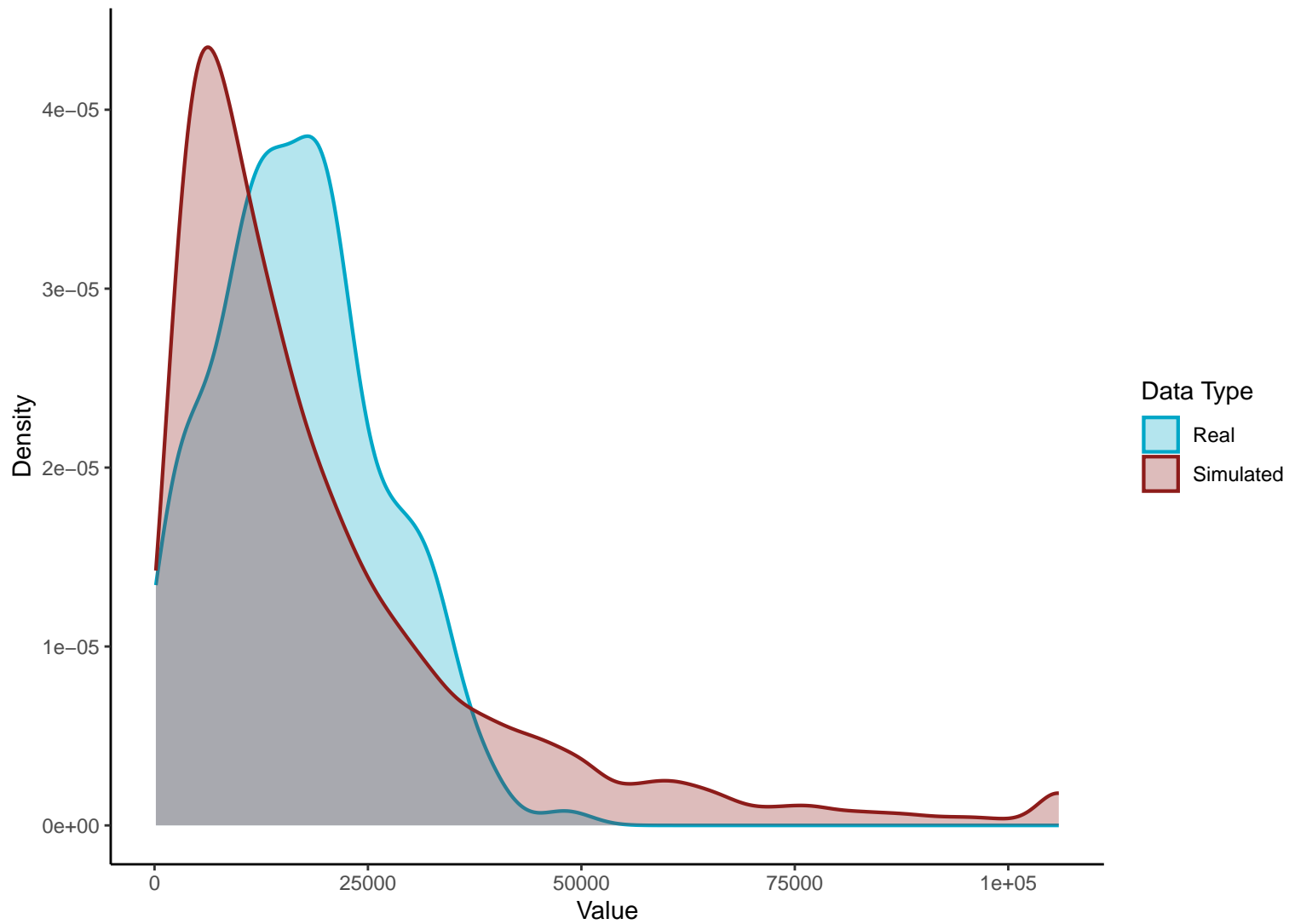
# Lachnospiraceae.ND3007.group



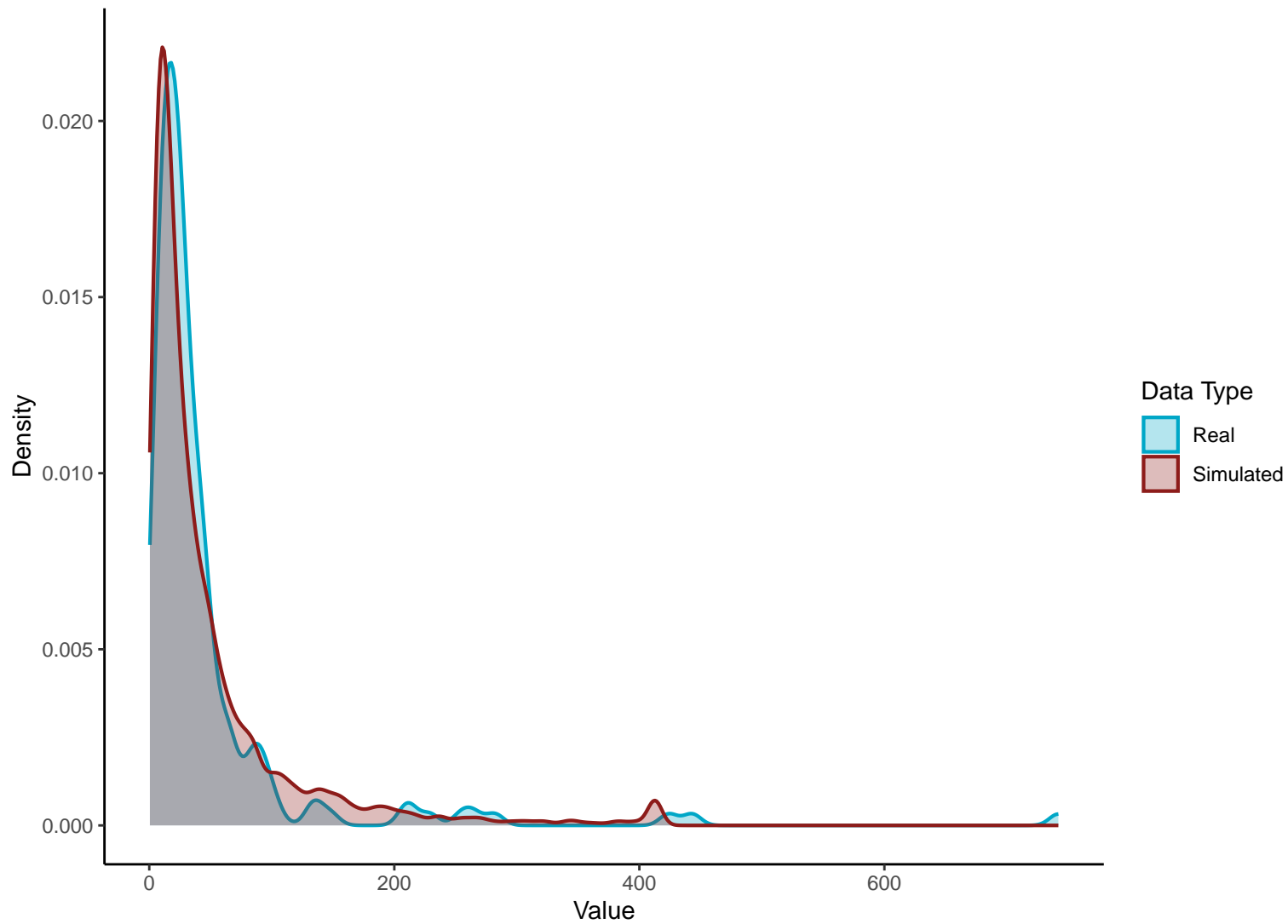
# Coprococcus



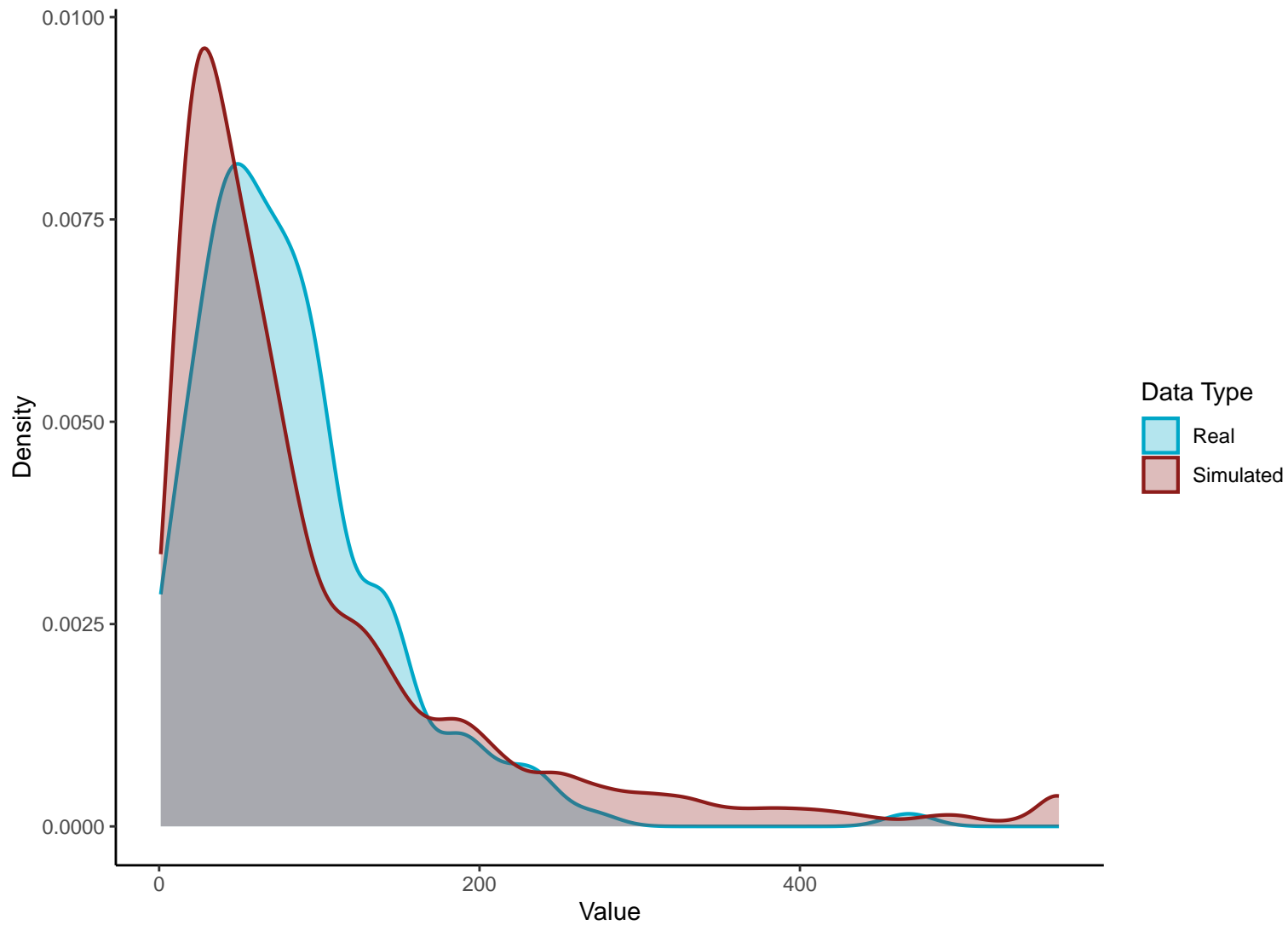
# Lactobacillus



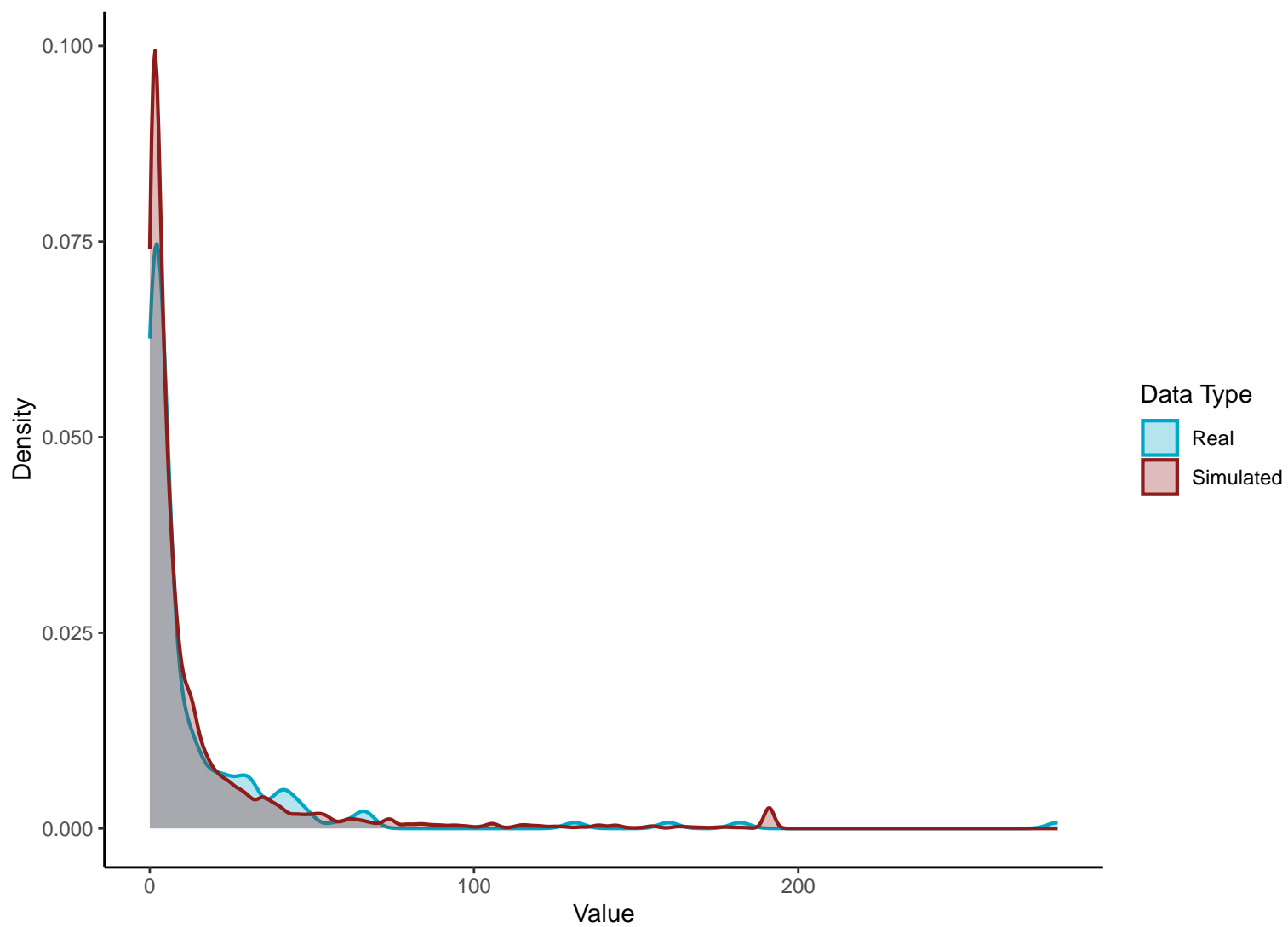
UCG.009



# Colidextribacter

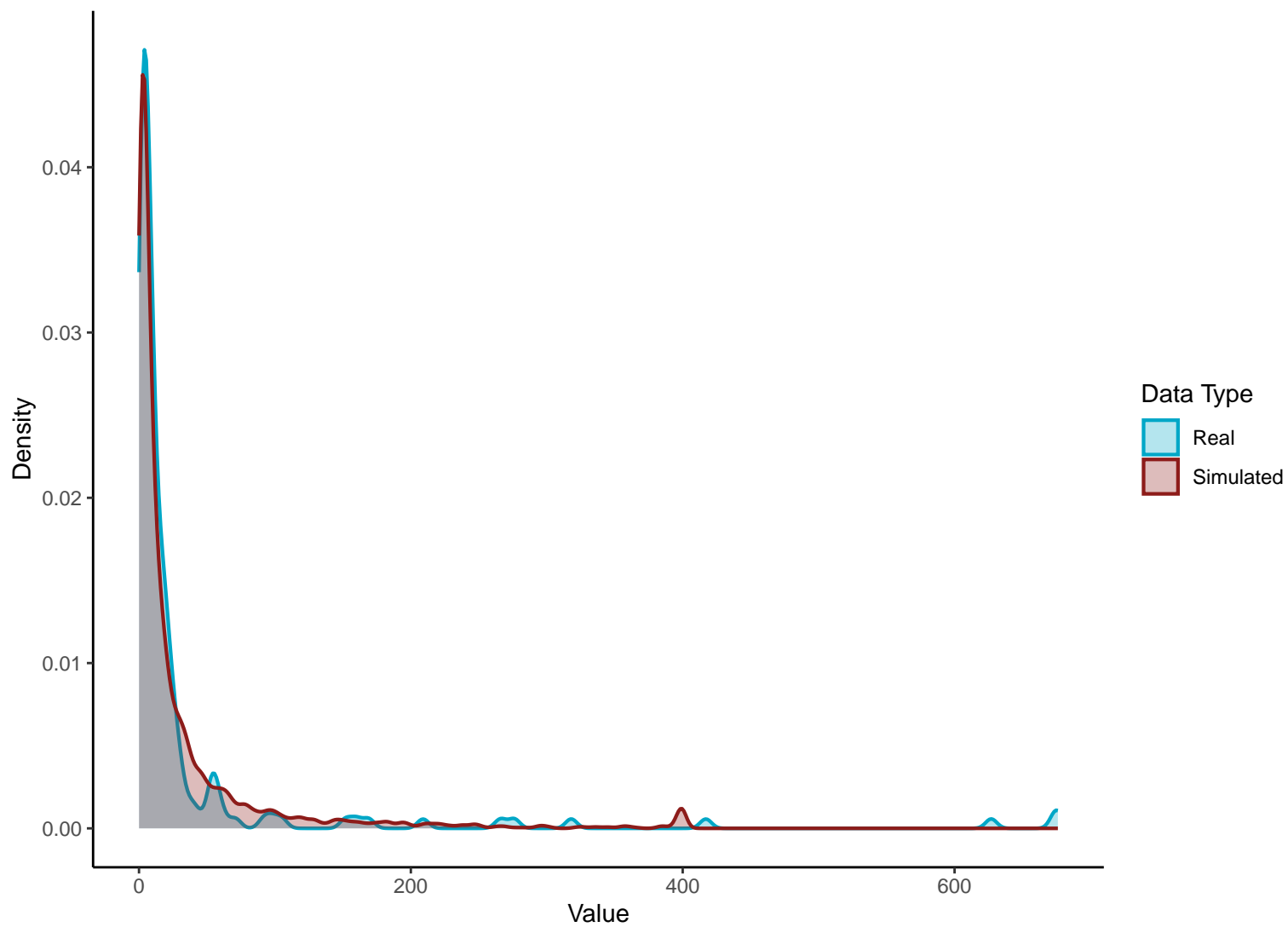


# Acidaminococcus

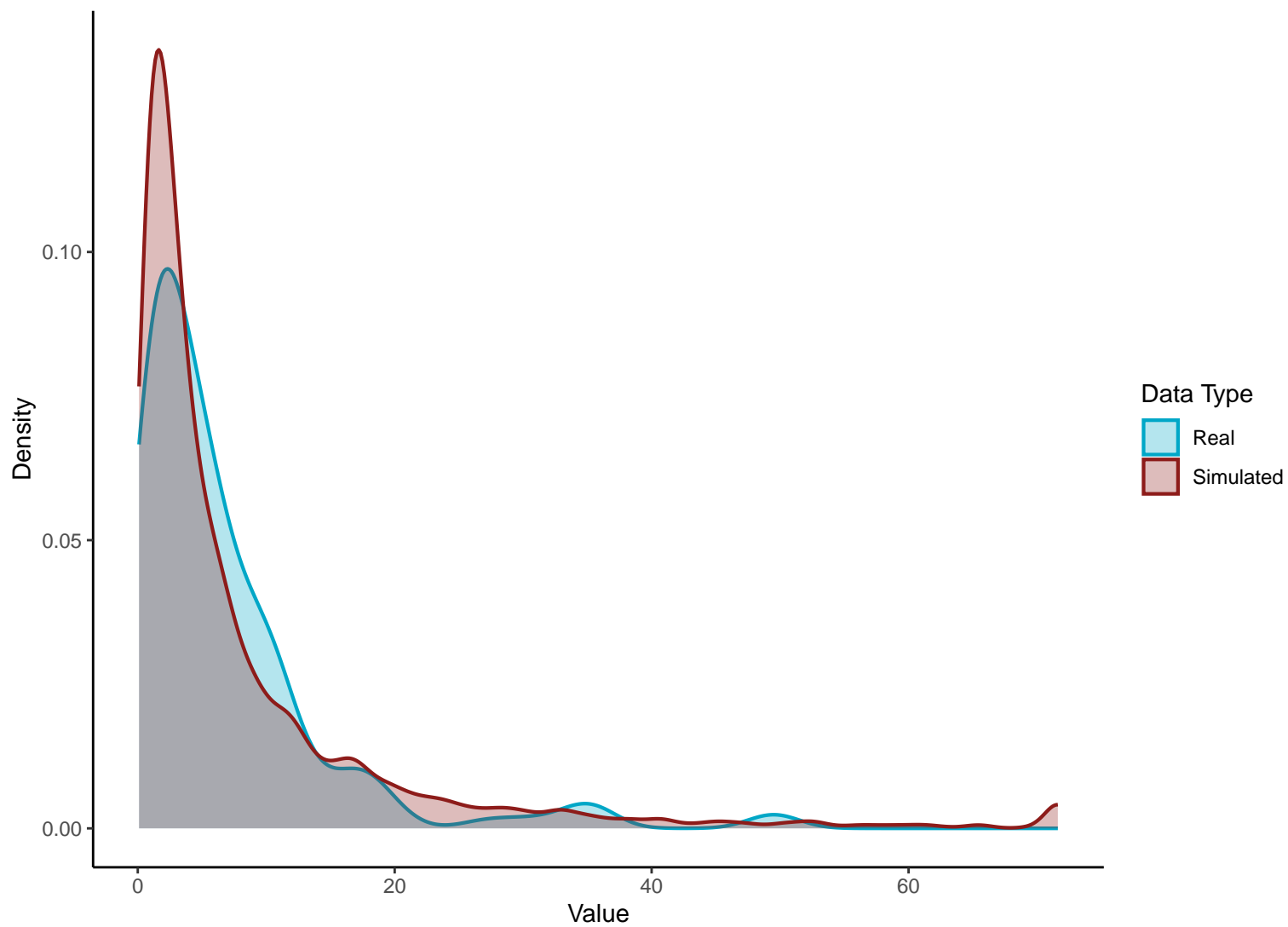




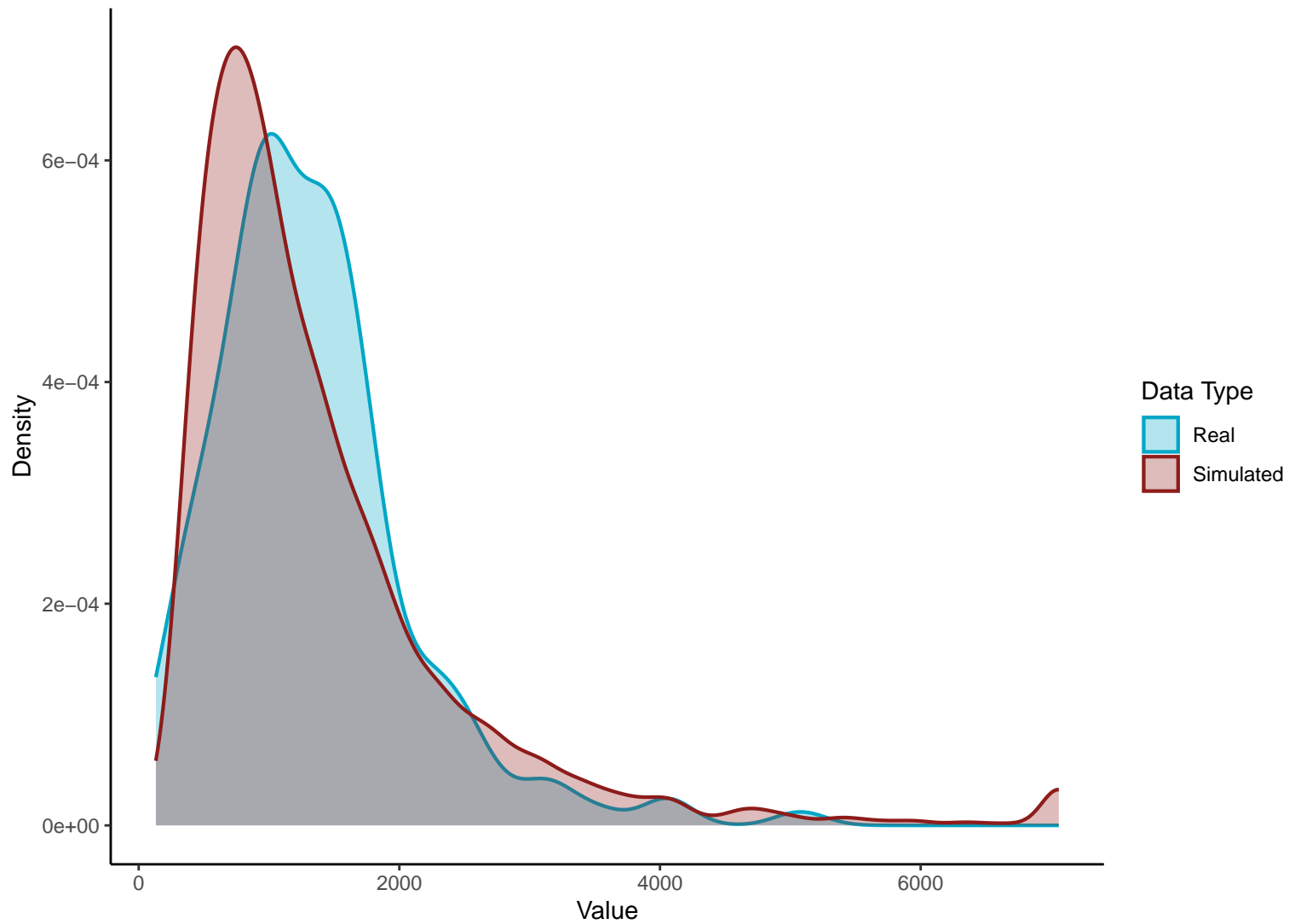
# Parabacteroides



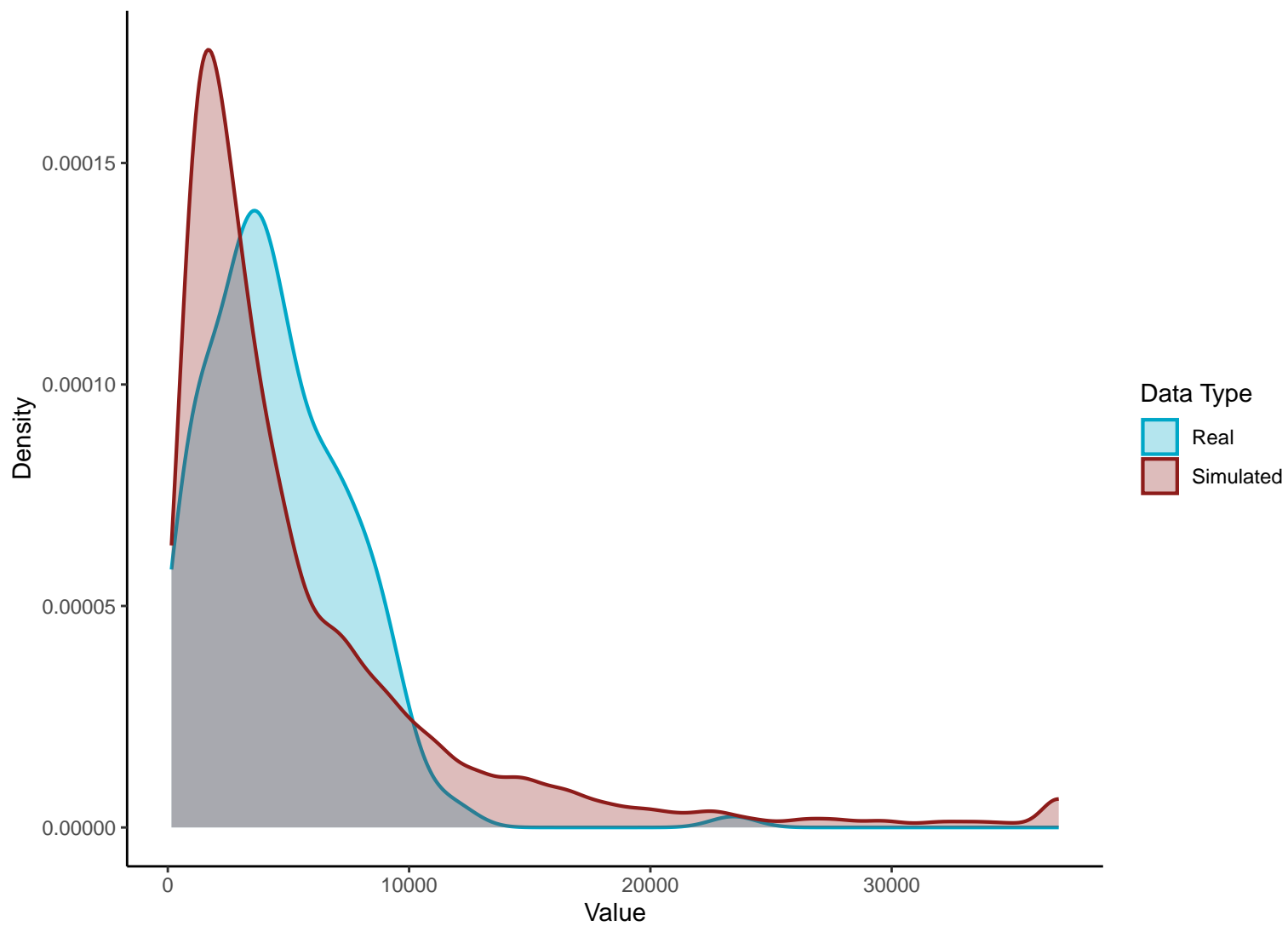
# Allisonella



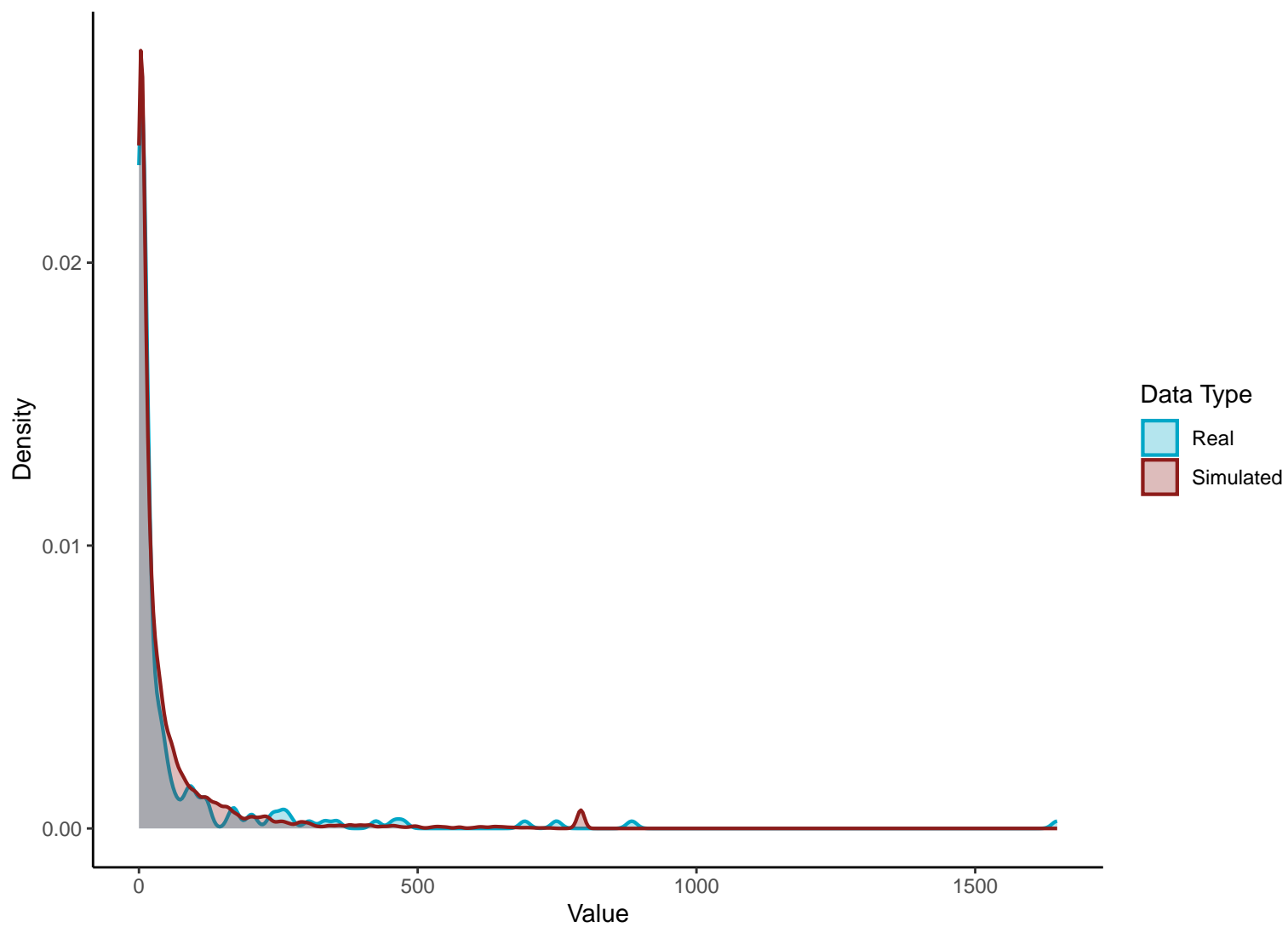
# Blautia



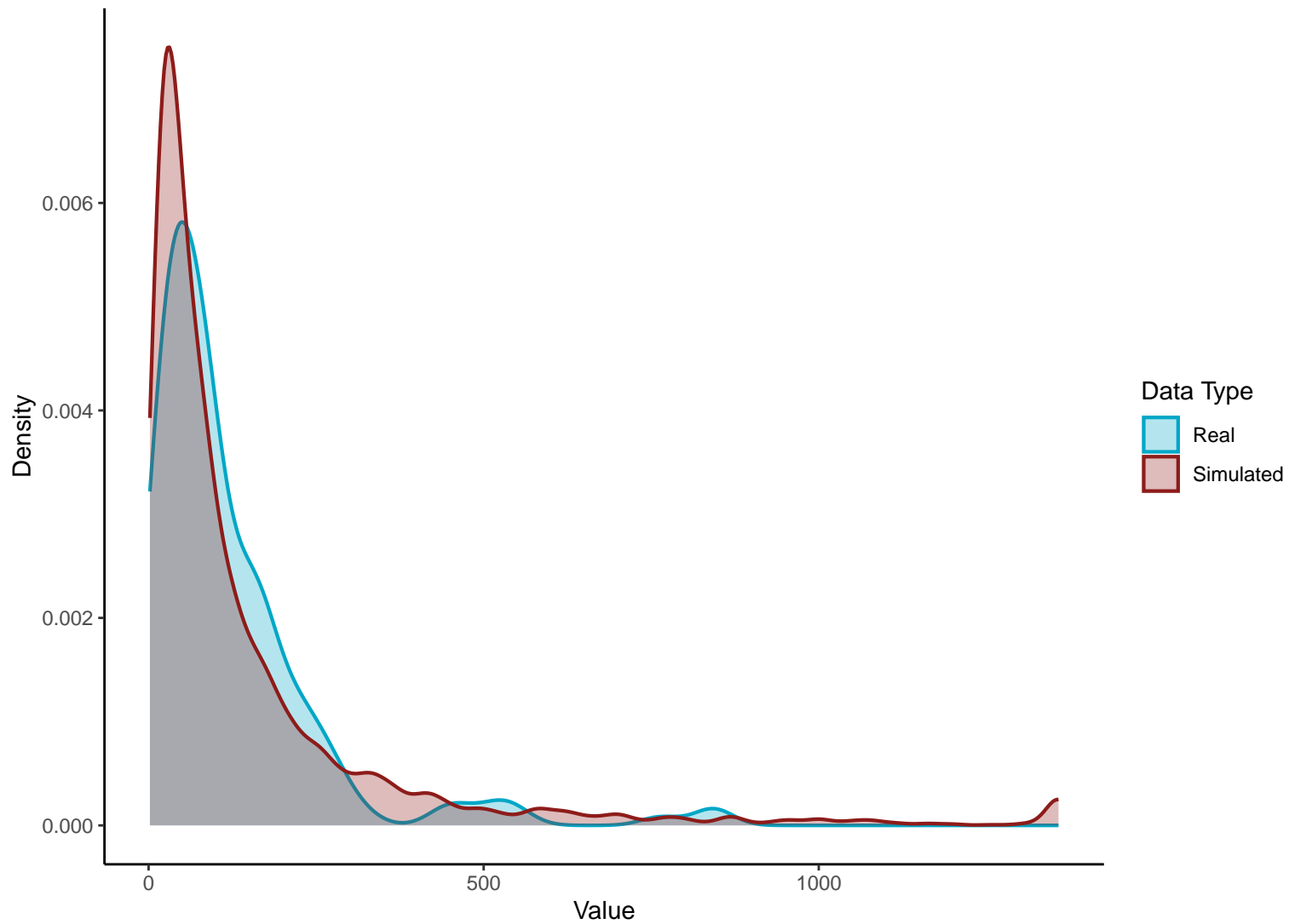
HT002



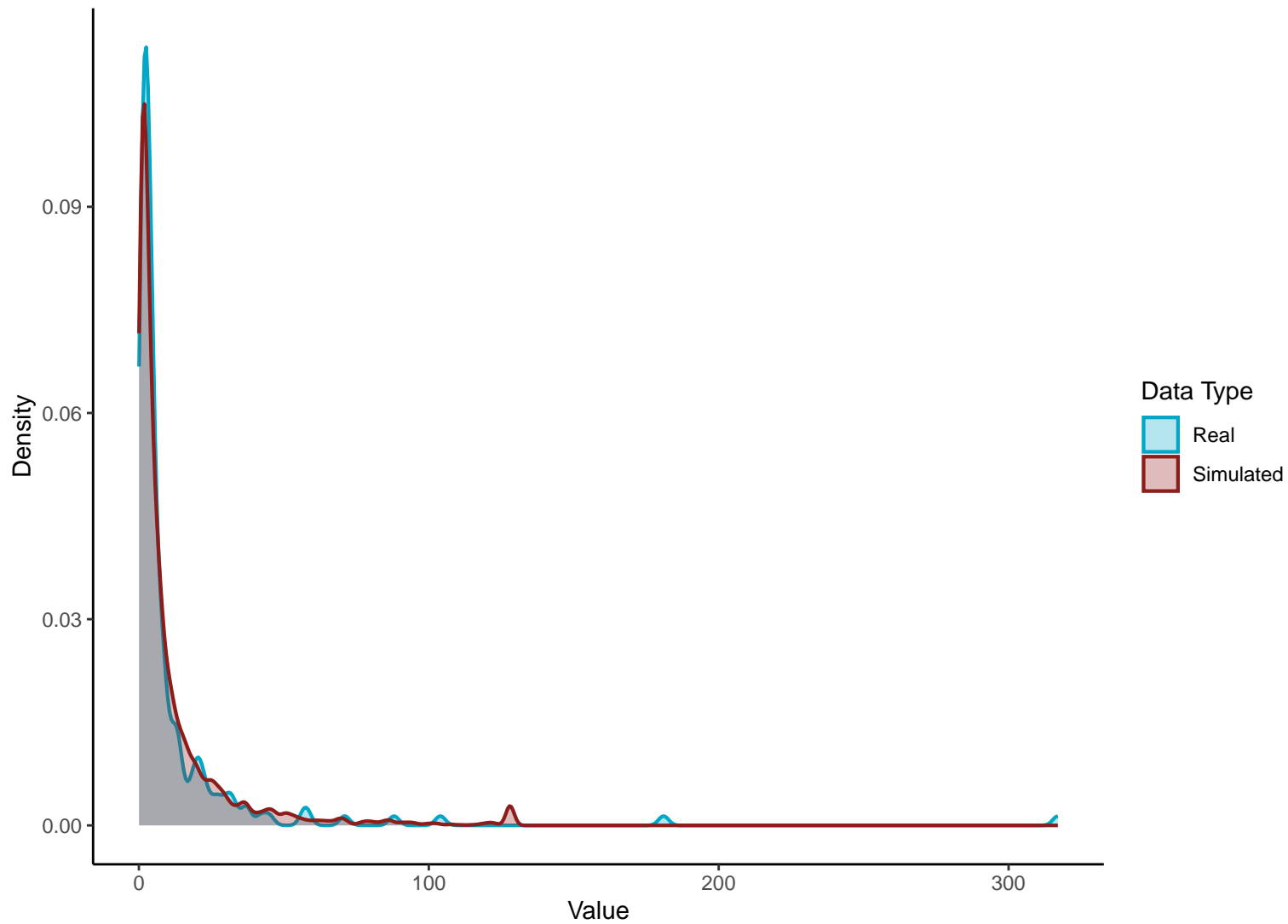
# Frisingicoccus



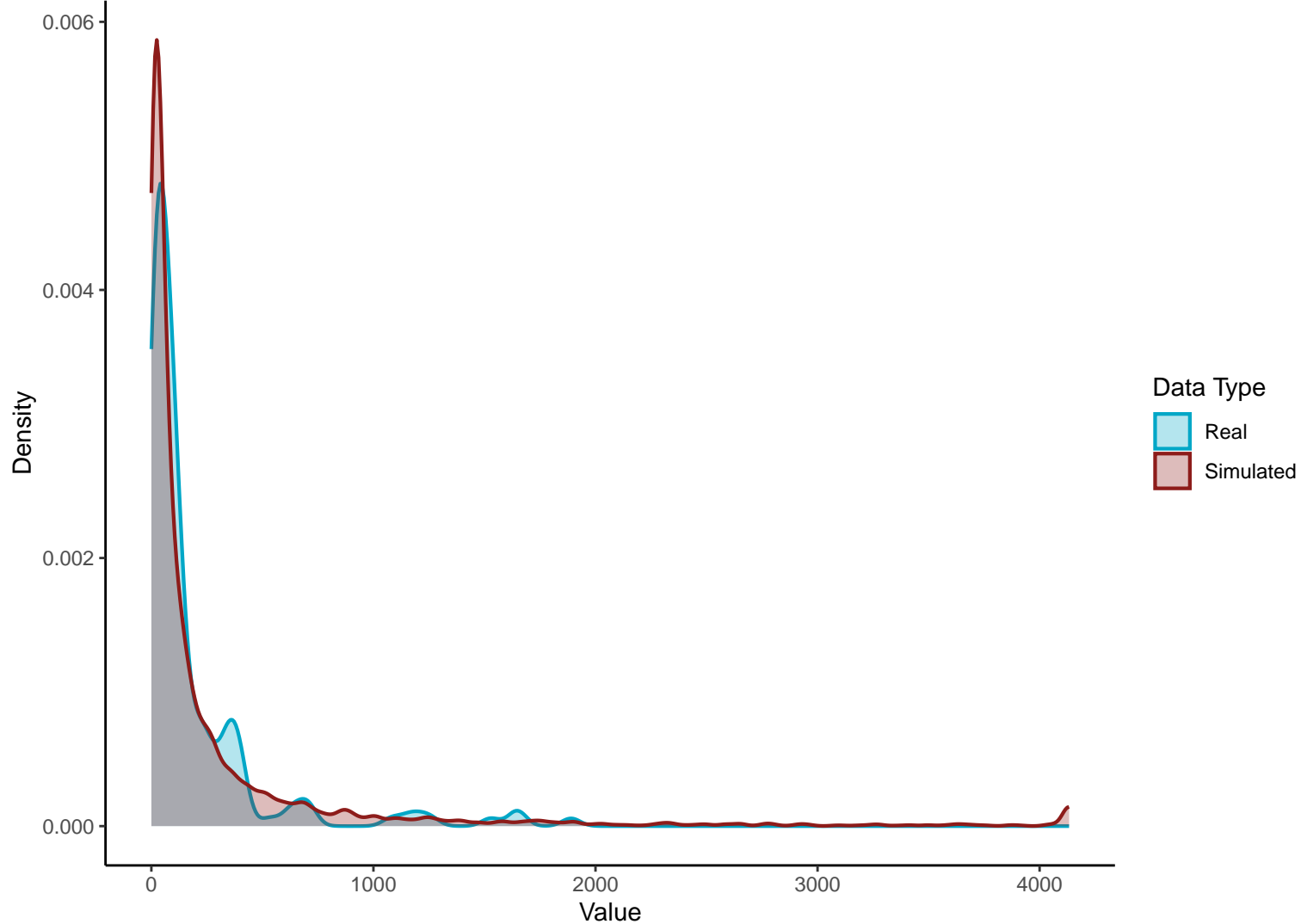
# Ligilactobacillus



# Sphaerochaeta

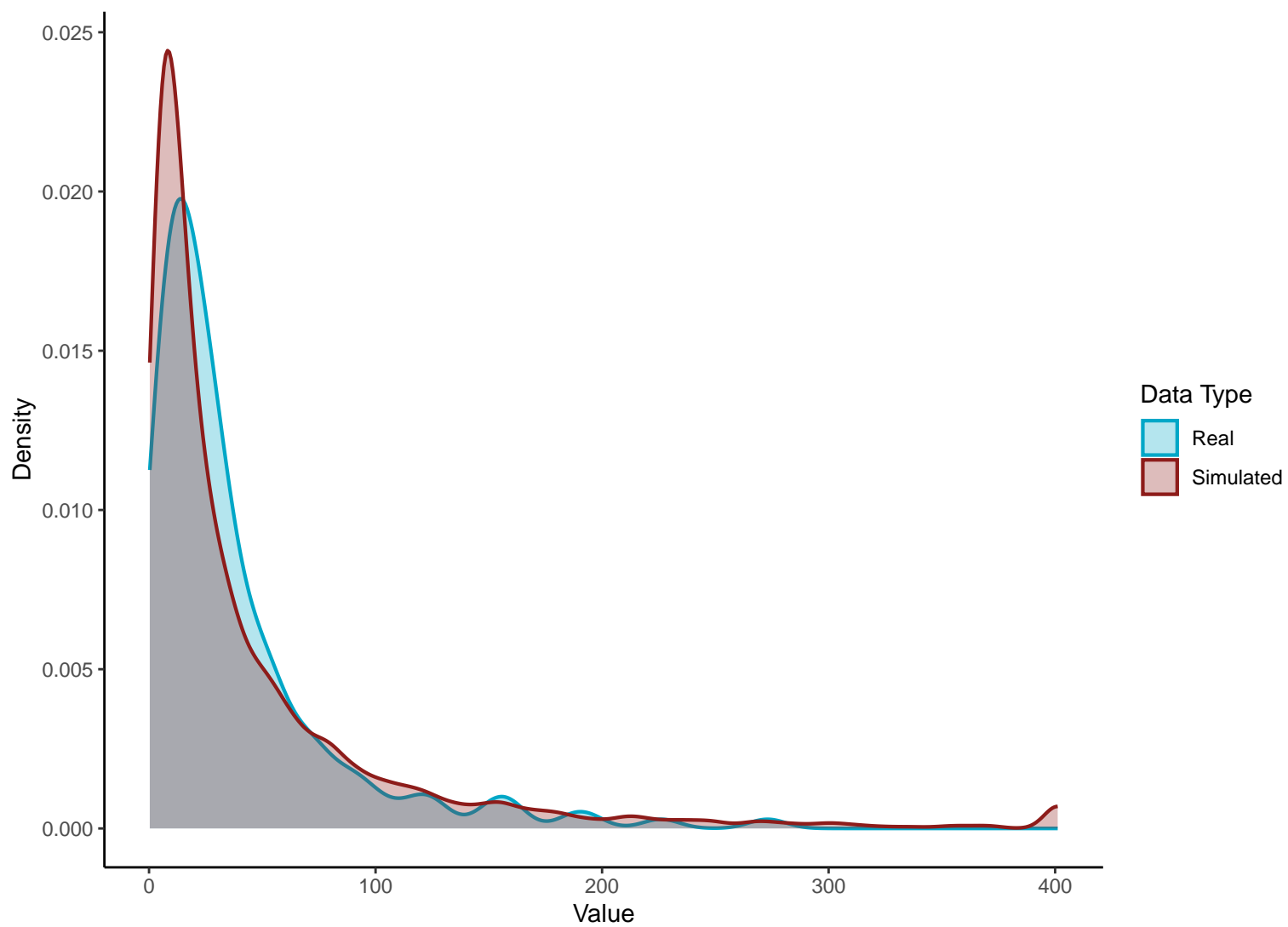


# Romboutsia

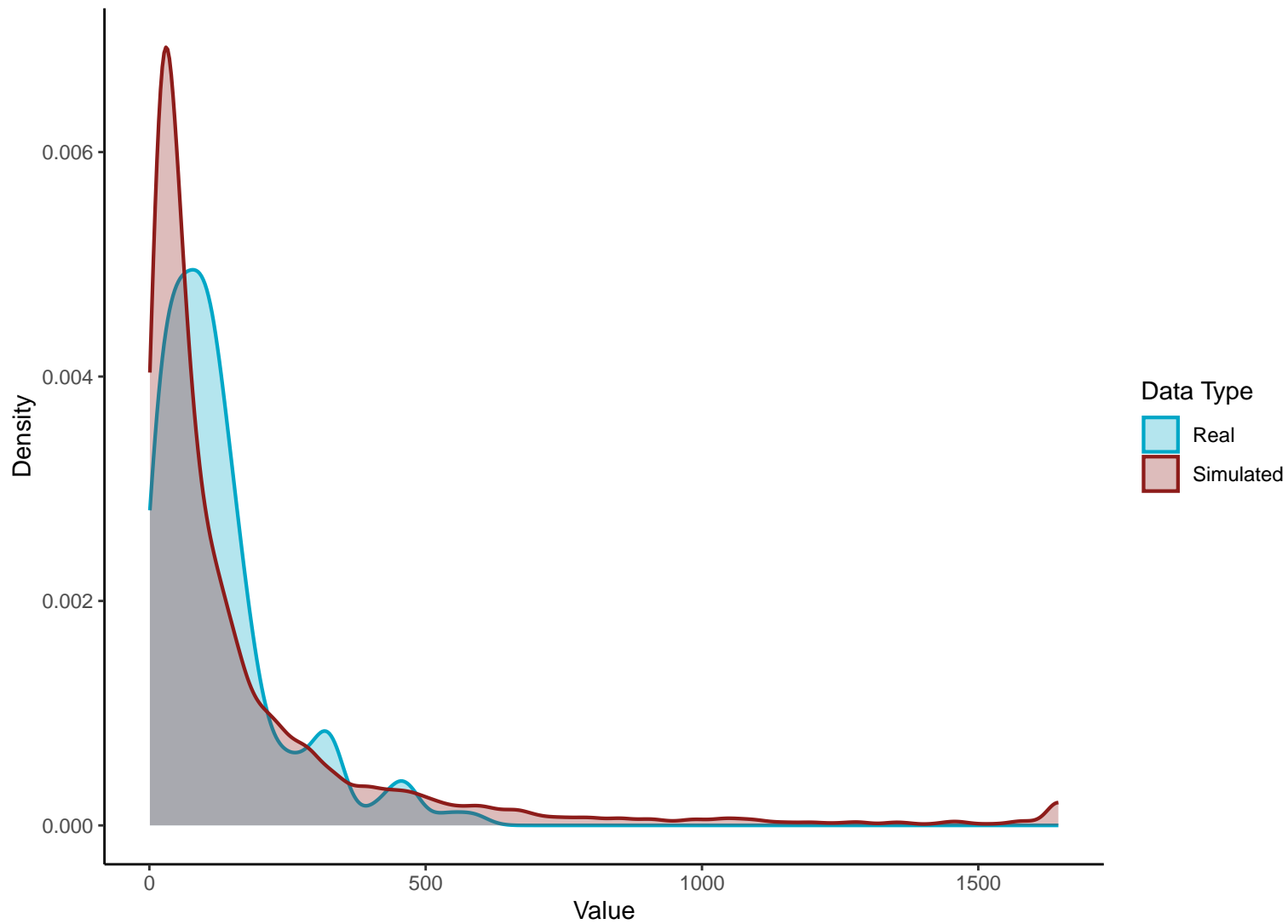




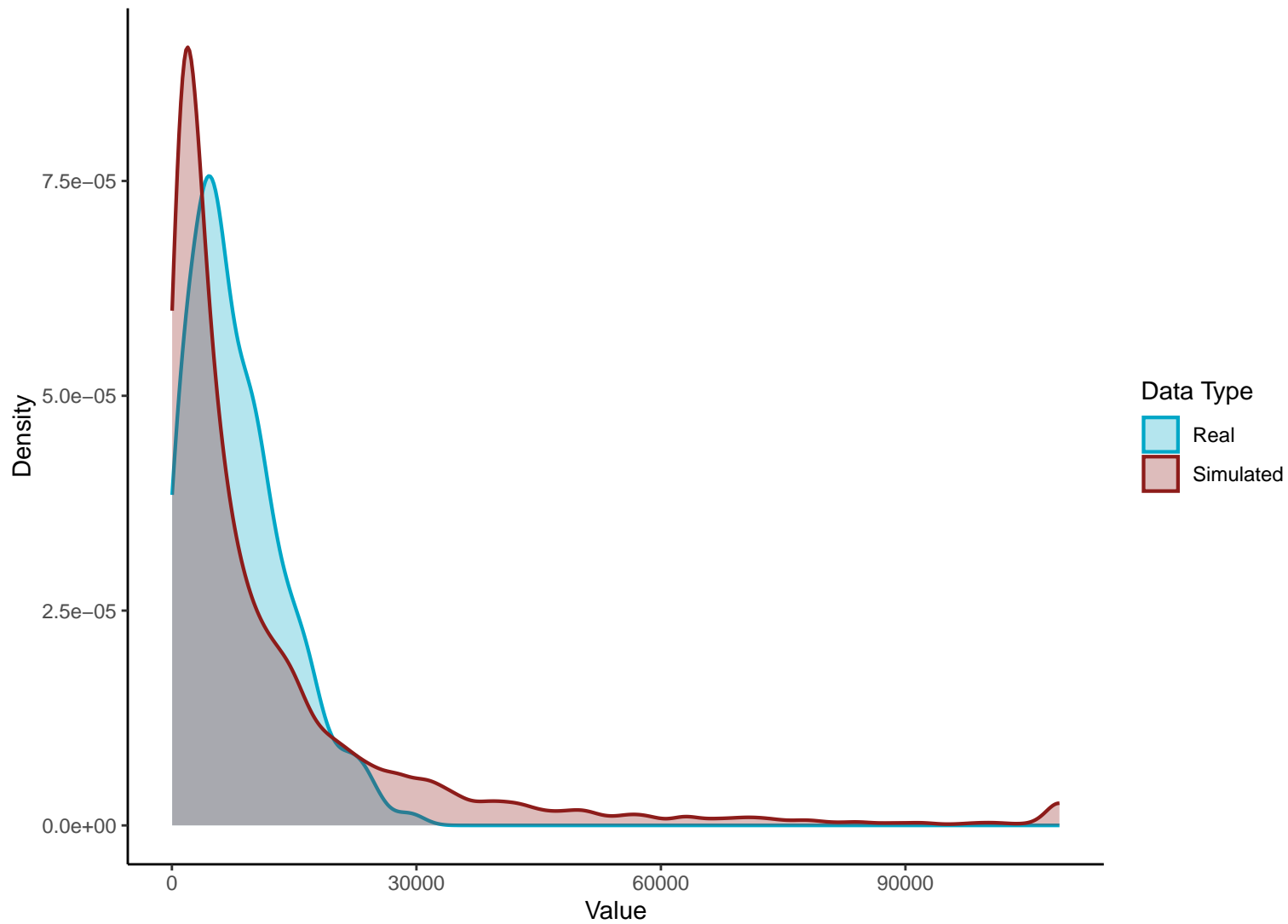
# Lachnospiraceae.UGC.001



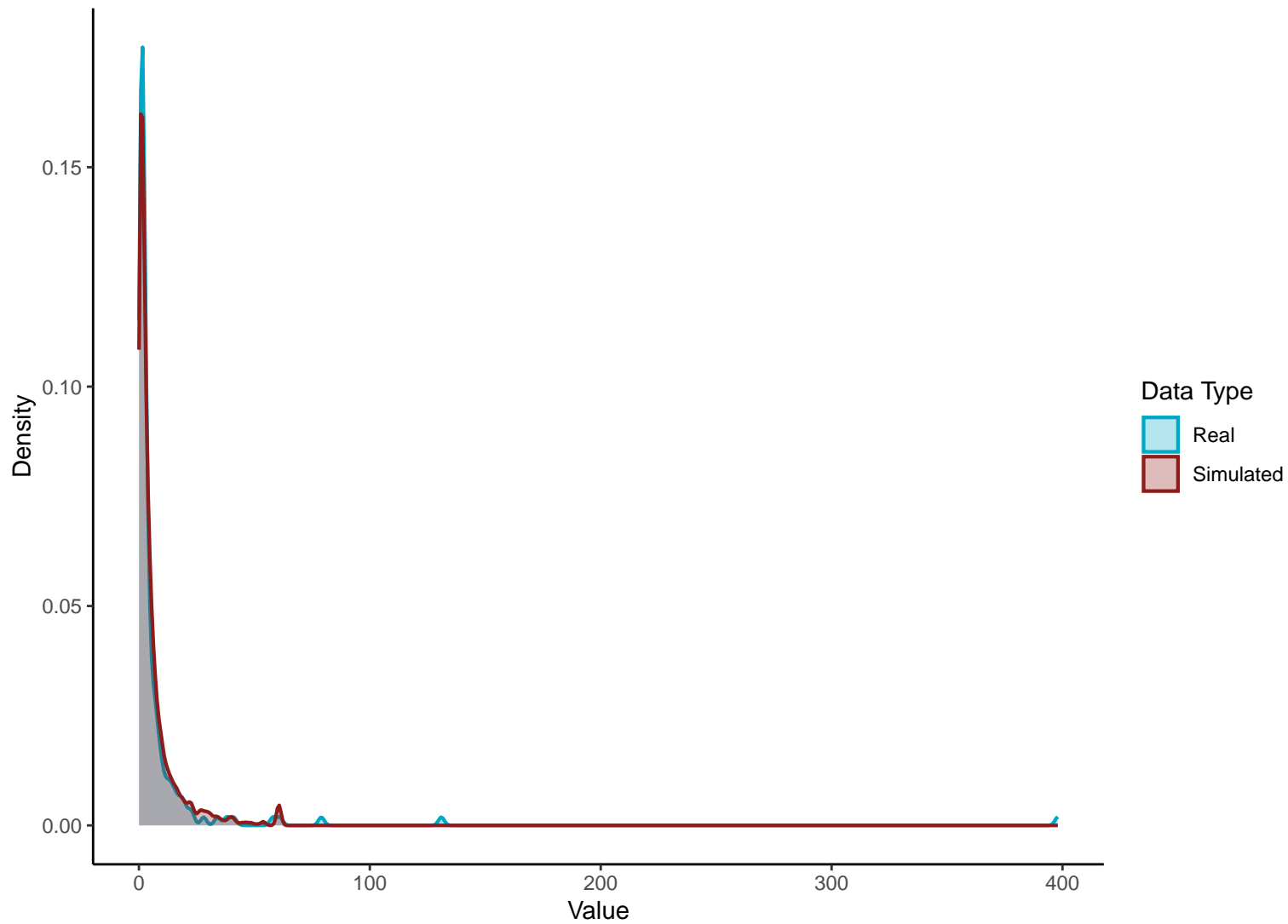
# Oscillibacter



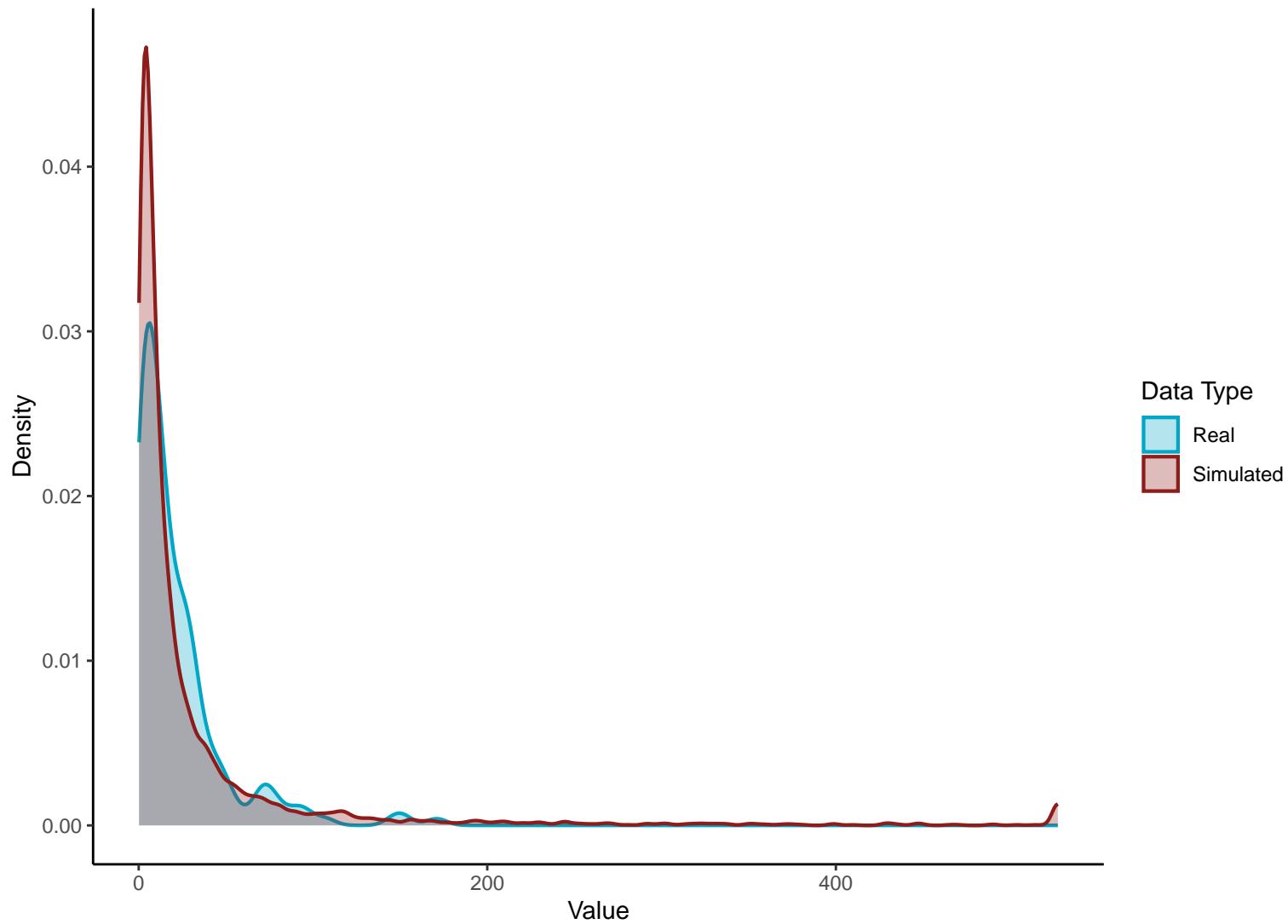
# Streptococcus



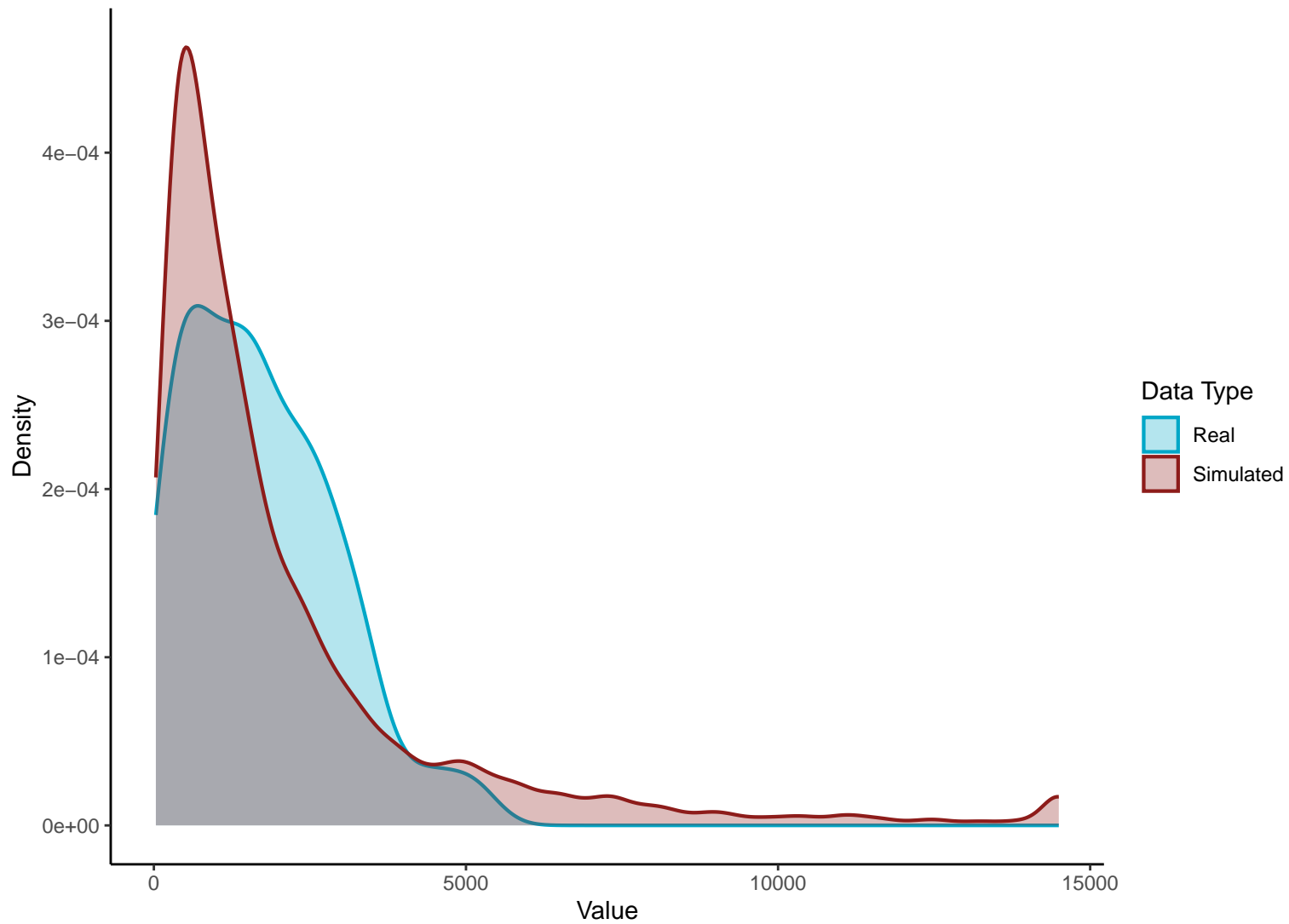
# Cellulosilyticum



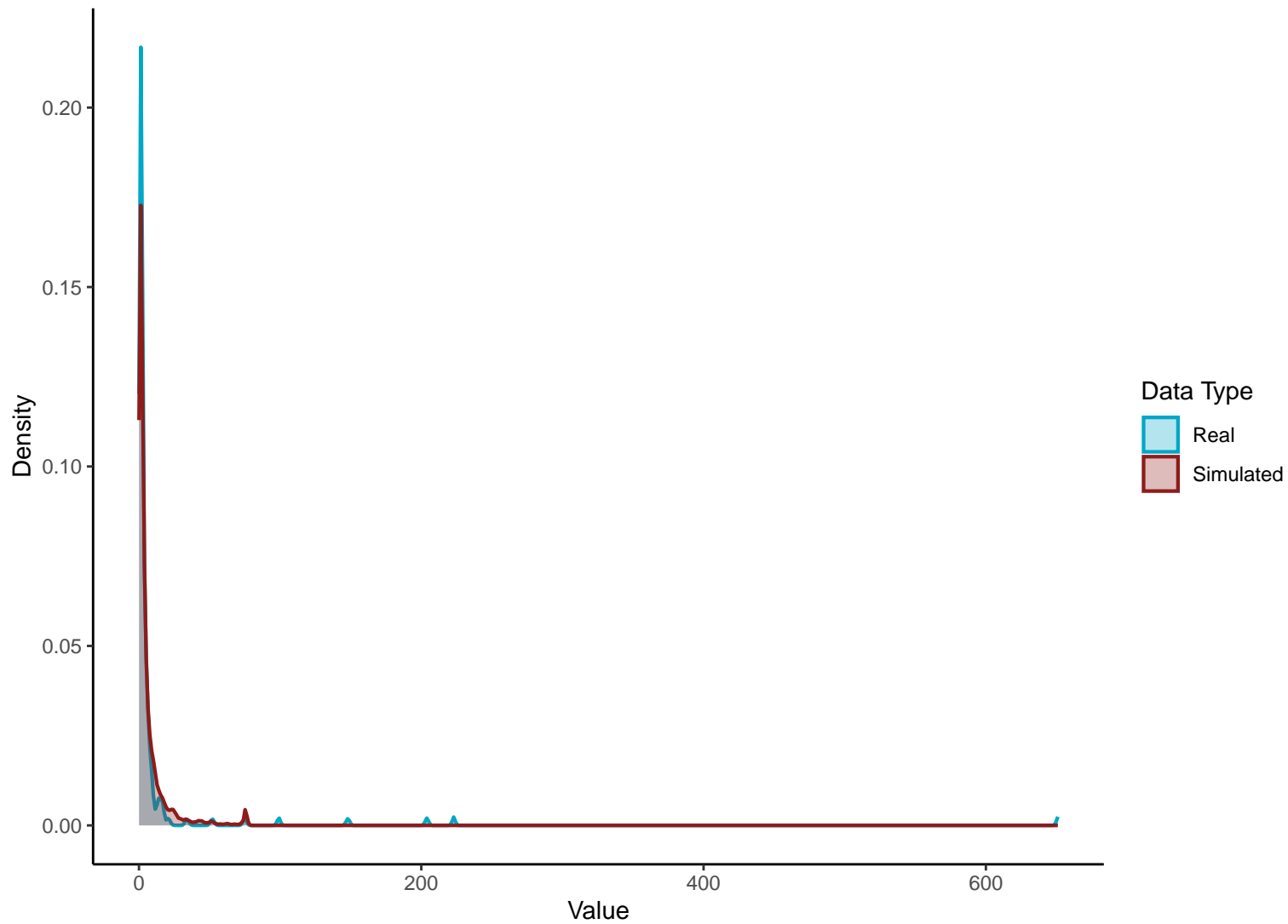
# Mitsuokella



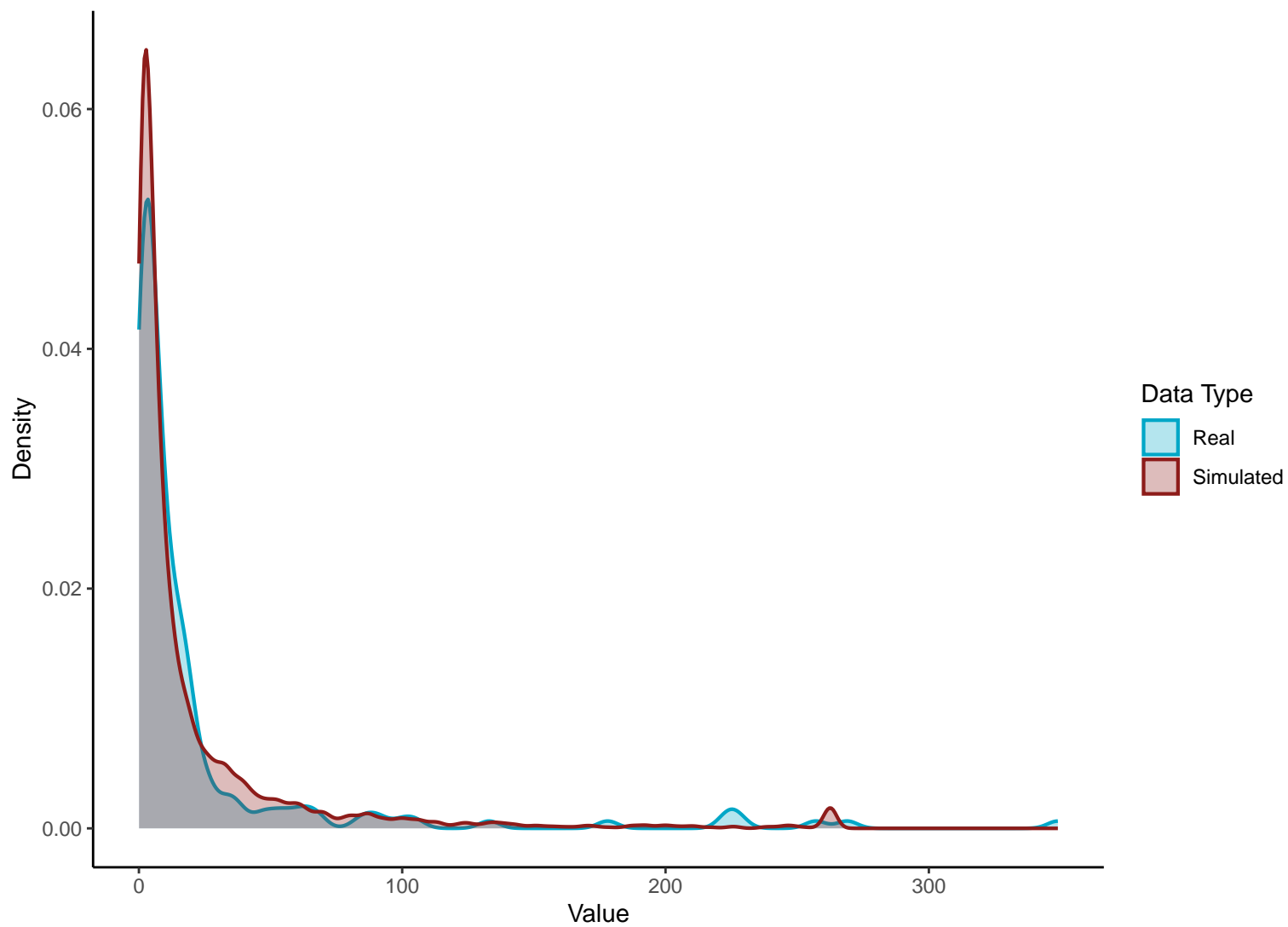
# Agathobacter



# Bacteroides

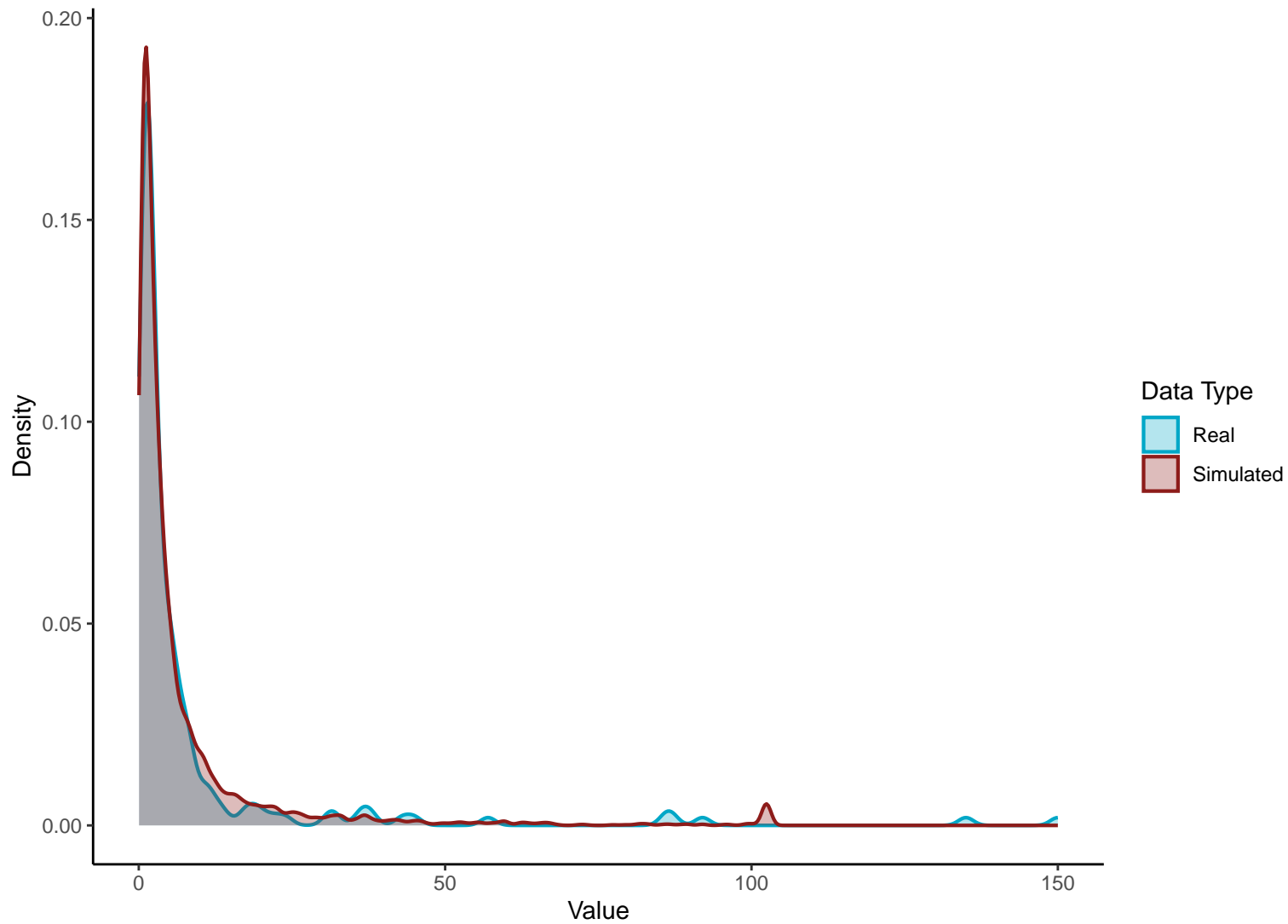


p.1088.a5.gut.group

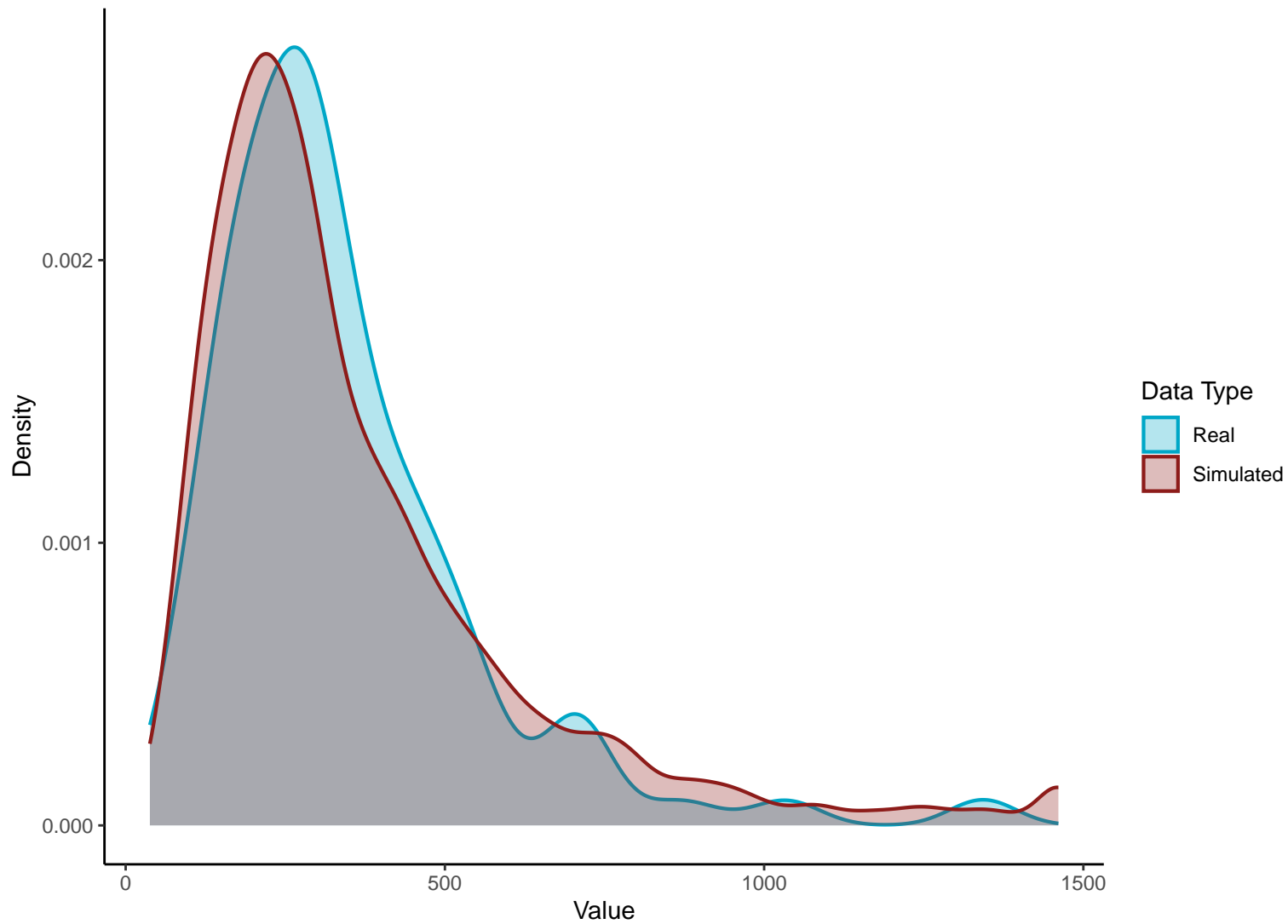




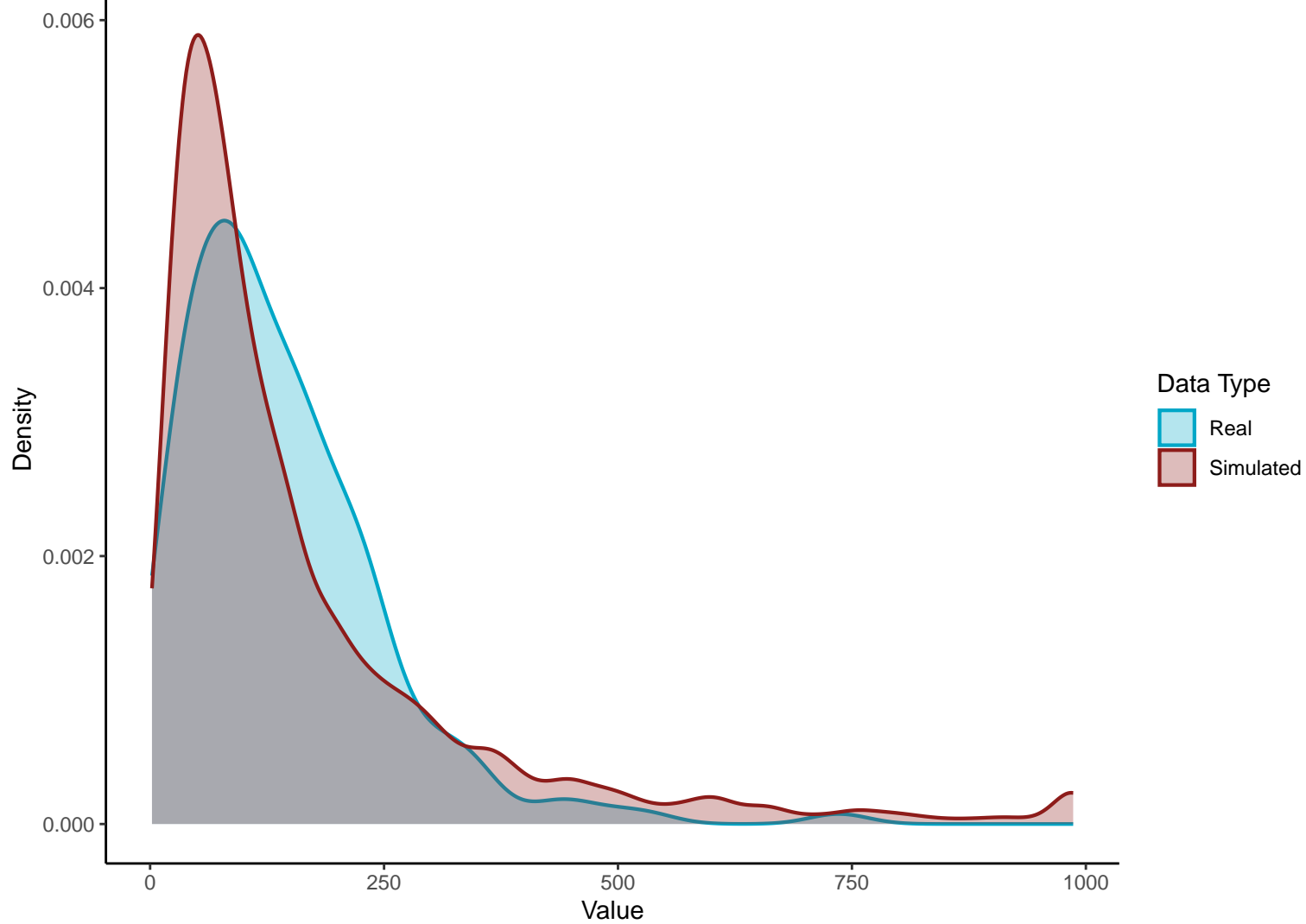
# Anaeroplasma



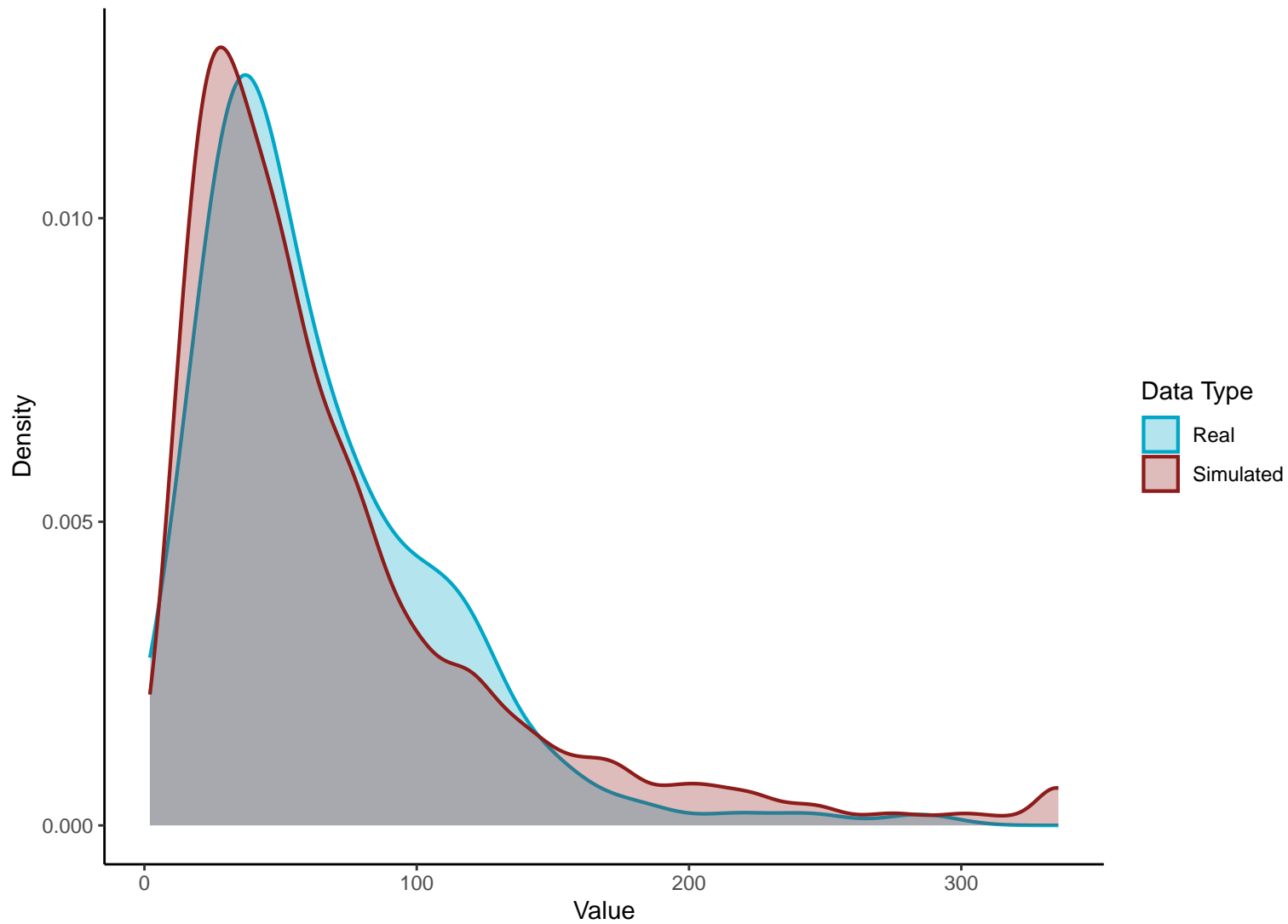
# Marvinbryantia



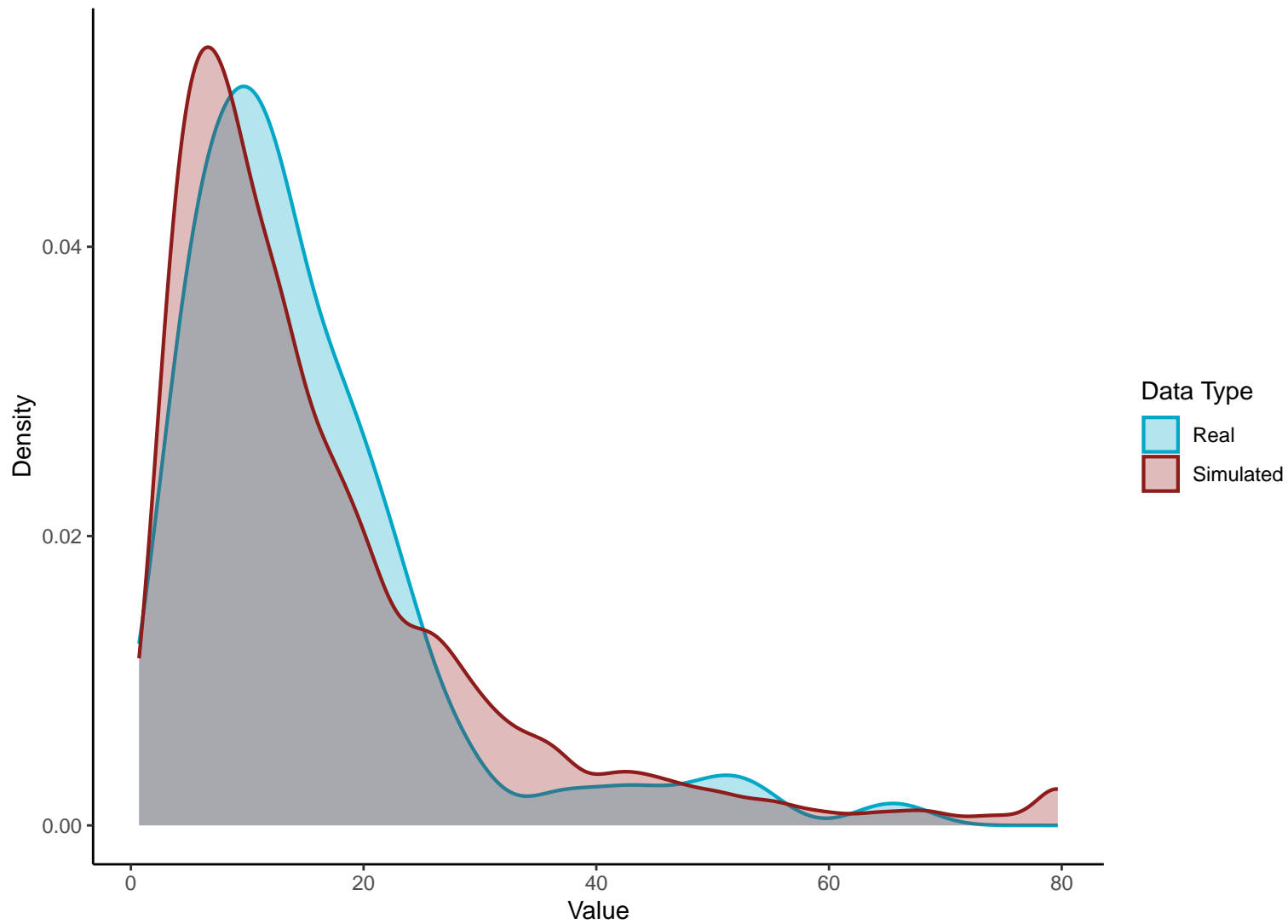
# Mogibacterium



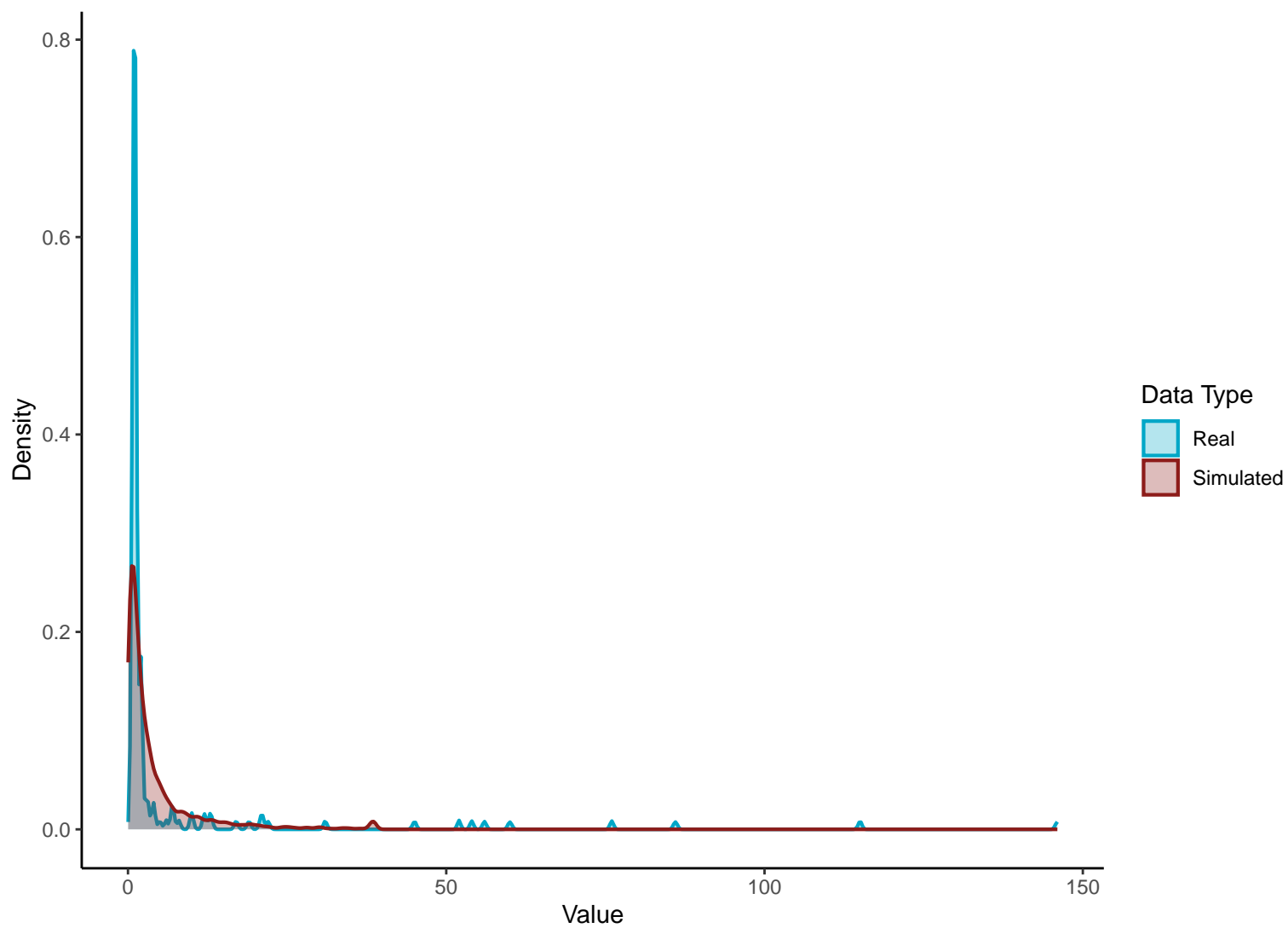
Family.XIII.UCG.001



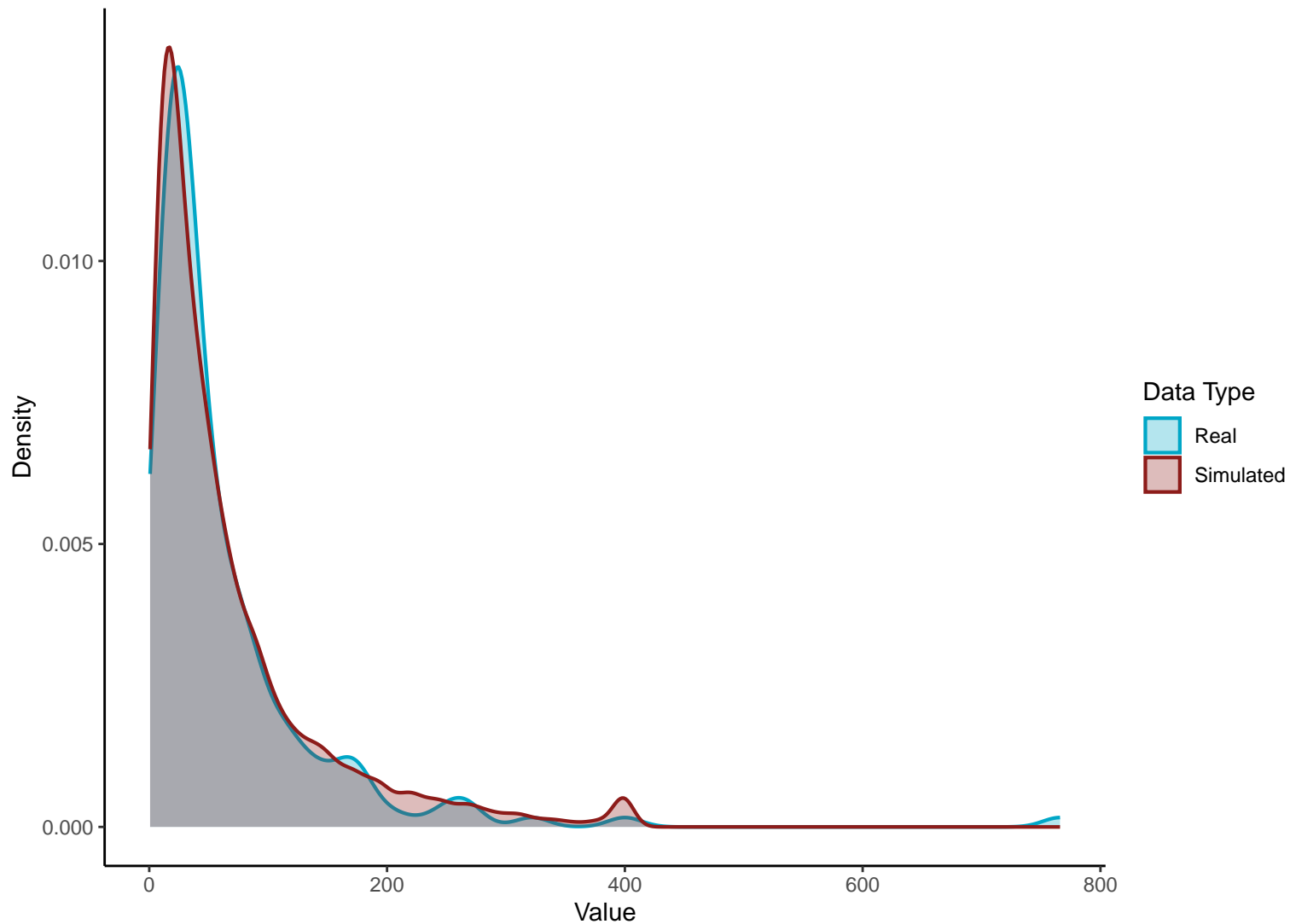
# Lachnospiraceae.UCG.010



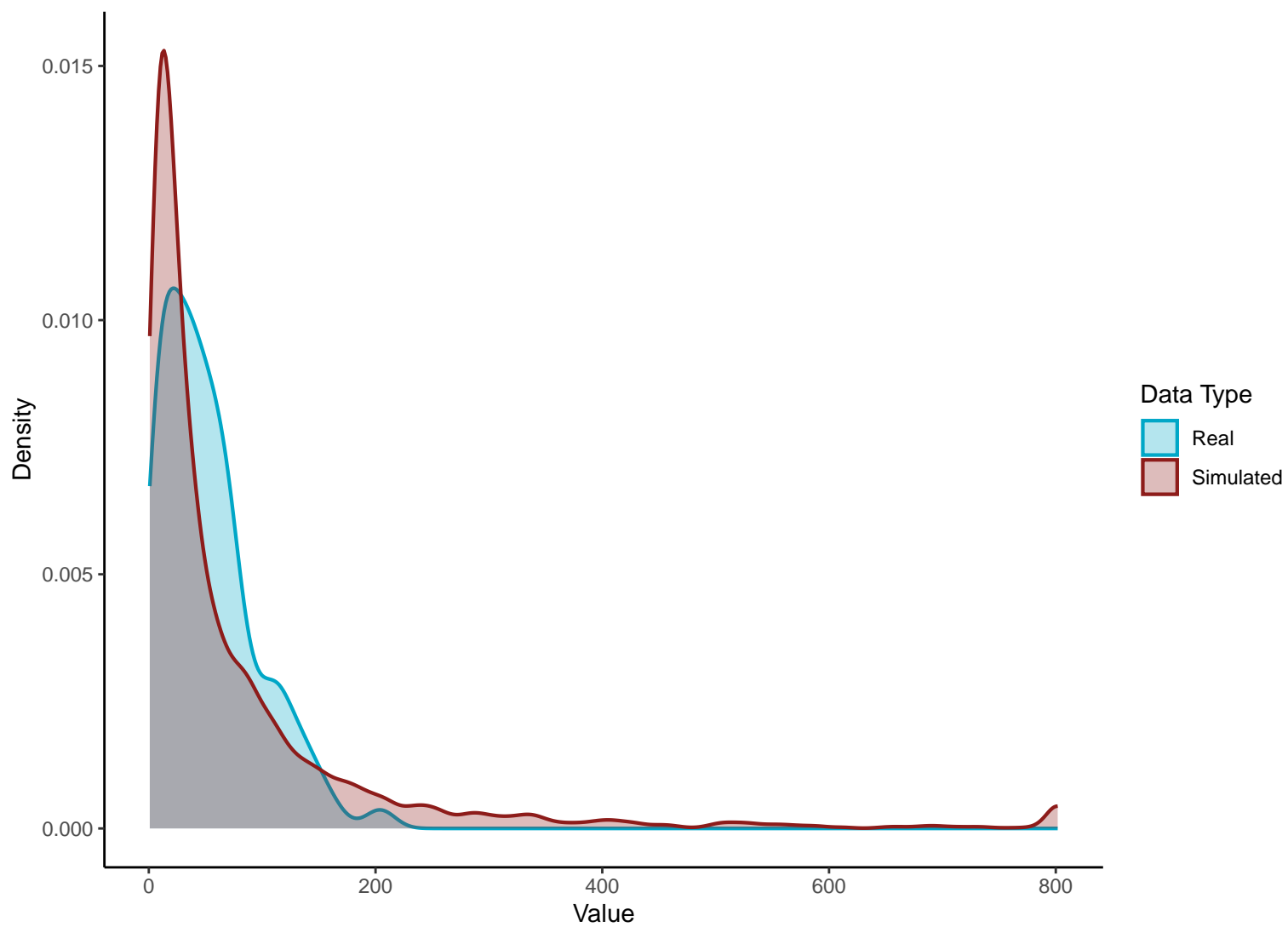
# Megamonas



# X.Eubacterium..nodatum.group

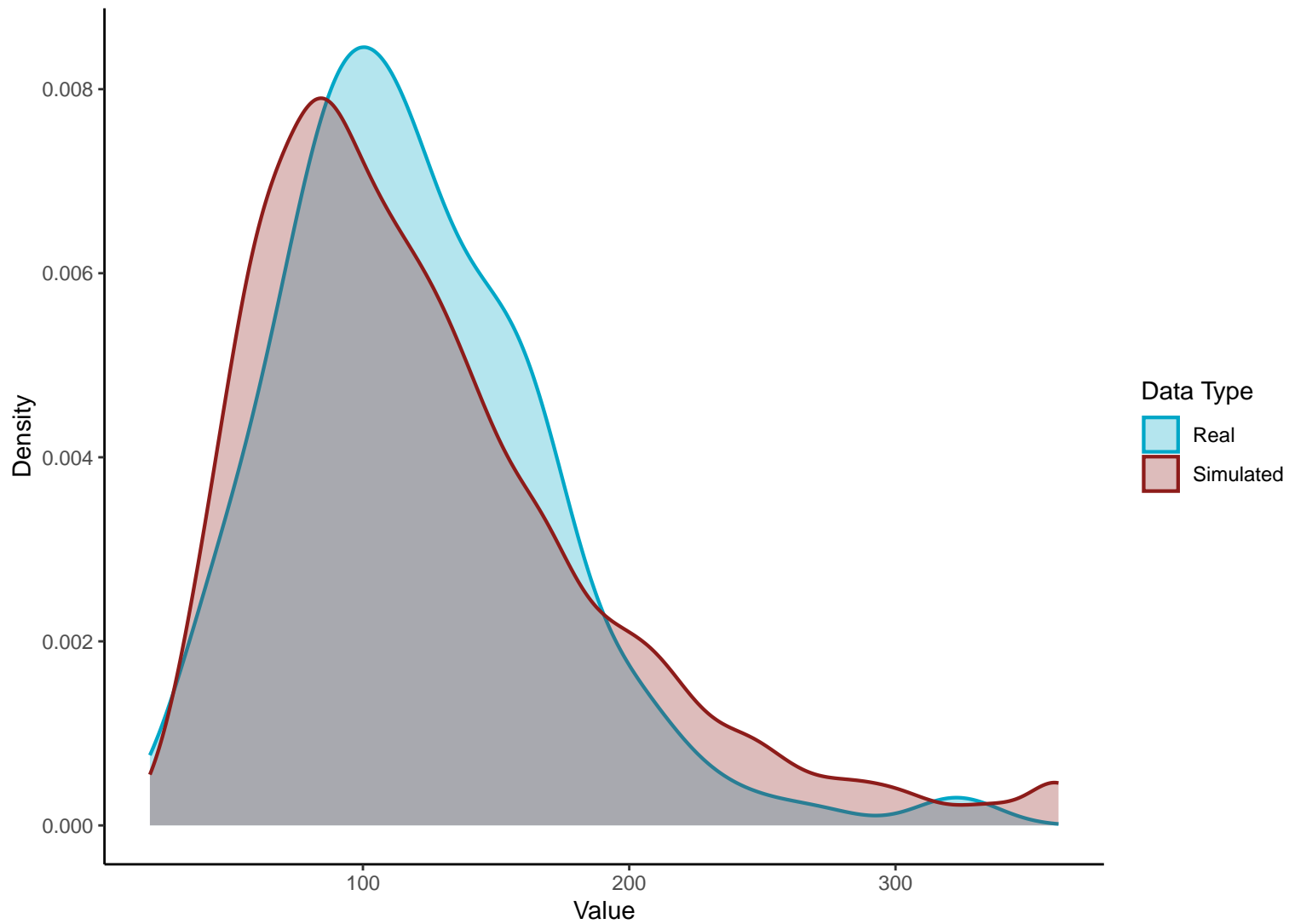


# Lachnospiraceae.NK3A20.group

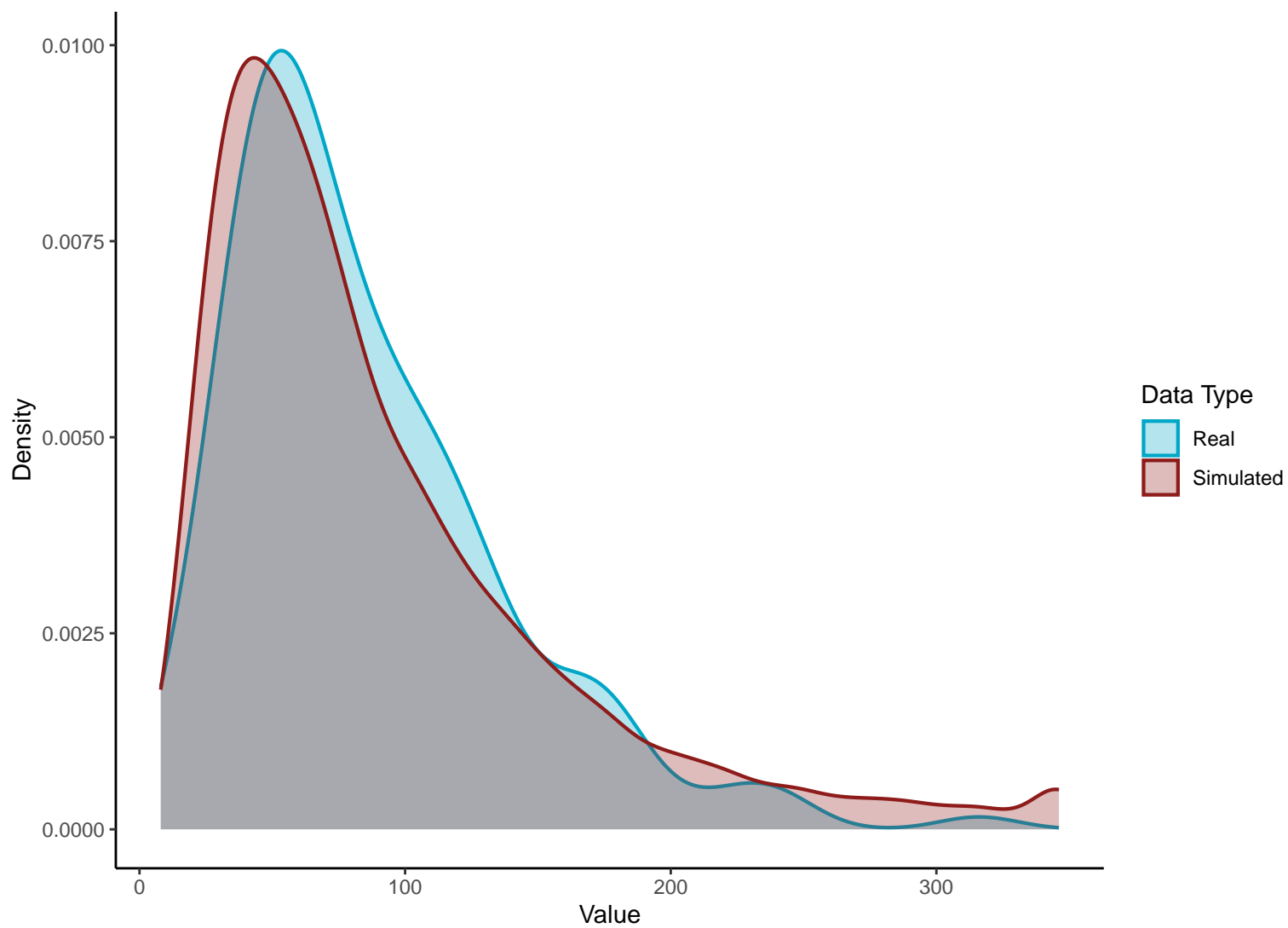




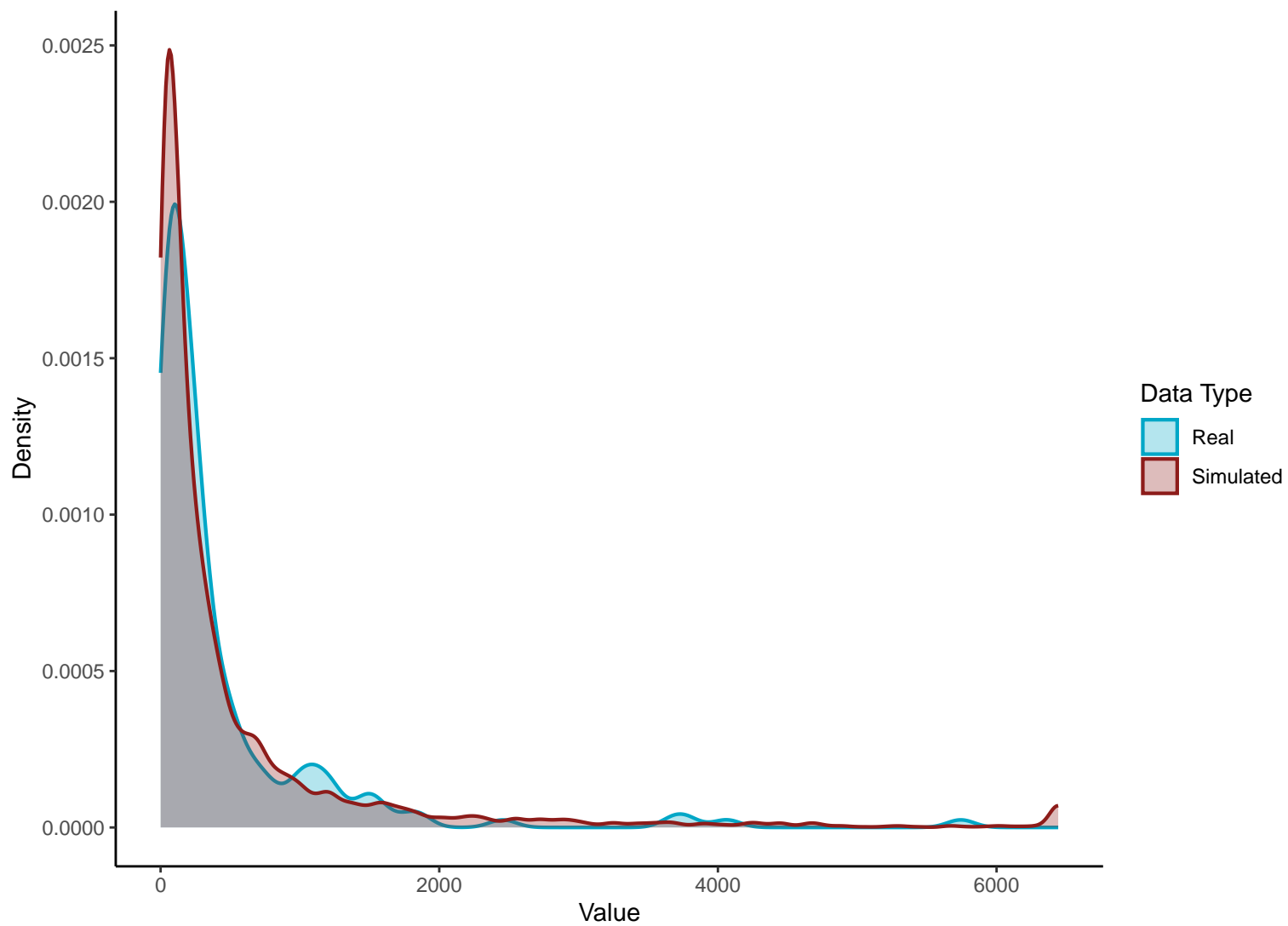
# Lachnospiraceae.FCS020.group



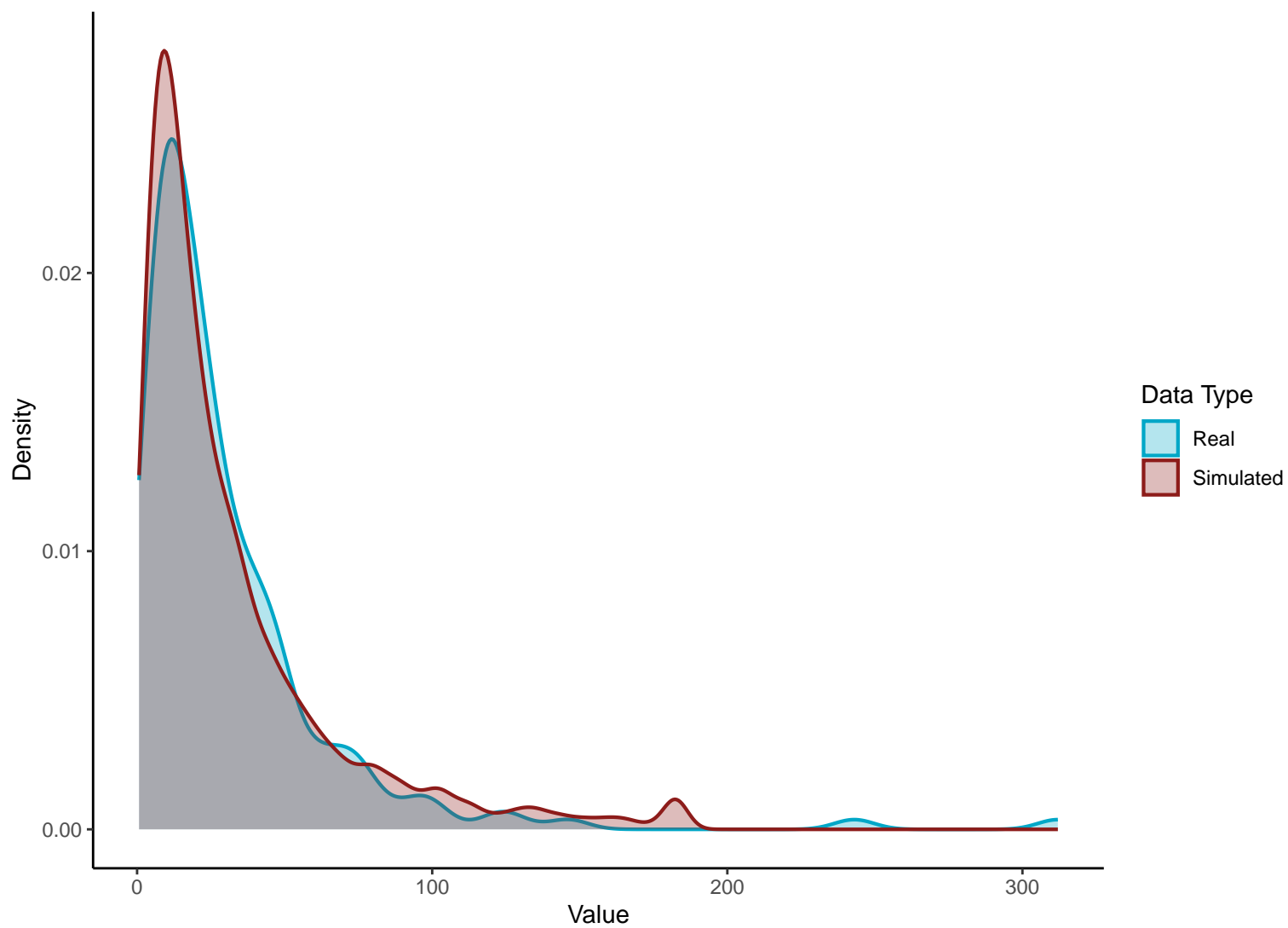
# Incertae.Sedis



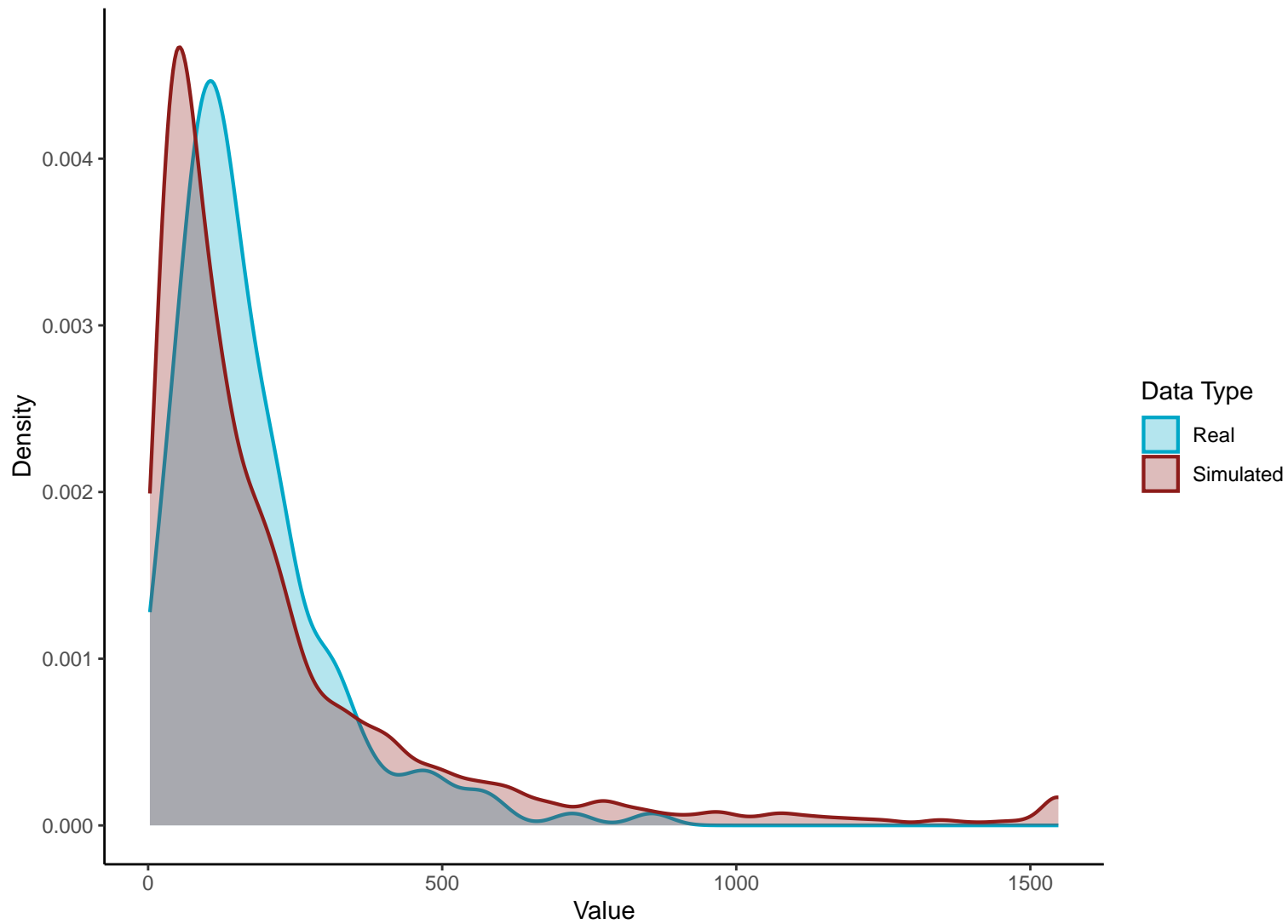
# Limosilactobacillus



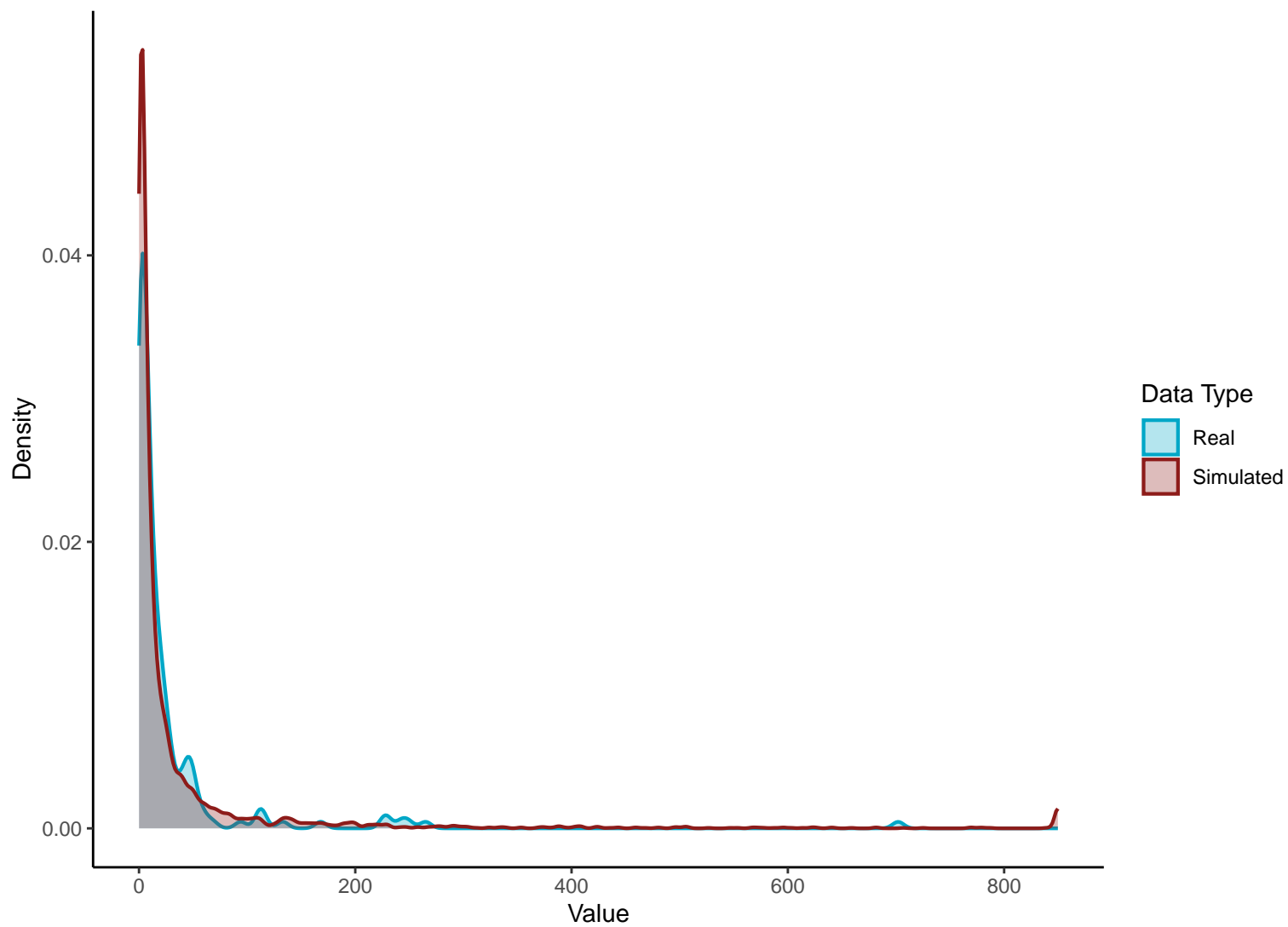
# Desulfovibrio



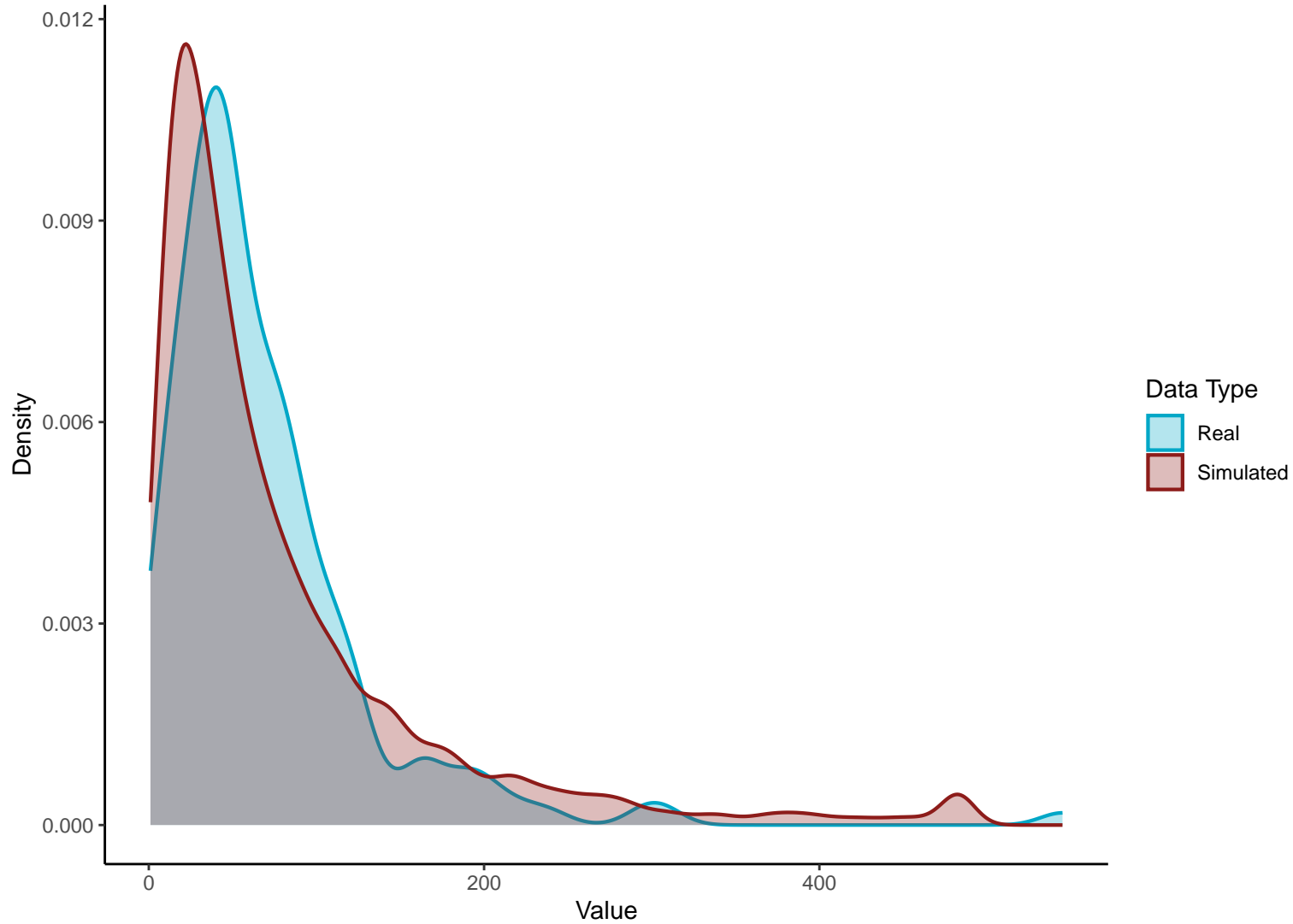
# X.Eubacterium..ruminantium.group



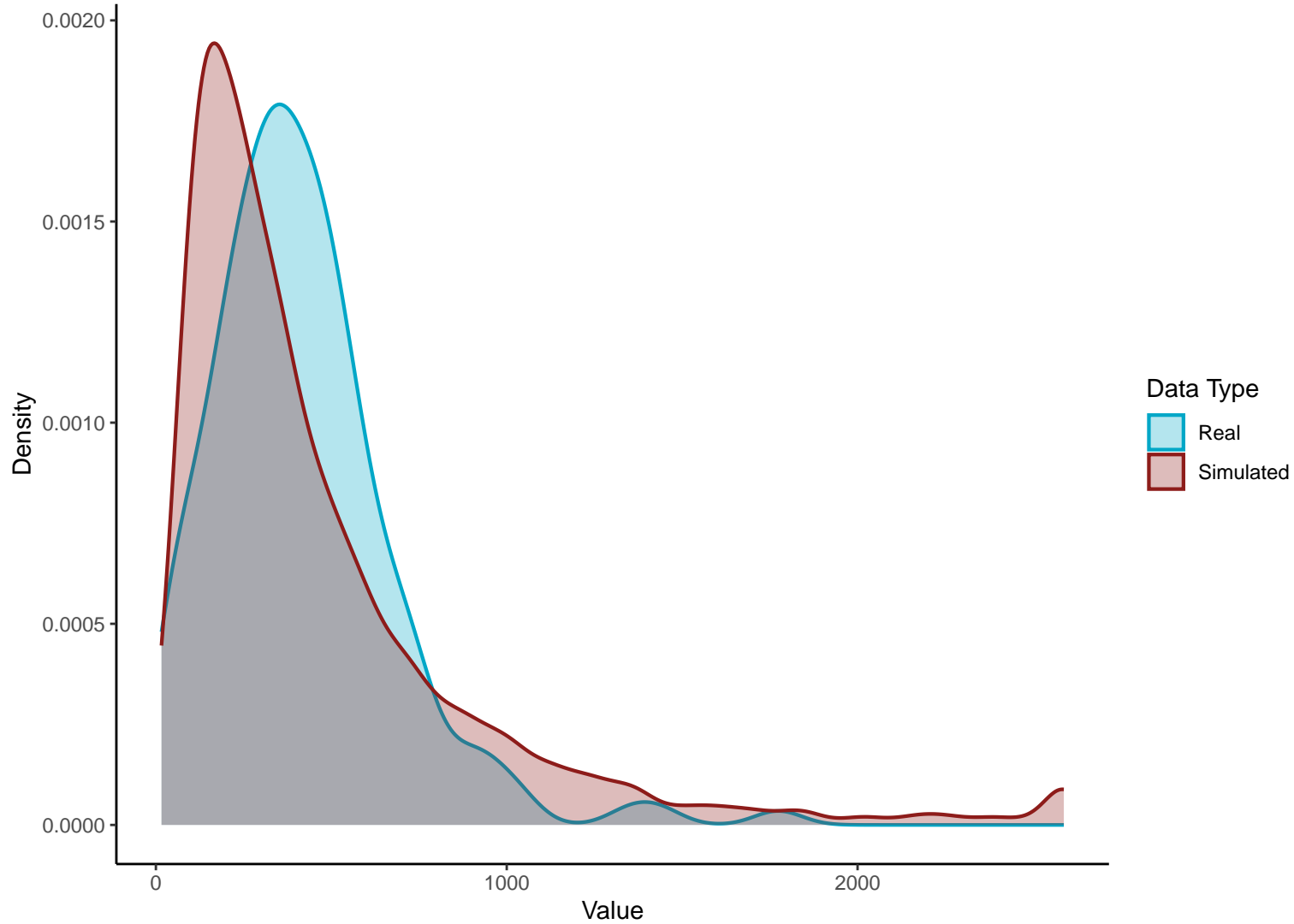
# Prevotellaceae.UGC.001



# Lachnospiraceae.NK4B4.group



# Holdemacteria





# Papillibacter

Density

0.00

0.05

0.10

0.15

0

10

20

30

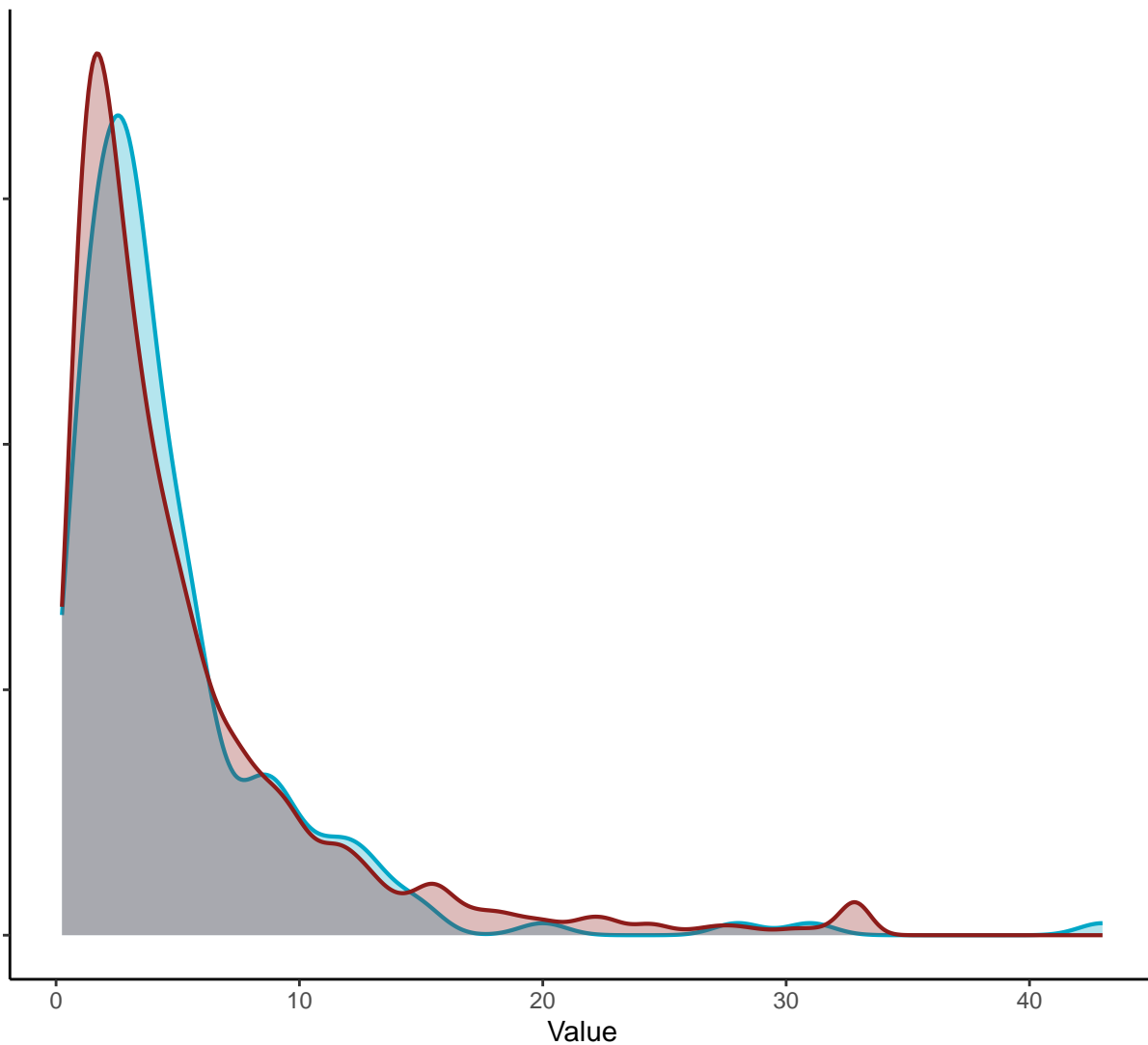
40

Value

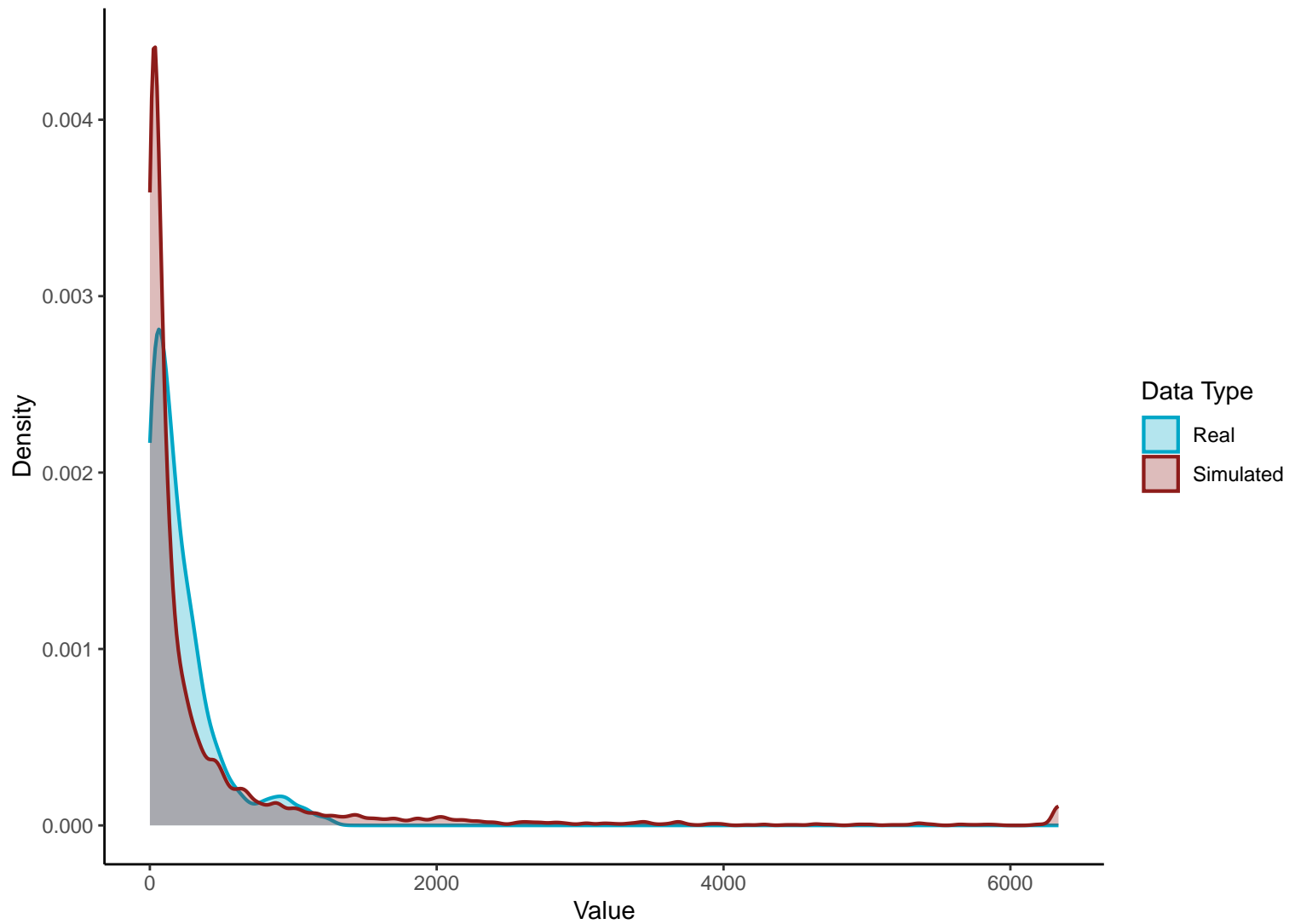
Data Type

Real

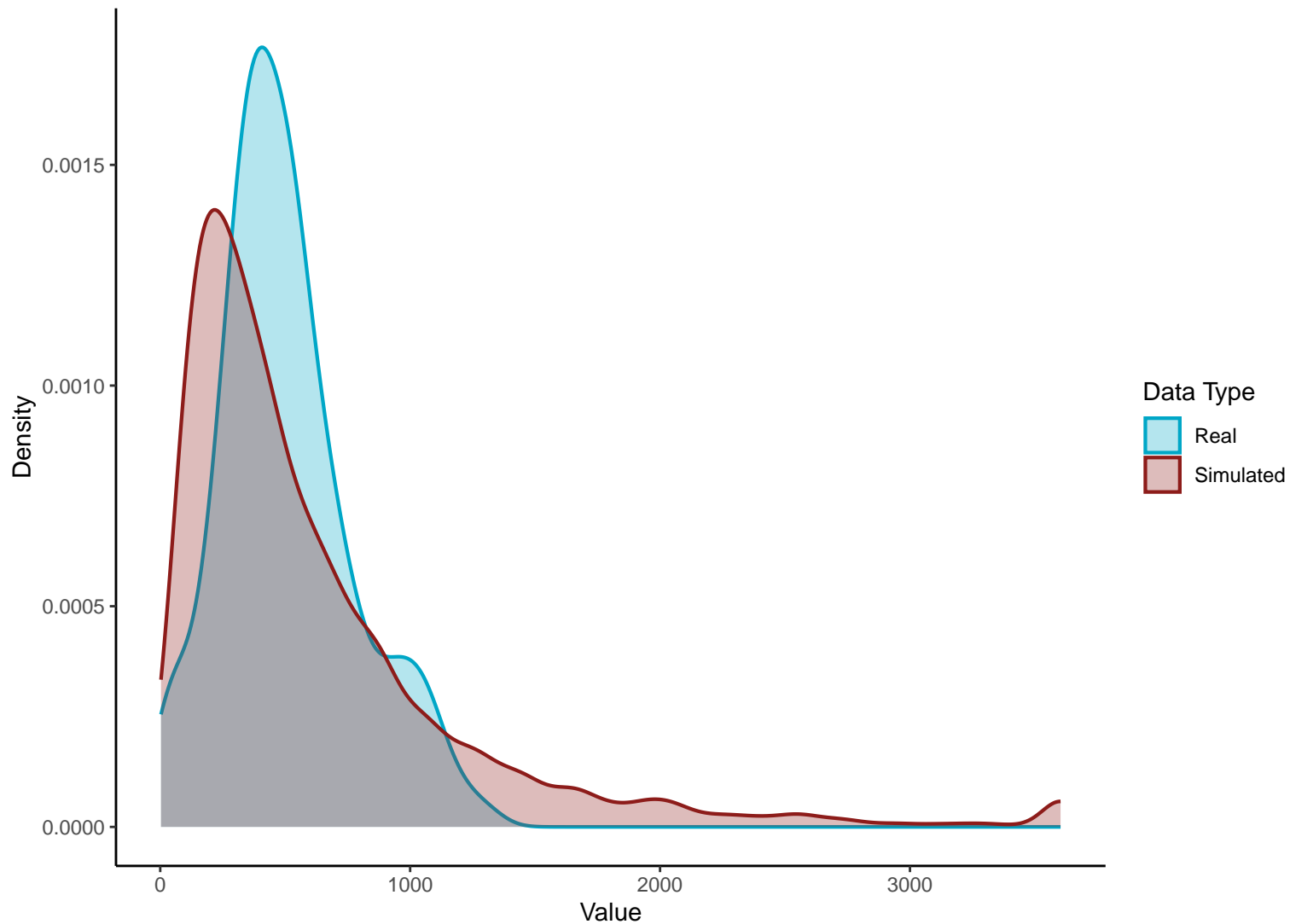
Simulated



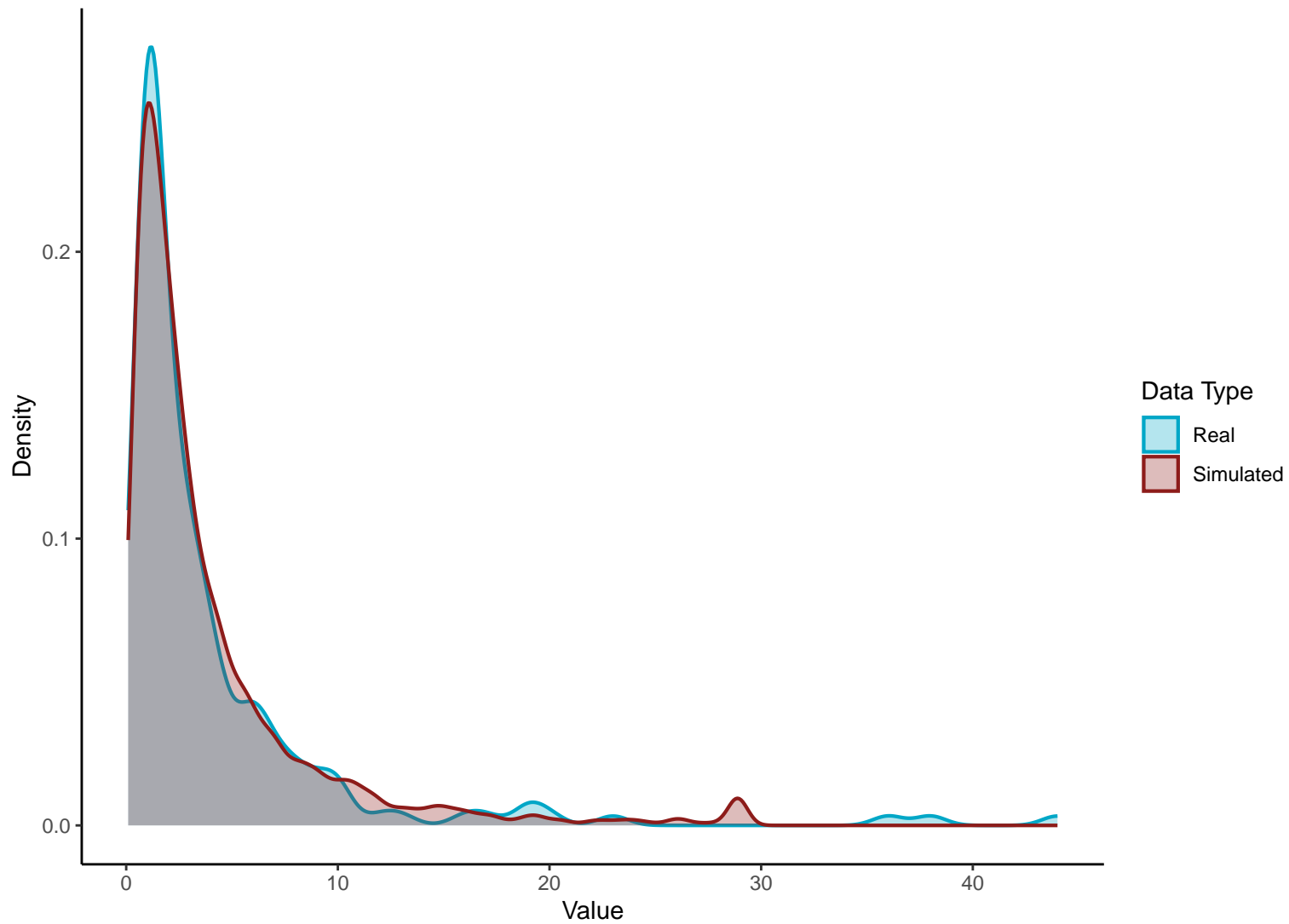
# Lachnospiraceae.AC2044.group



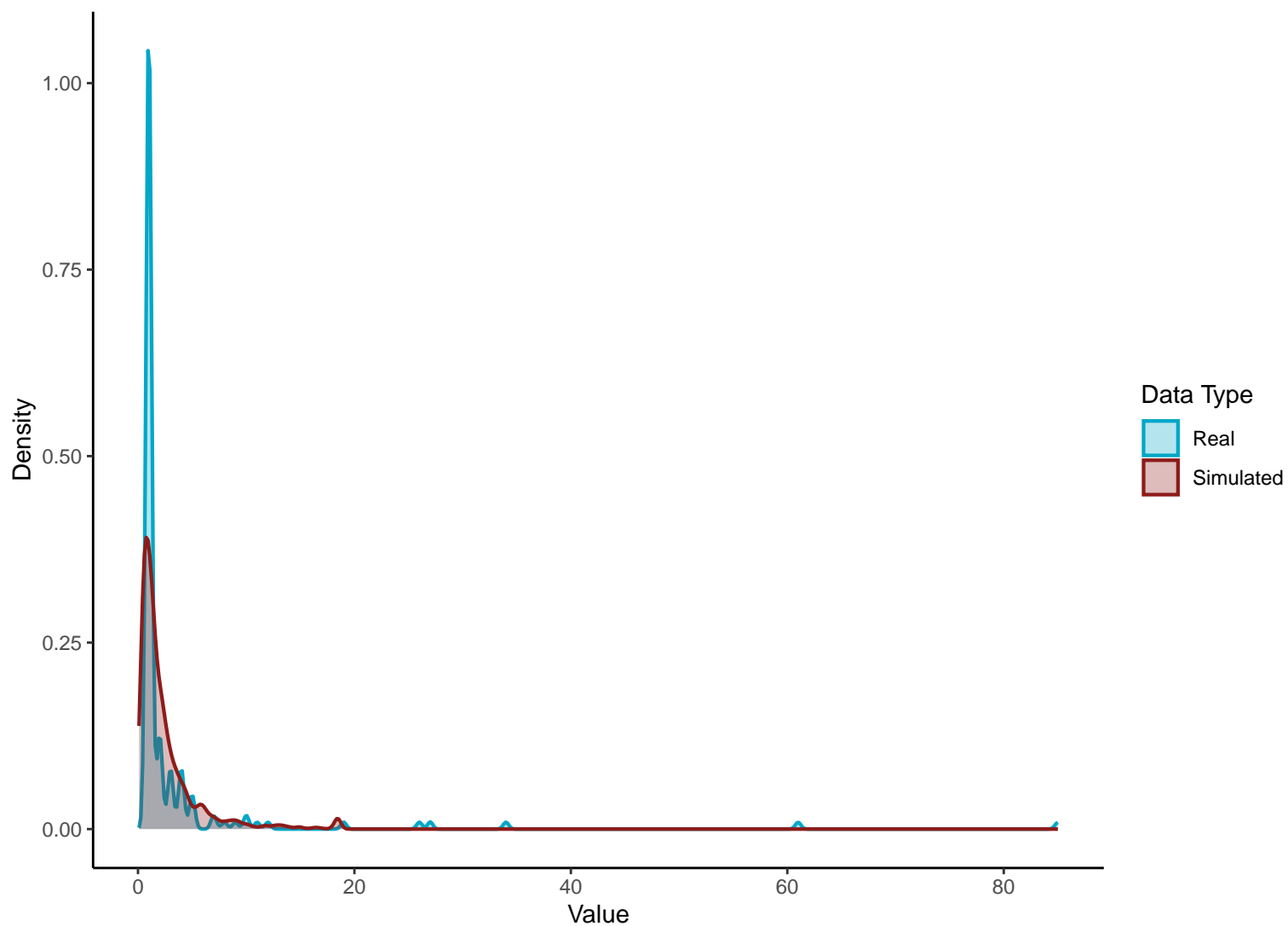
# Phascolarctobacterium



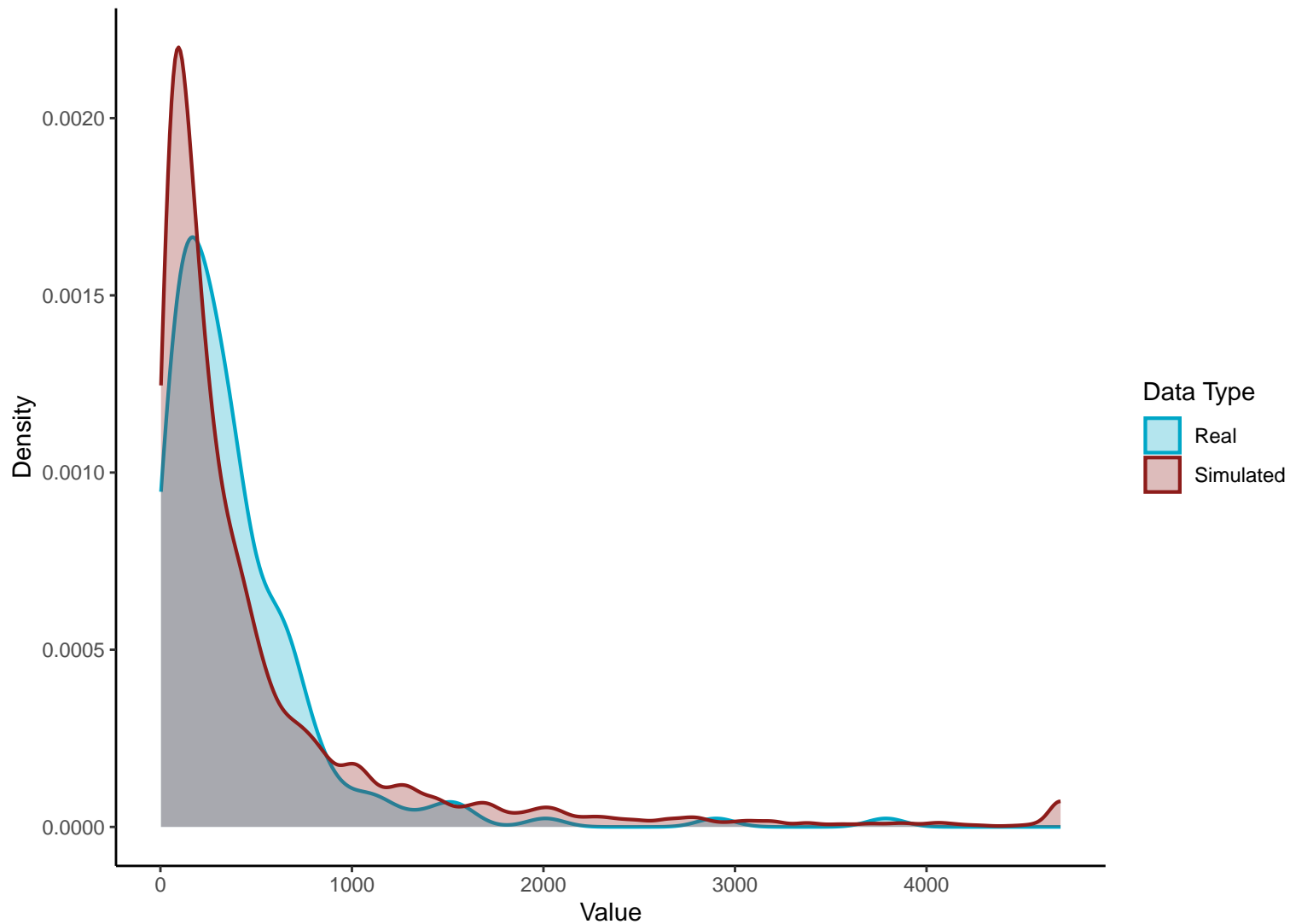
# Fibrobacter



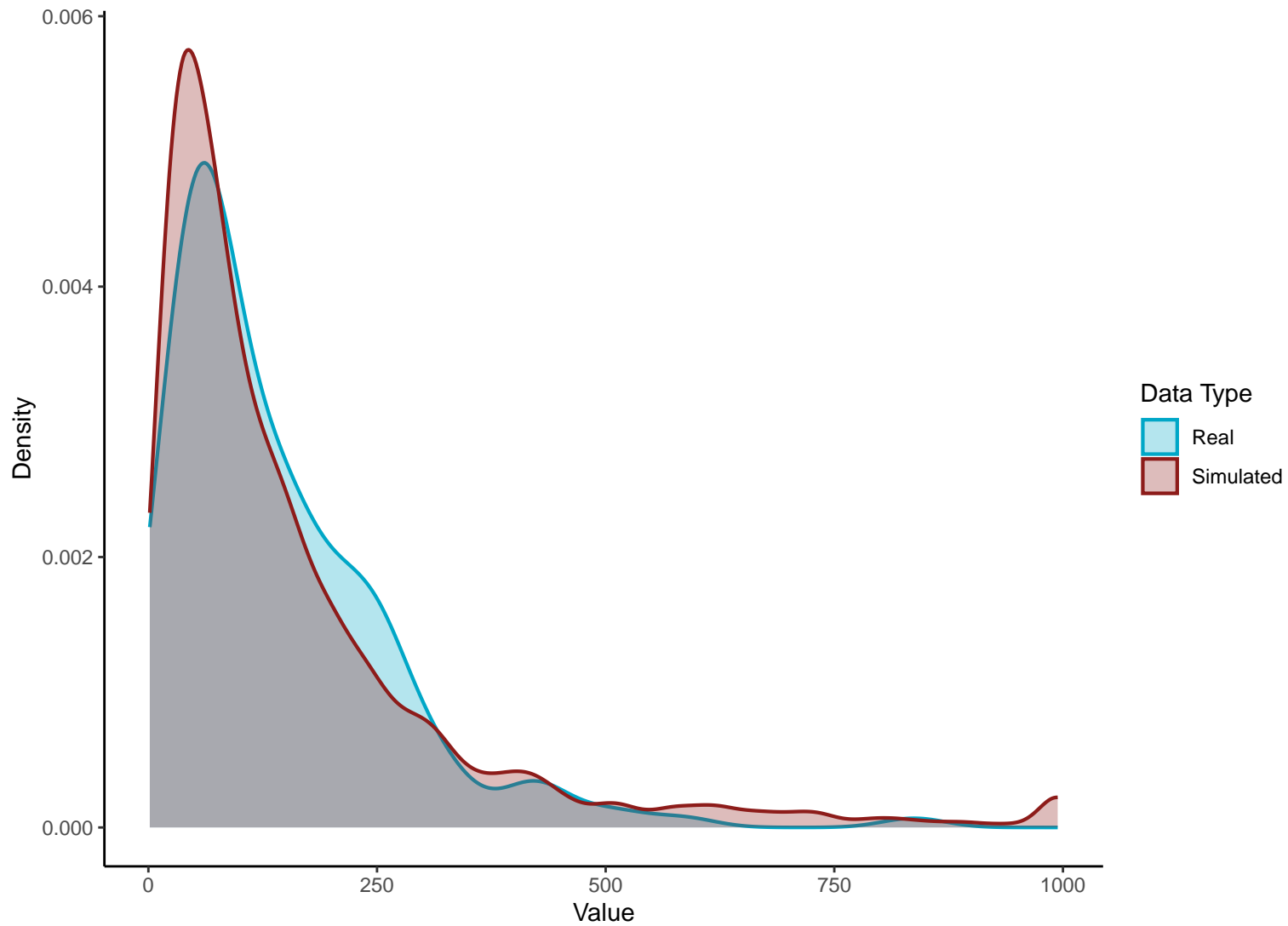
# Akkermansia



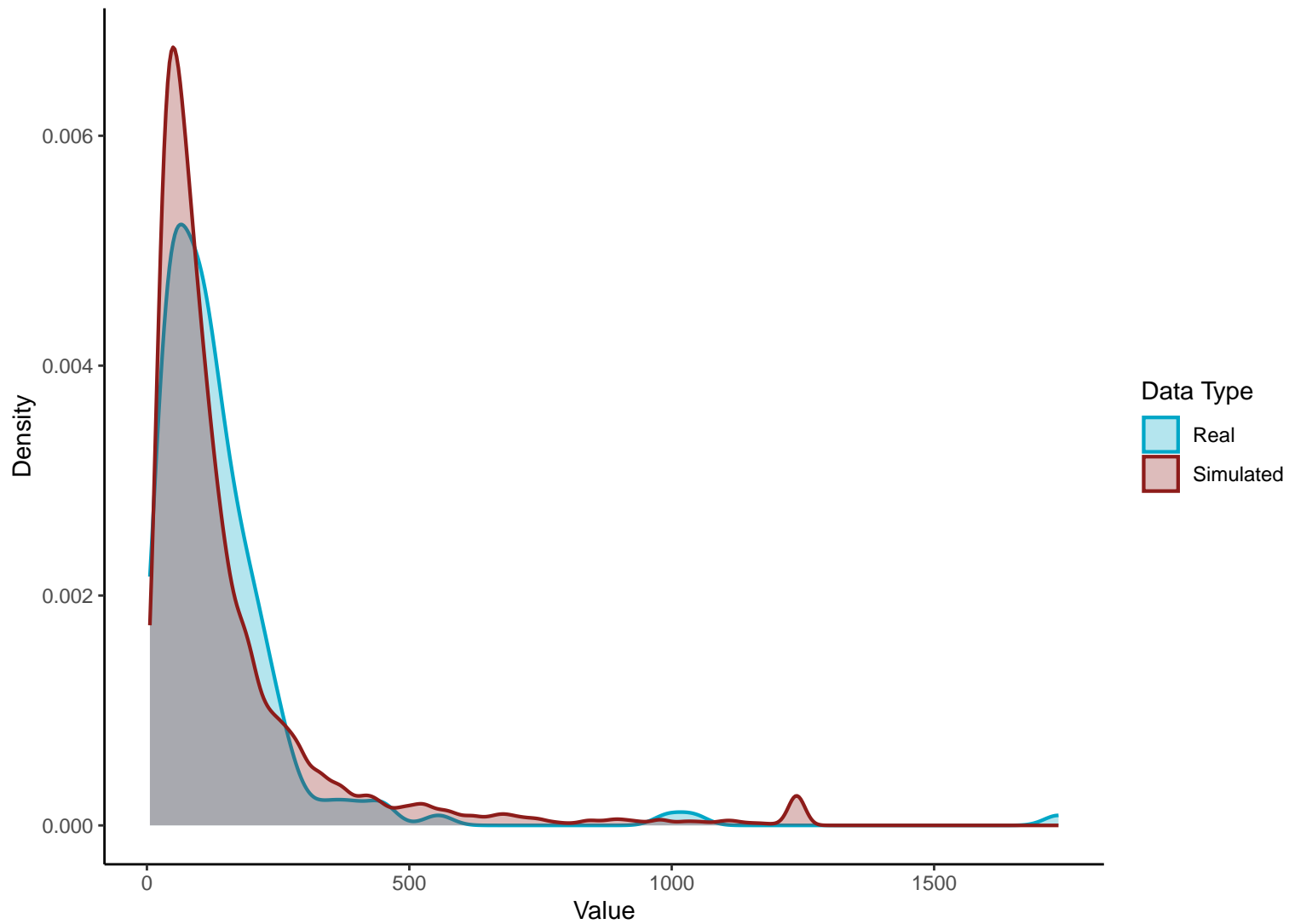
UCG.002



# Olsenella

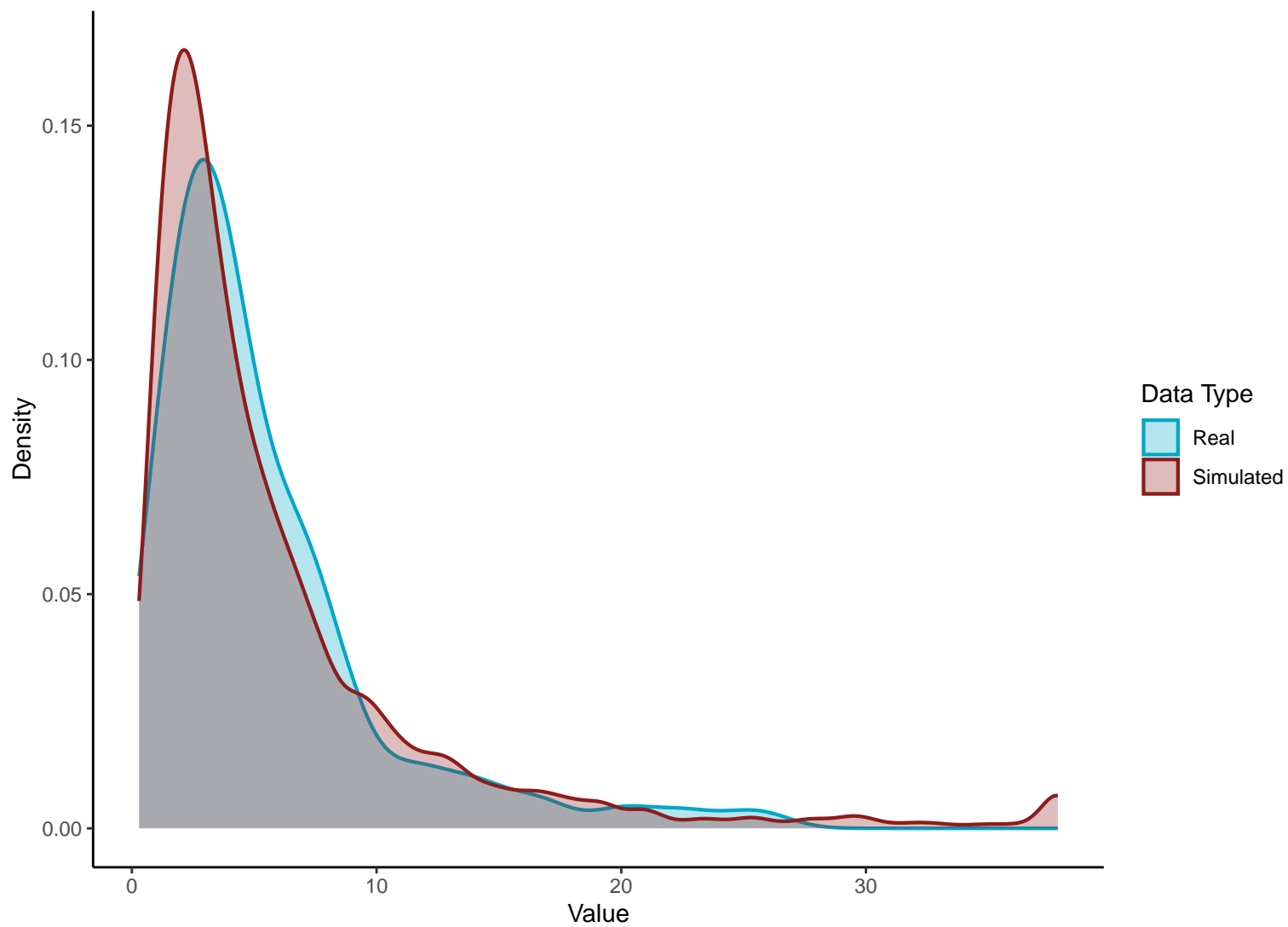


# Shuttleworthia

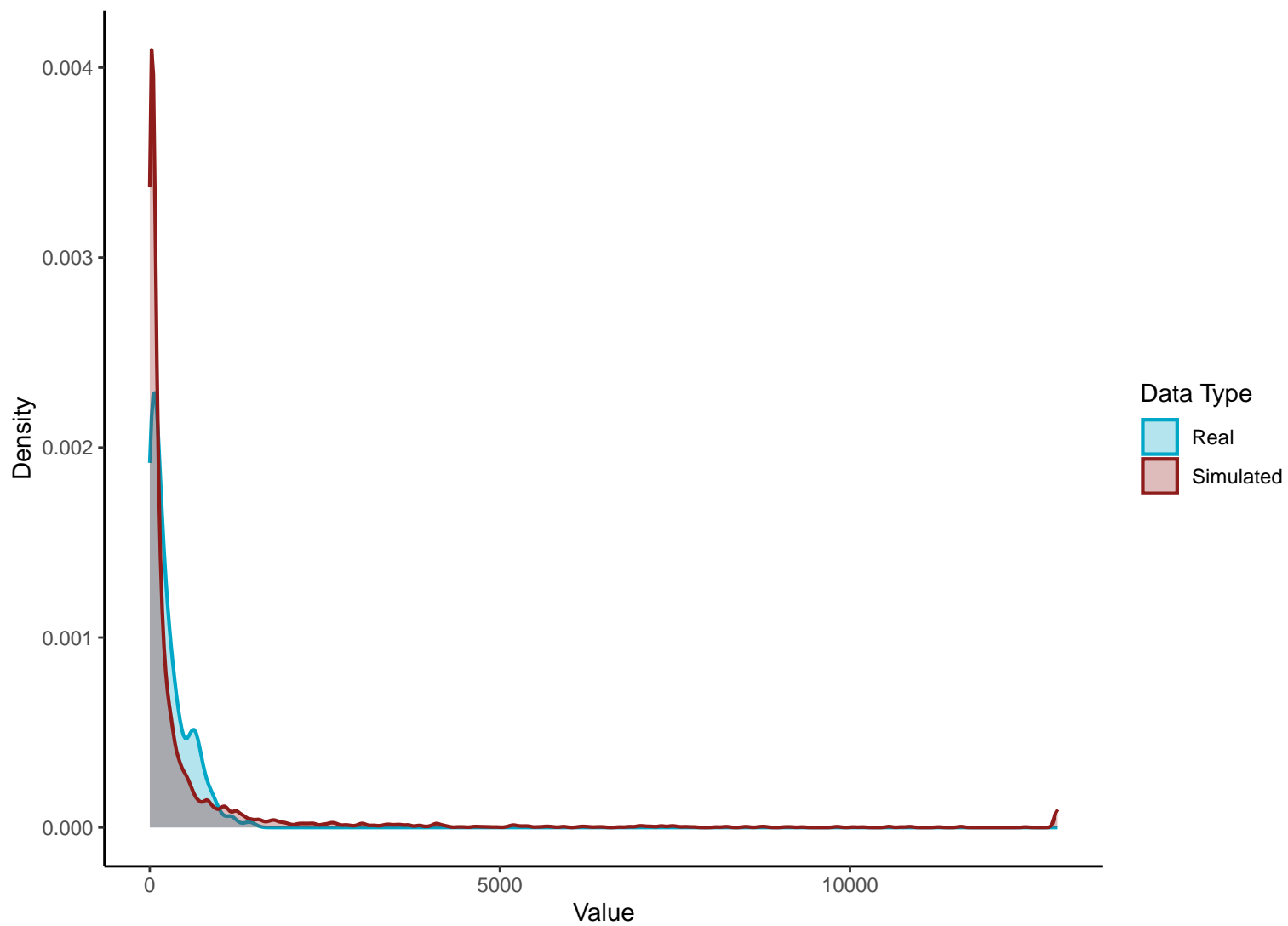




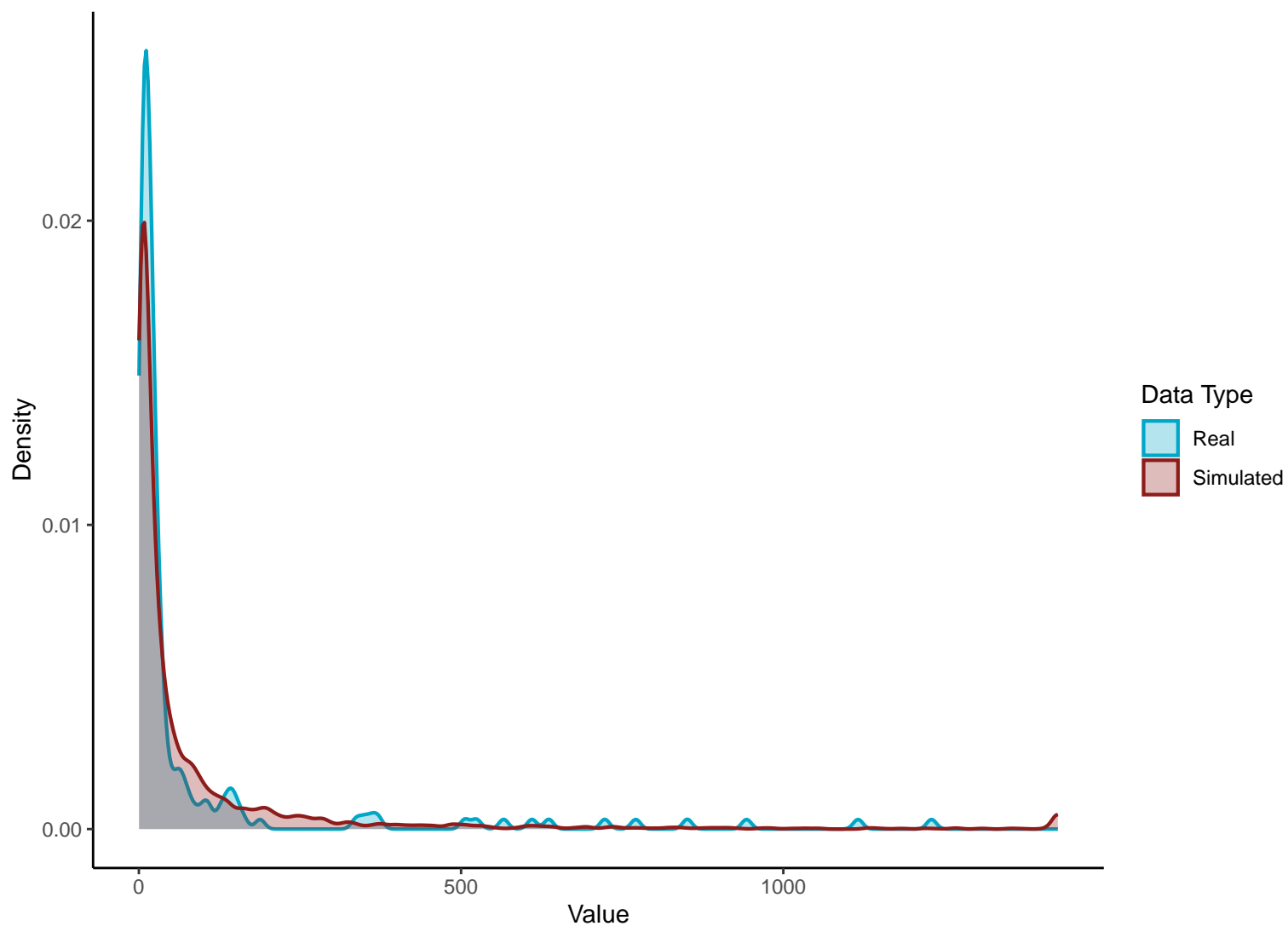
# Pygmaibacter



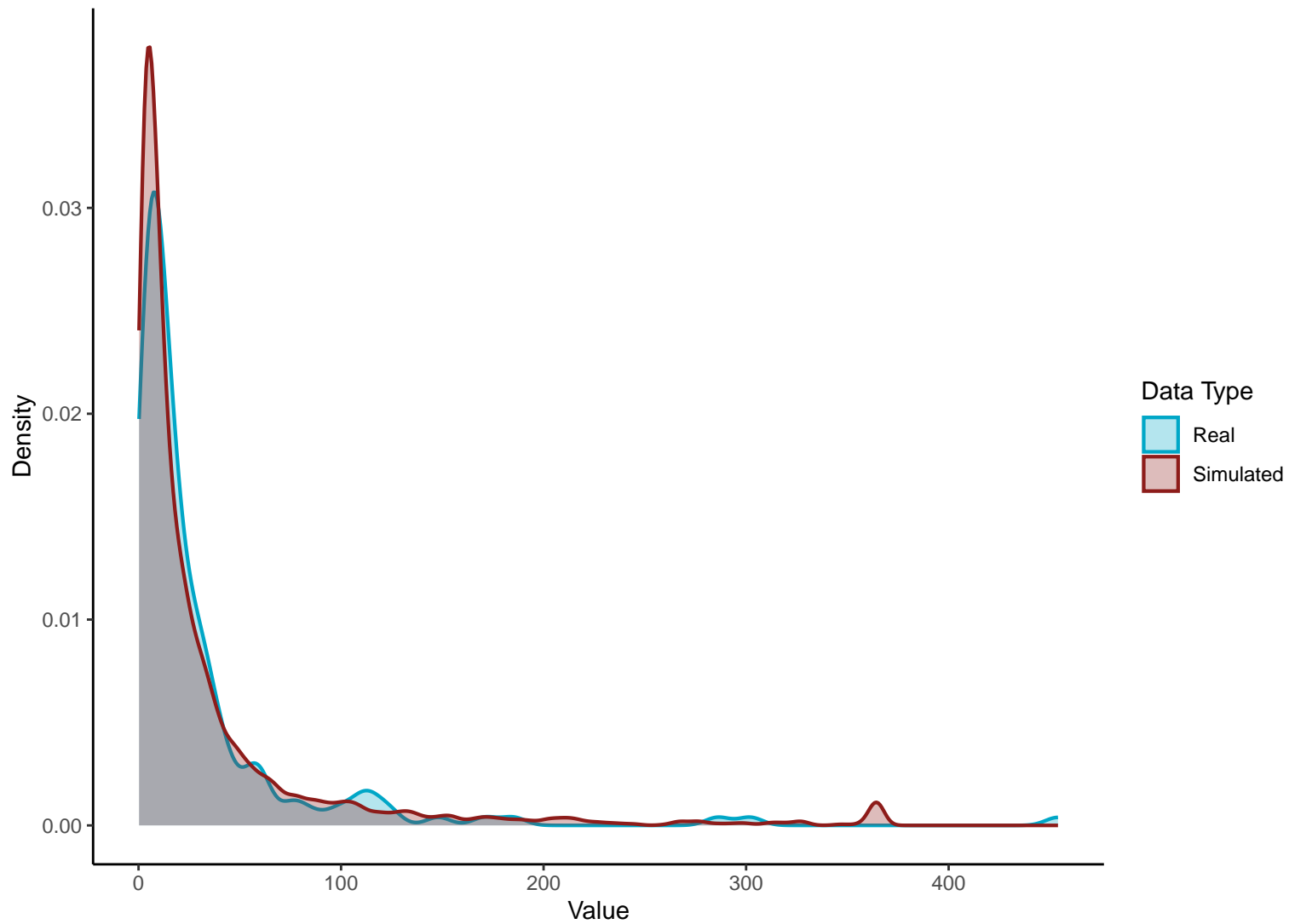
# Dialister



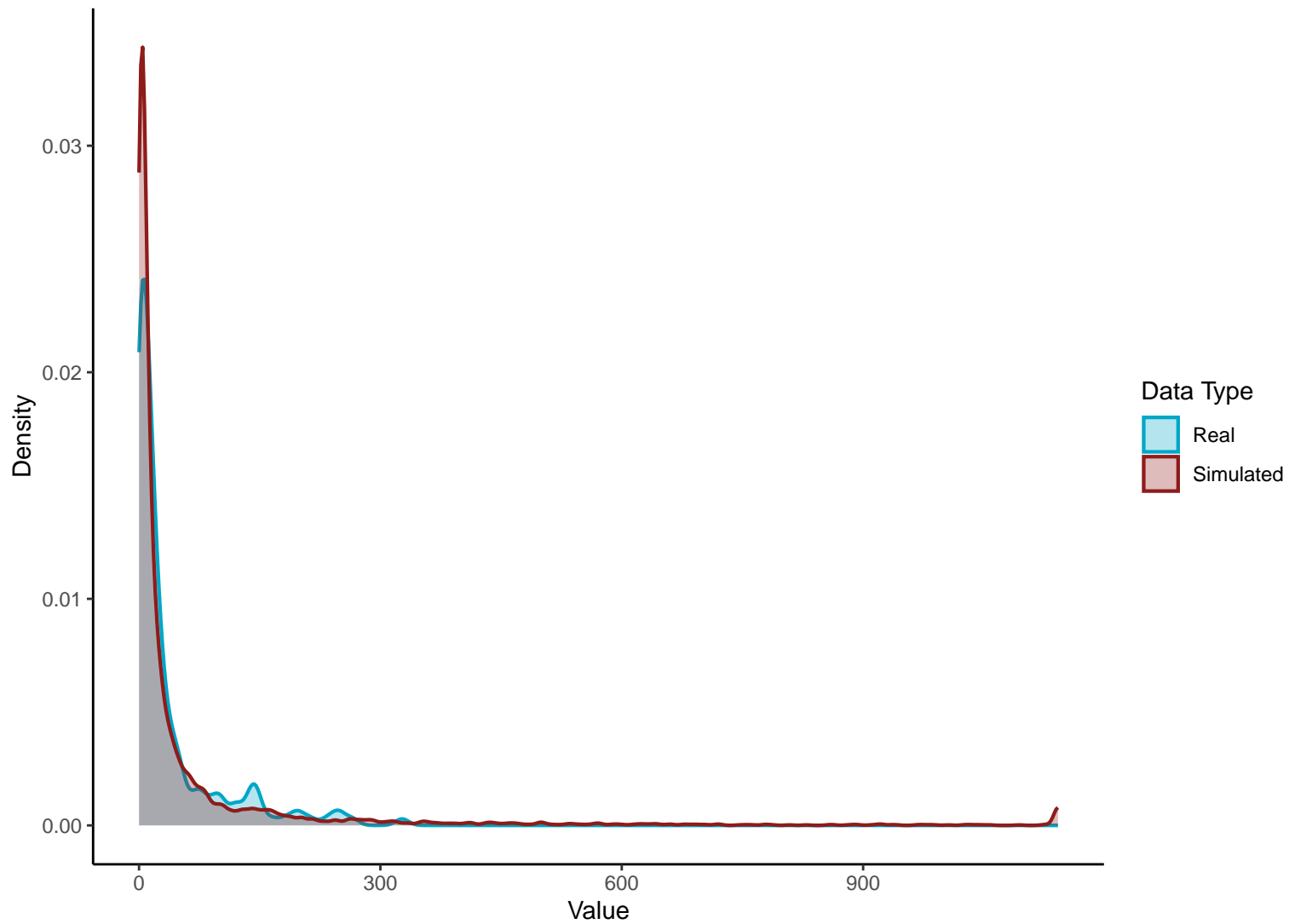
# Acetitomaculum



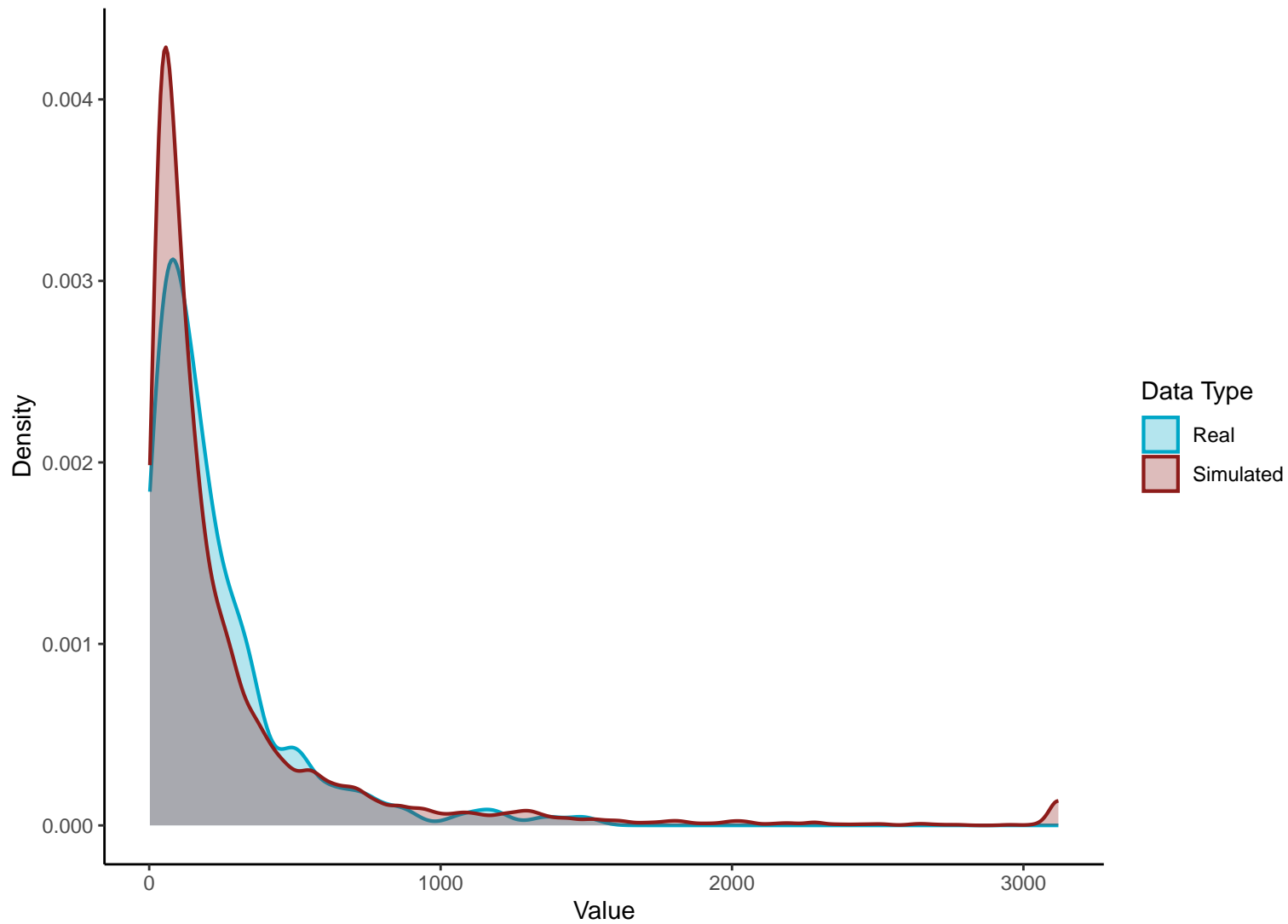
# Campylobacter



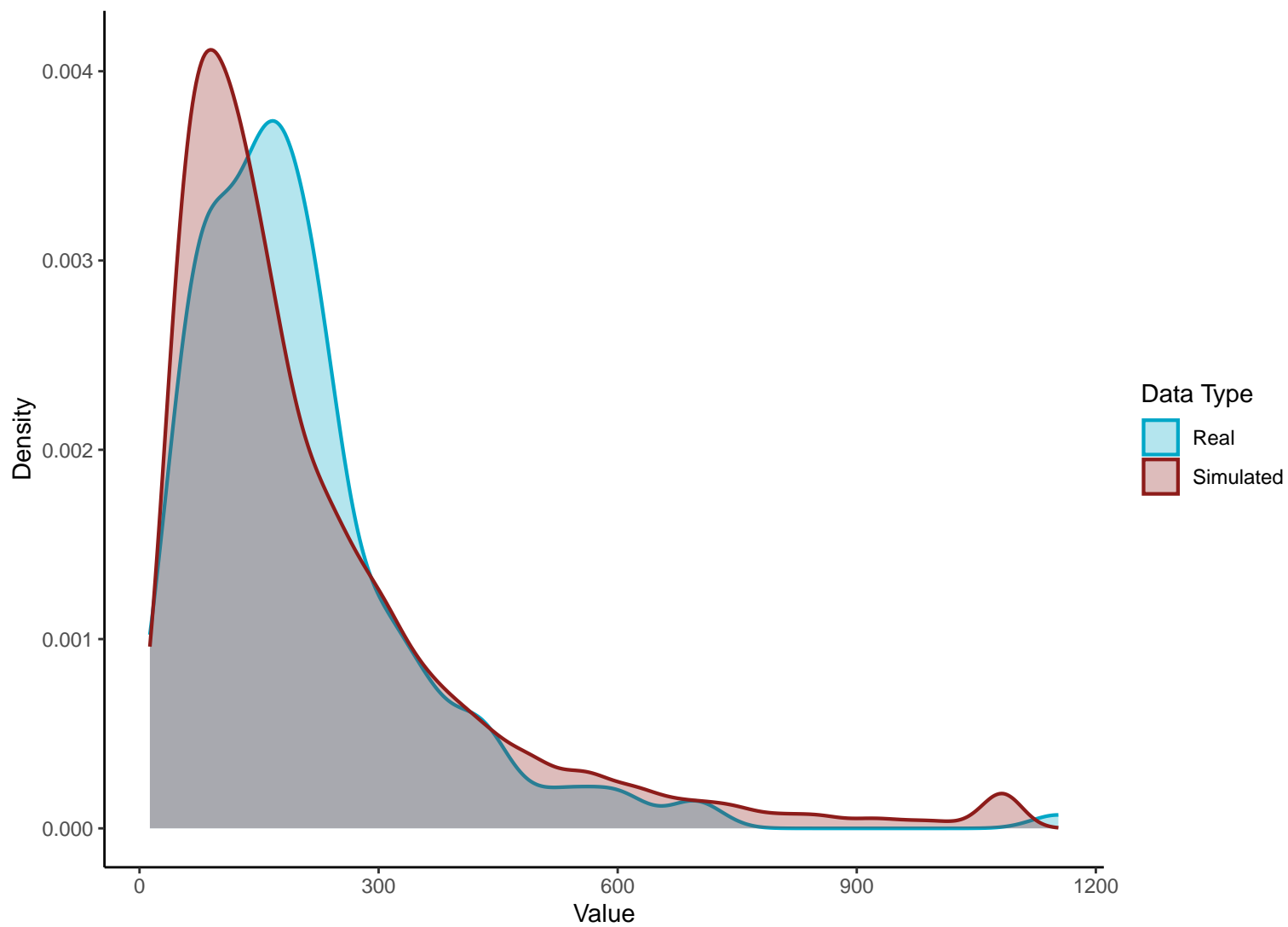
# Anaerosporobacter



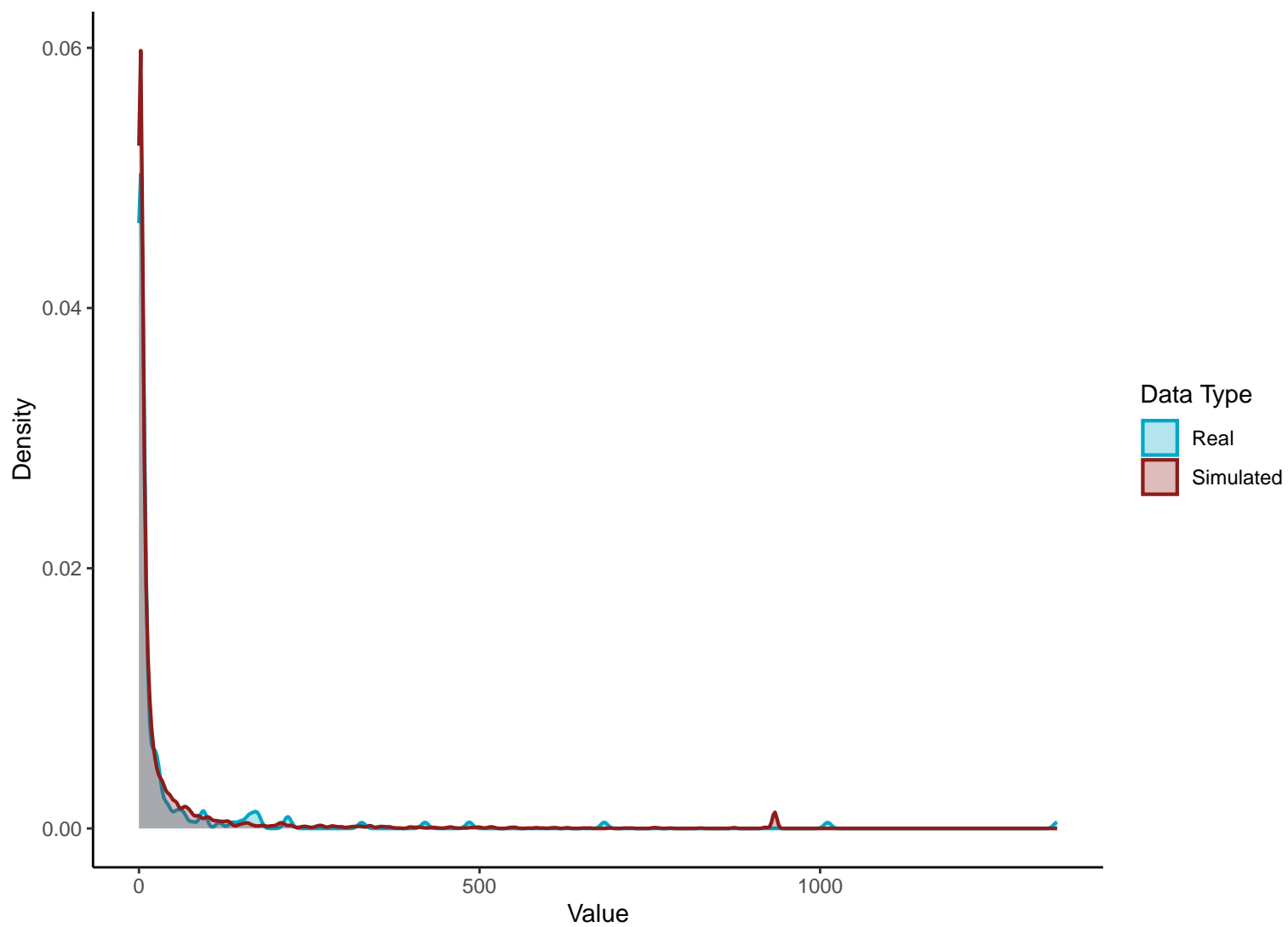
# Anaerostipes



# Collinsella

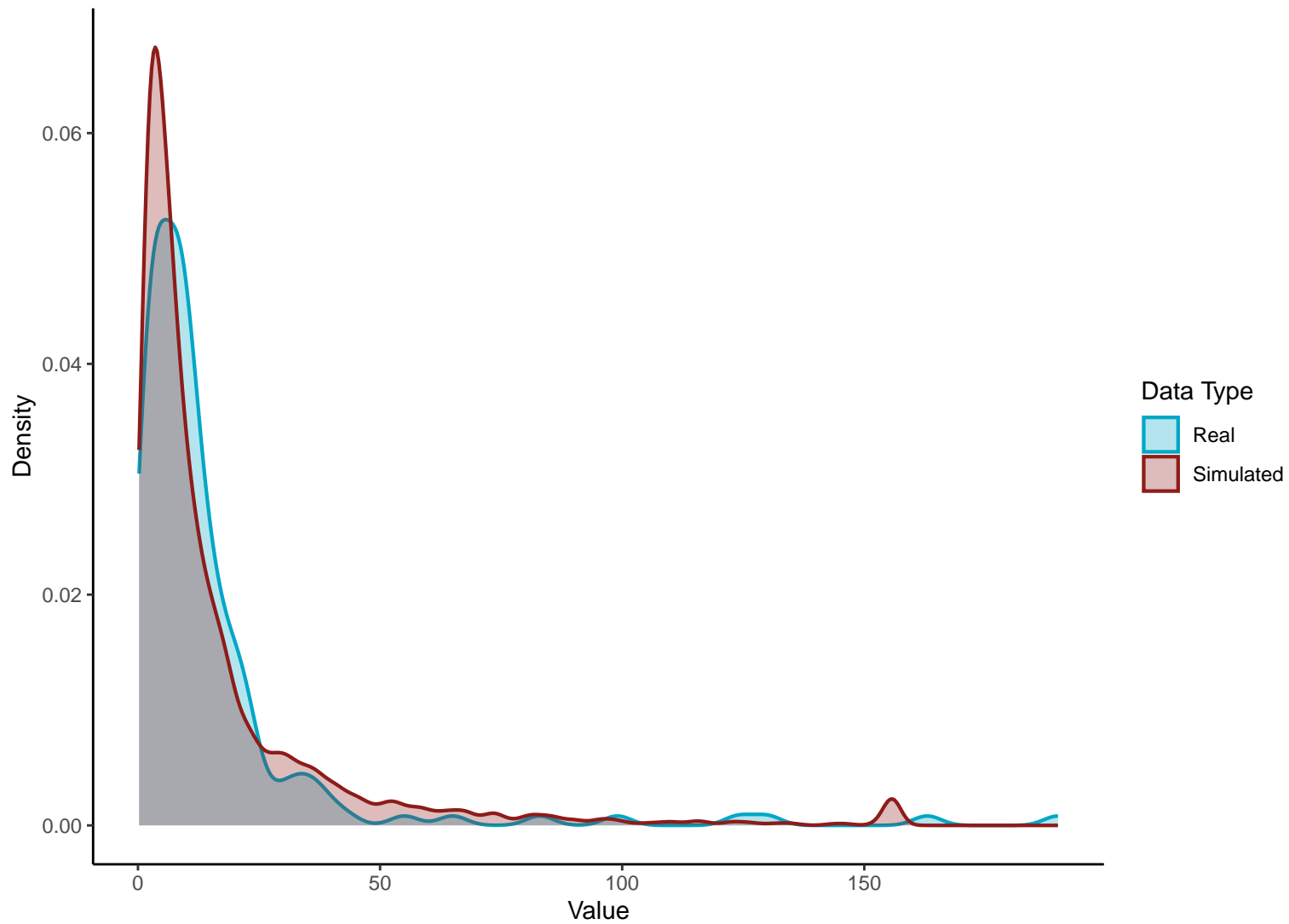


# Sarcina

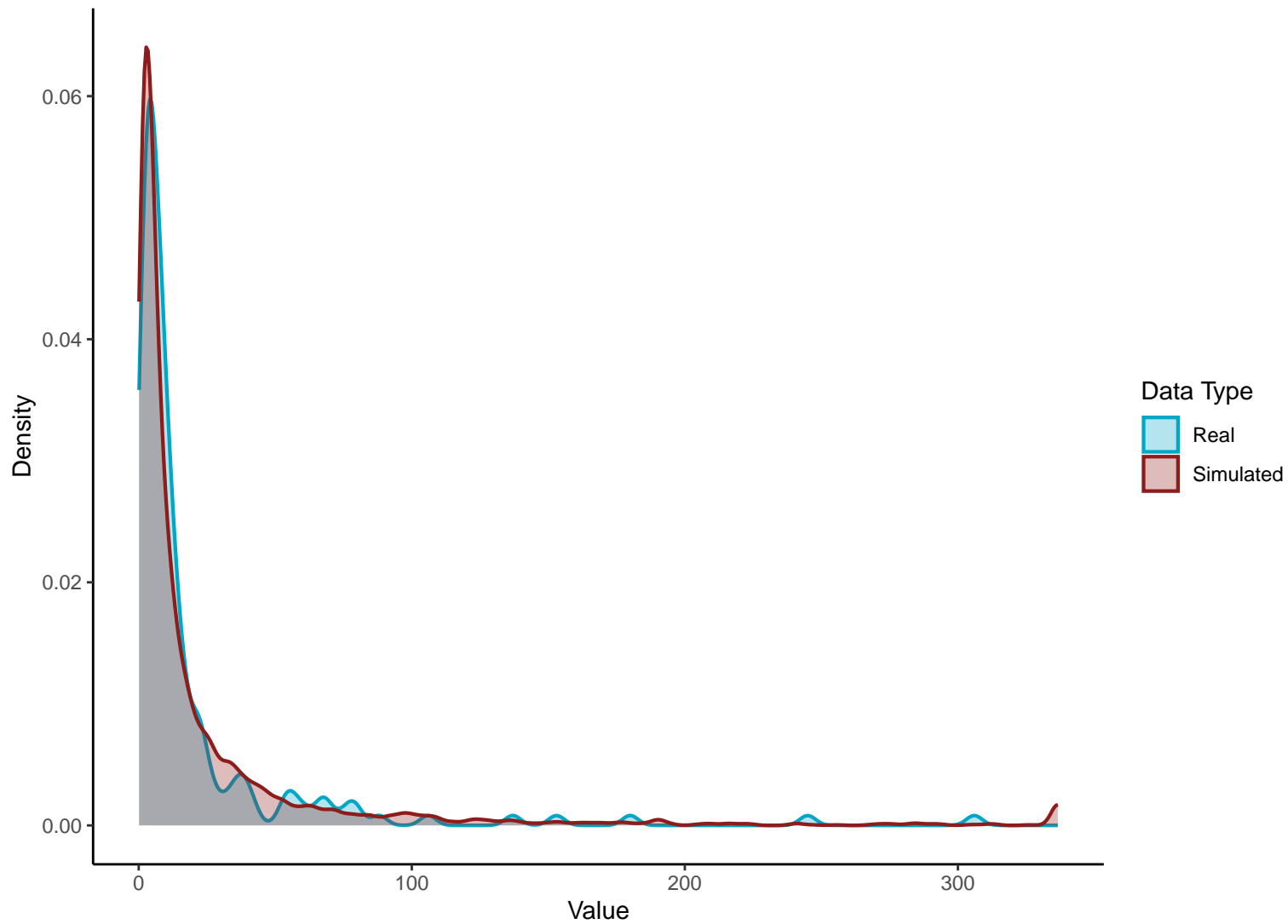




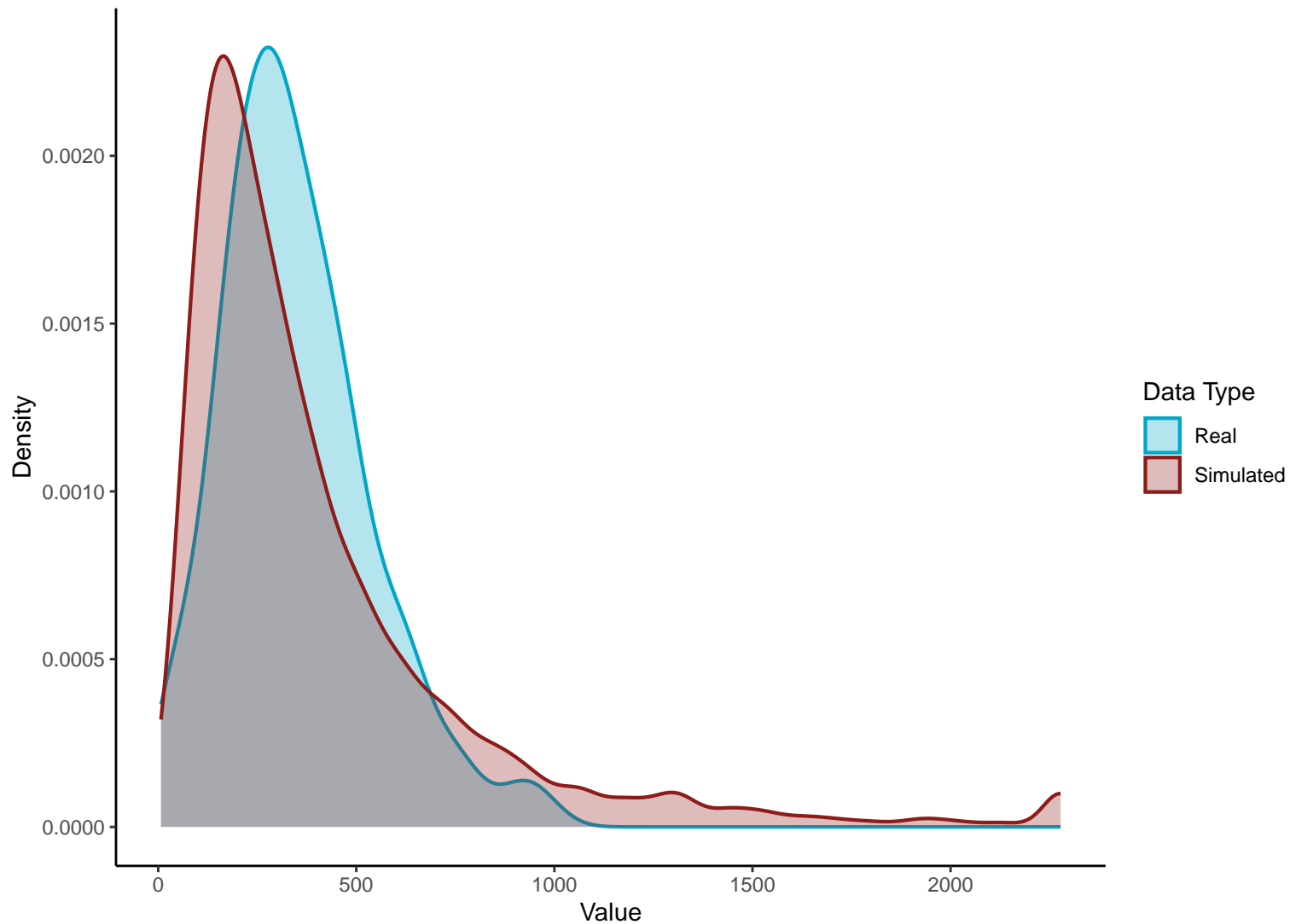
# X.Eubacterium..eligens.group



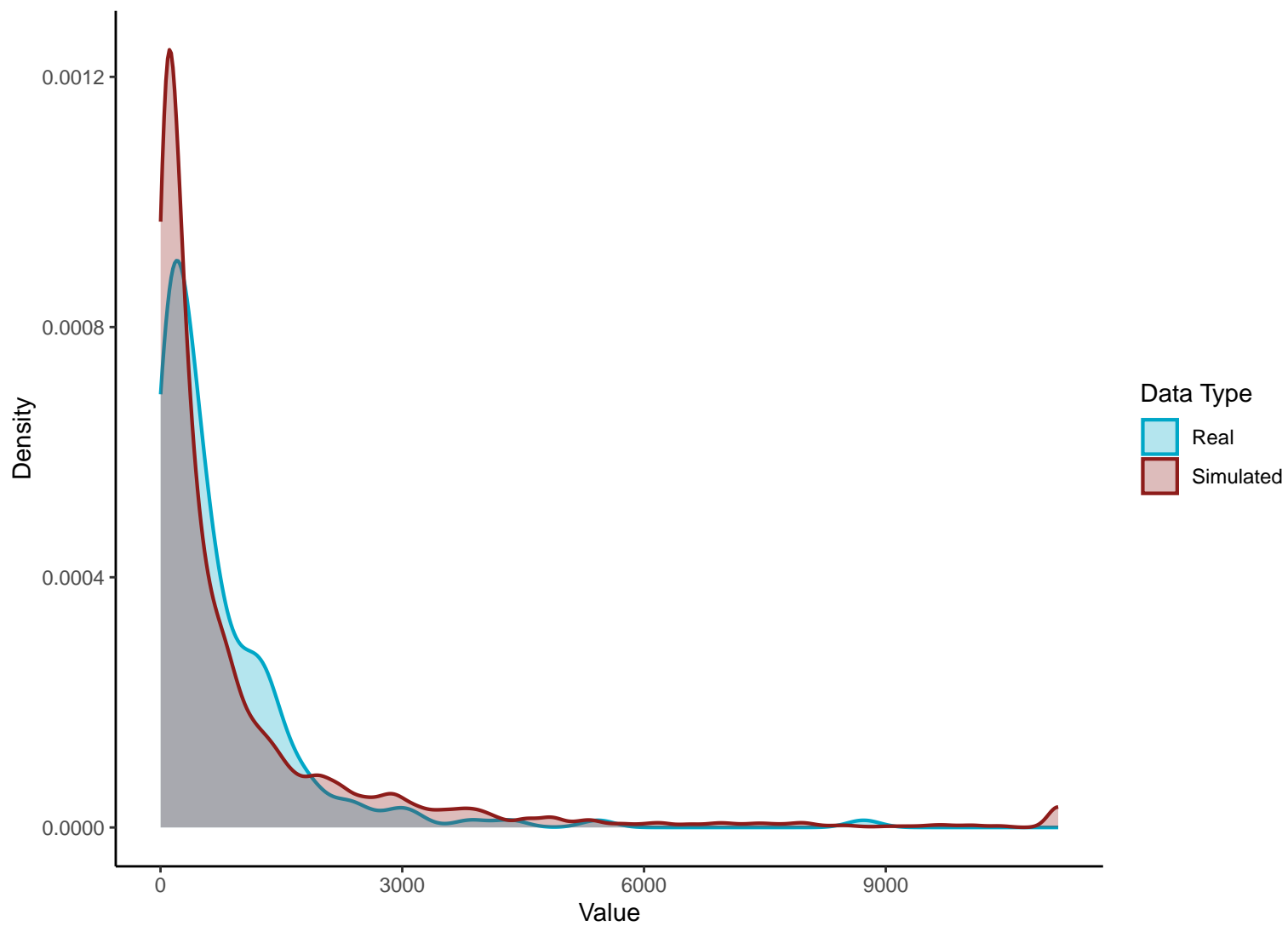
# Corynebacterium



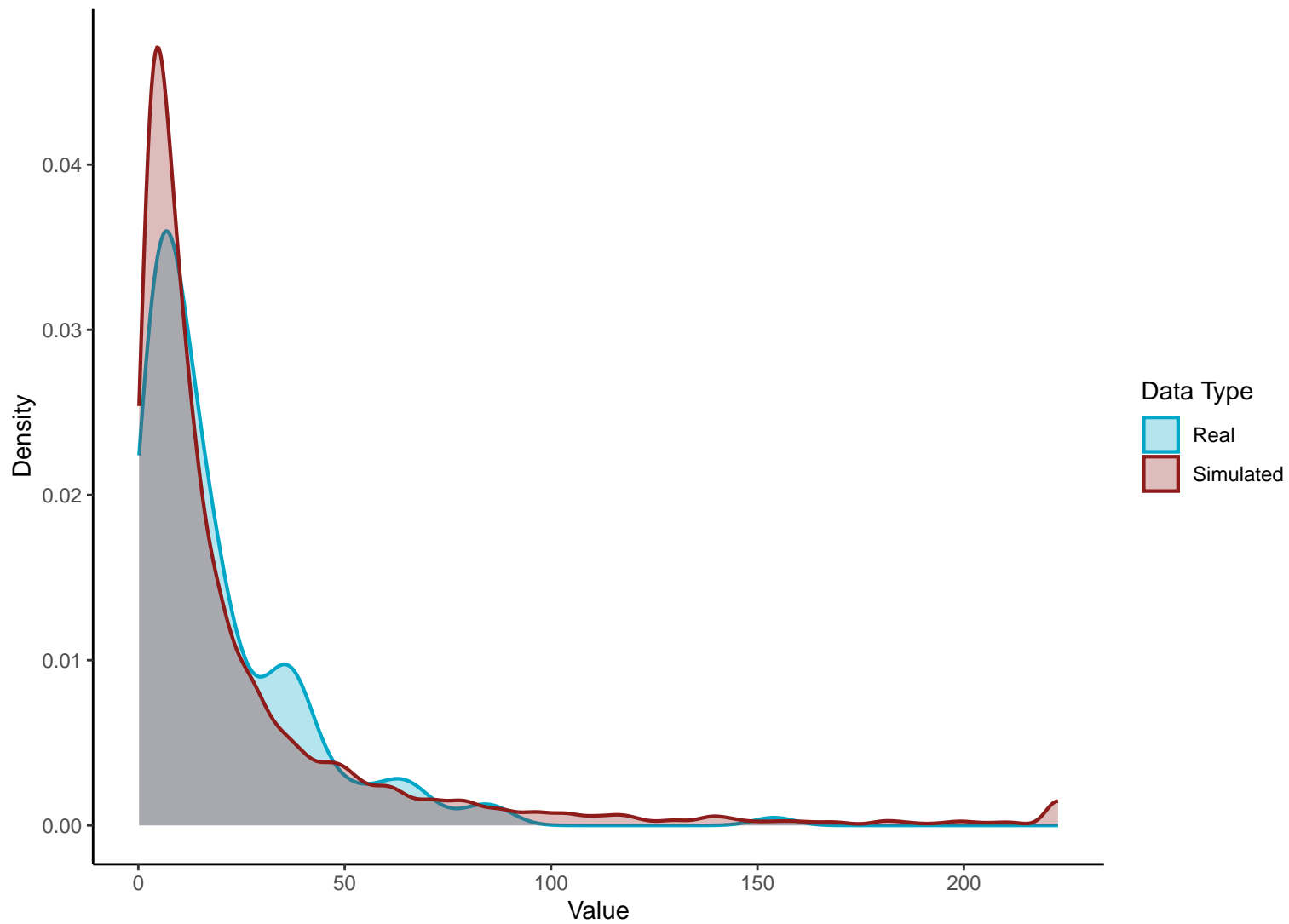
# X.Ruminococcus..gauvreauii.group



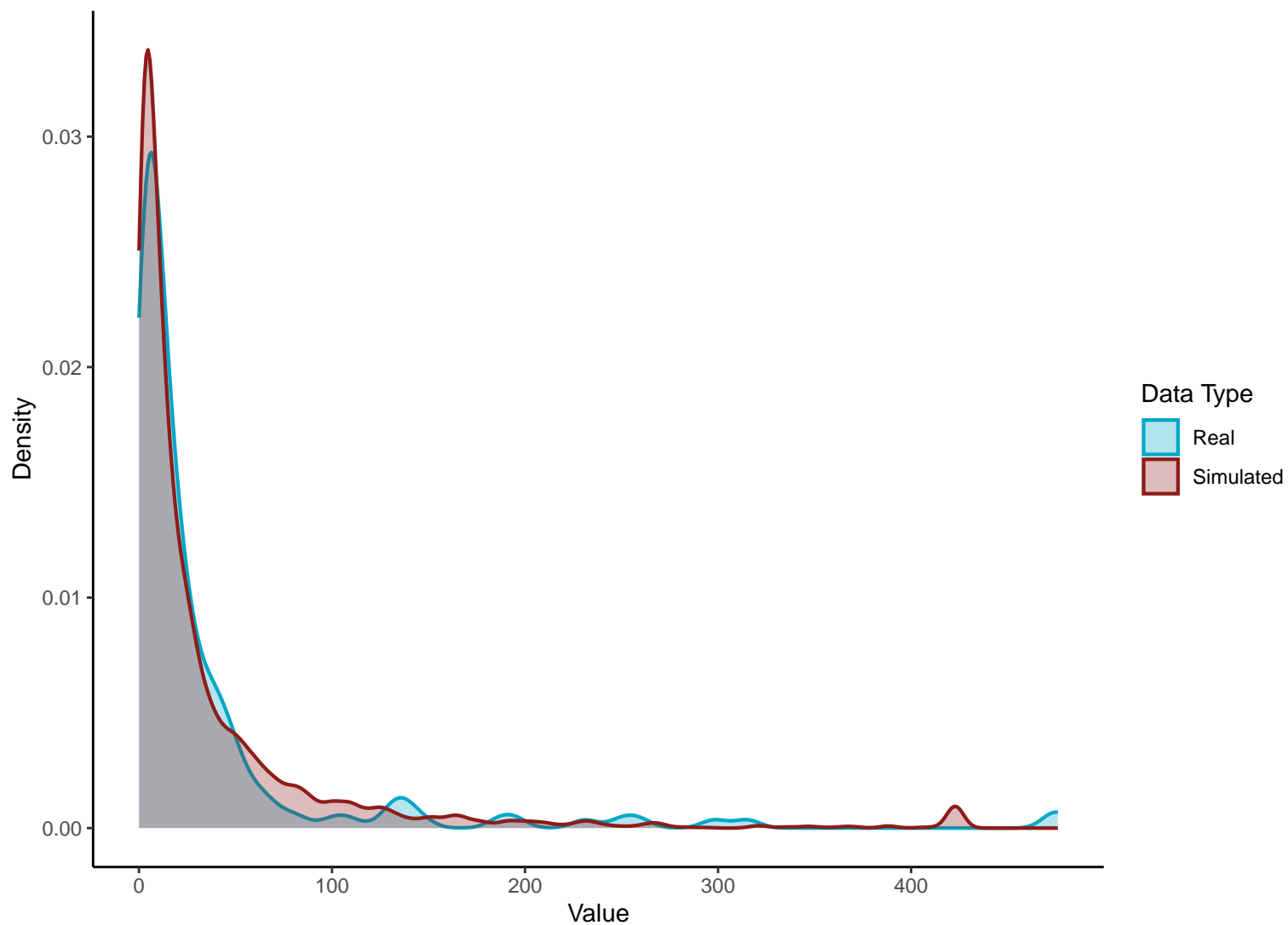
# Megasphaera



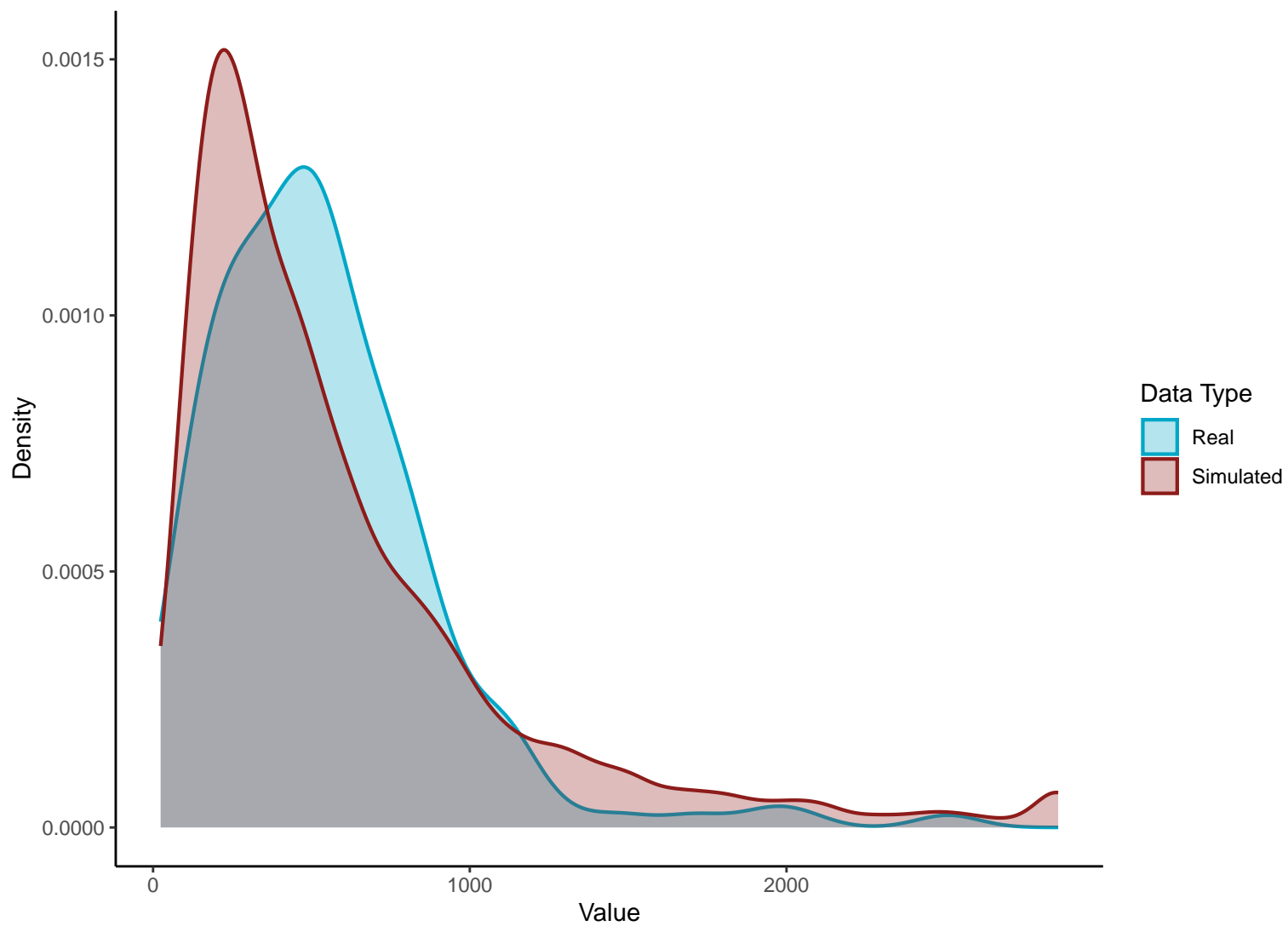
# Candidatus.Saccharimonas



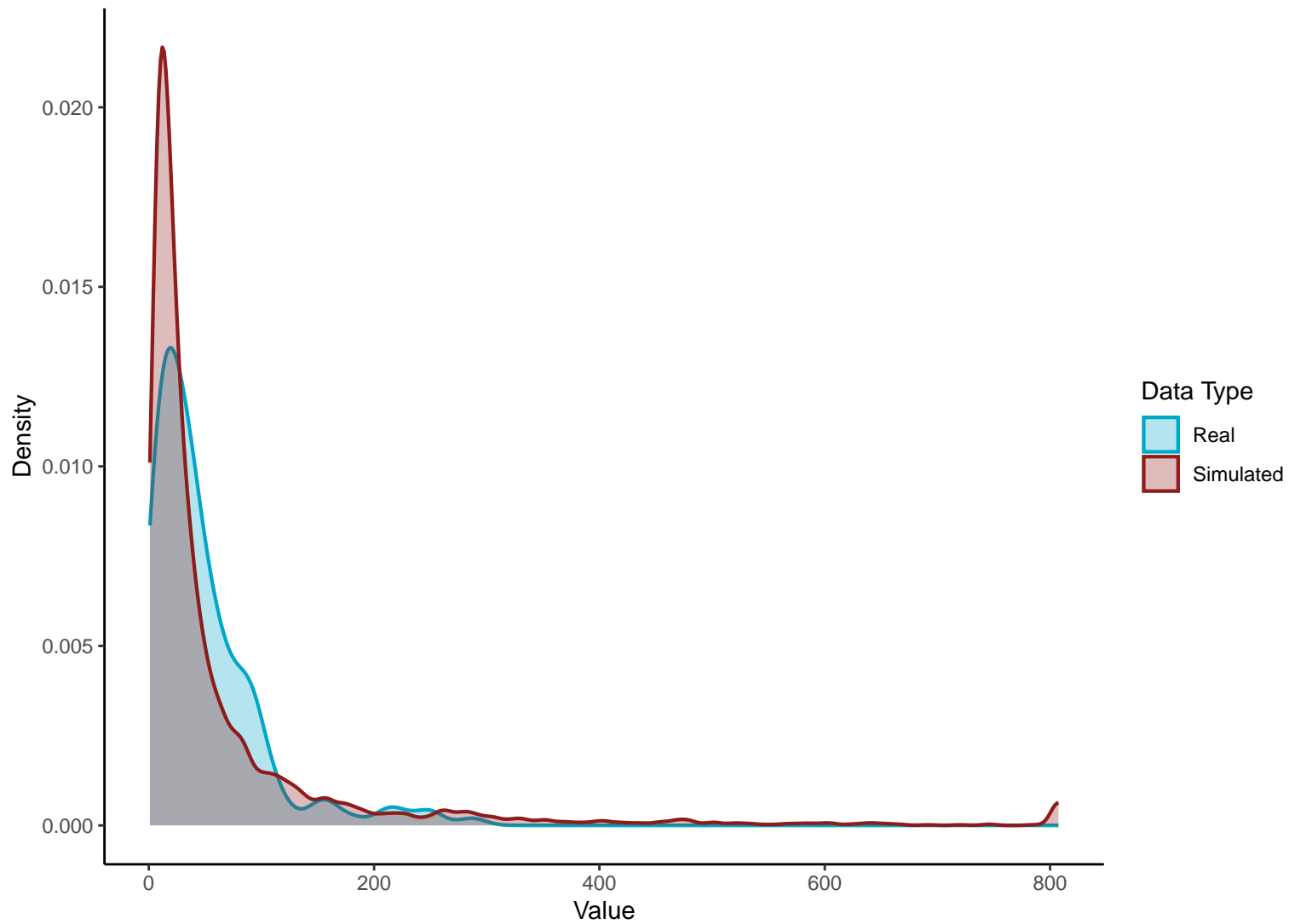
# Lachnospira



Dorea

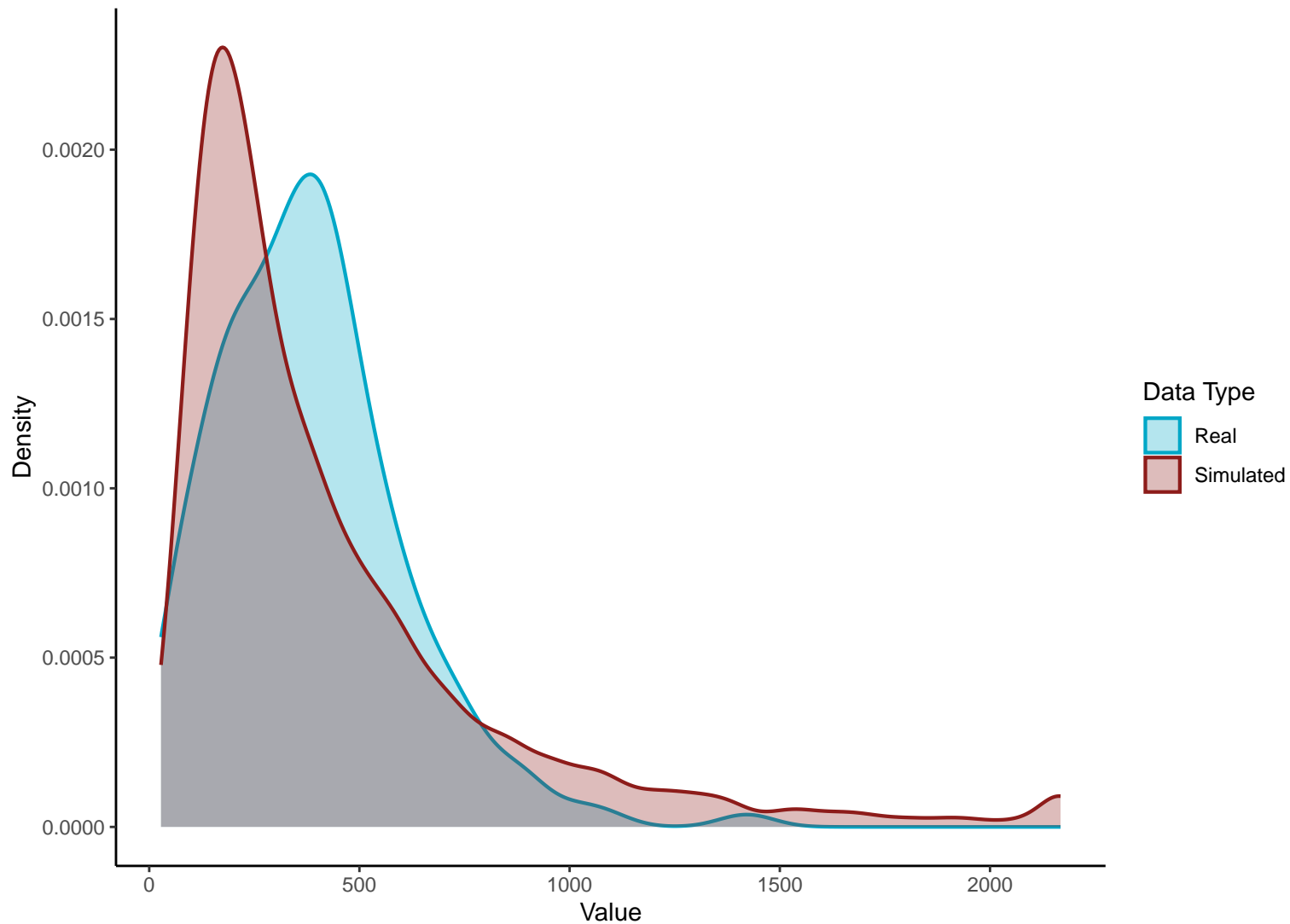


# Candidatus.Soleaferrea

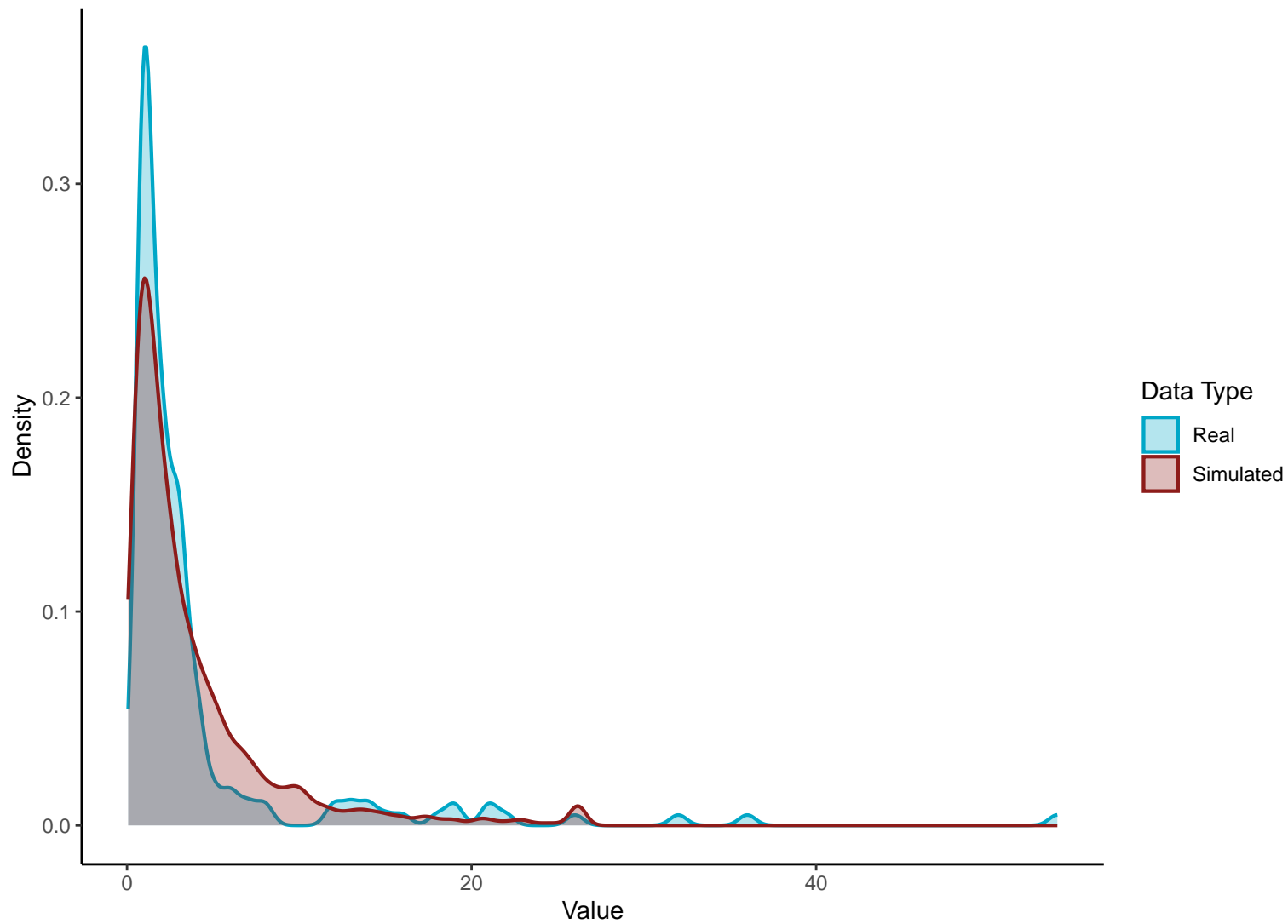




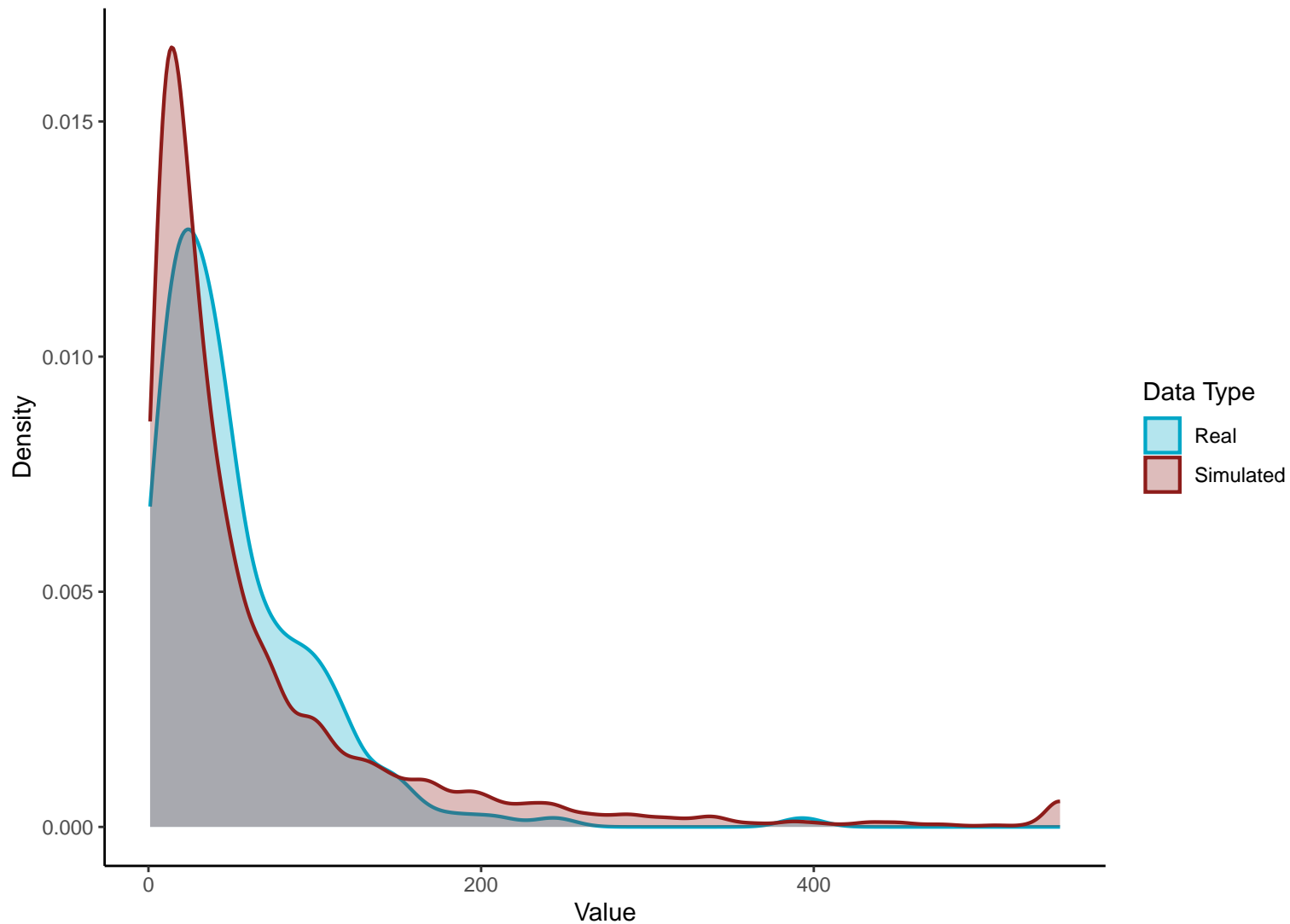
# Oribacterium



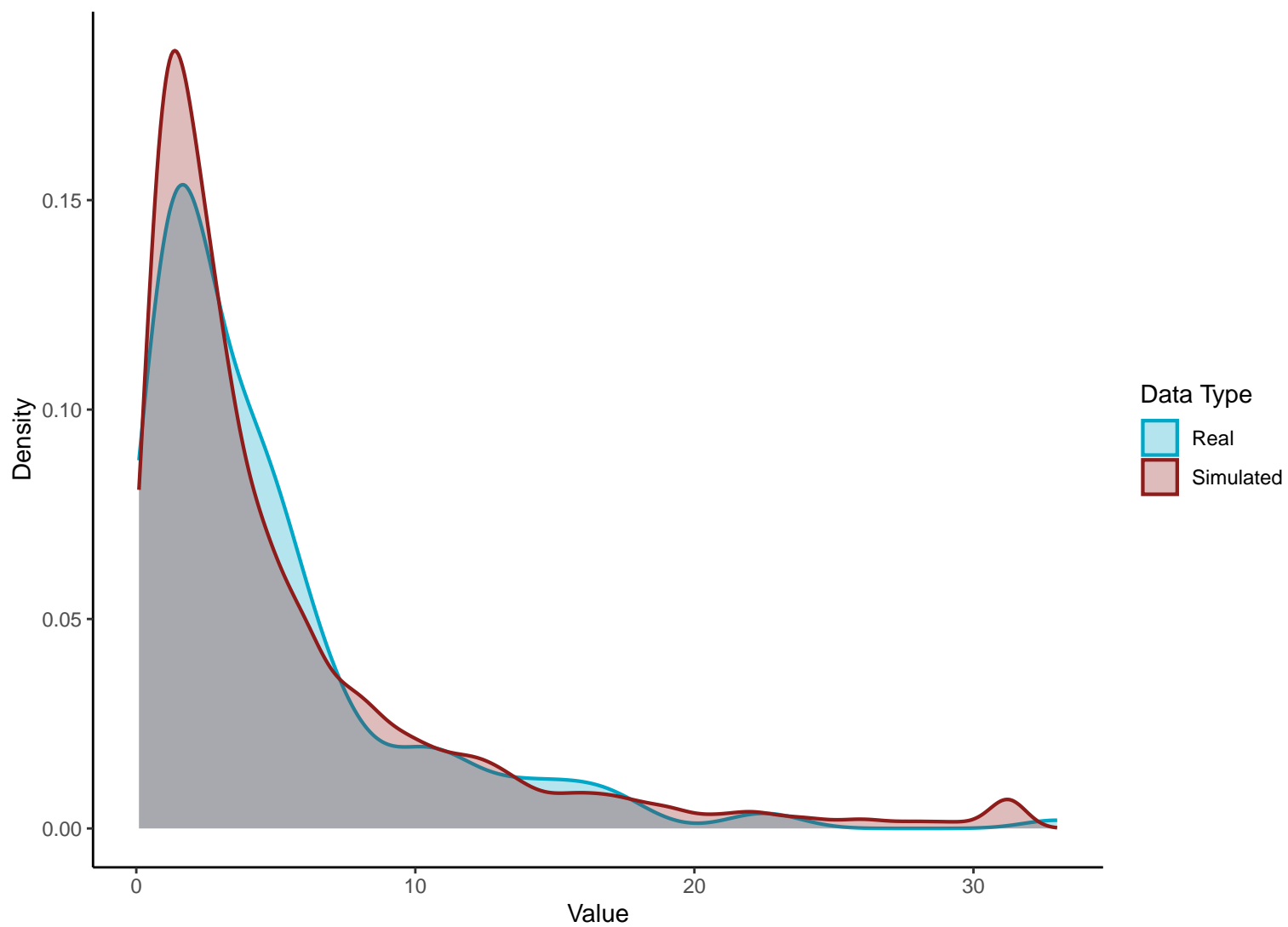
# Helicobacter



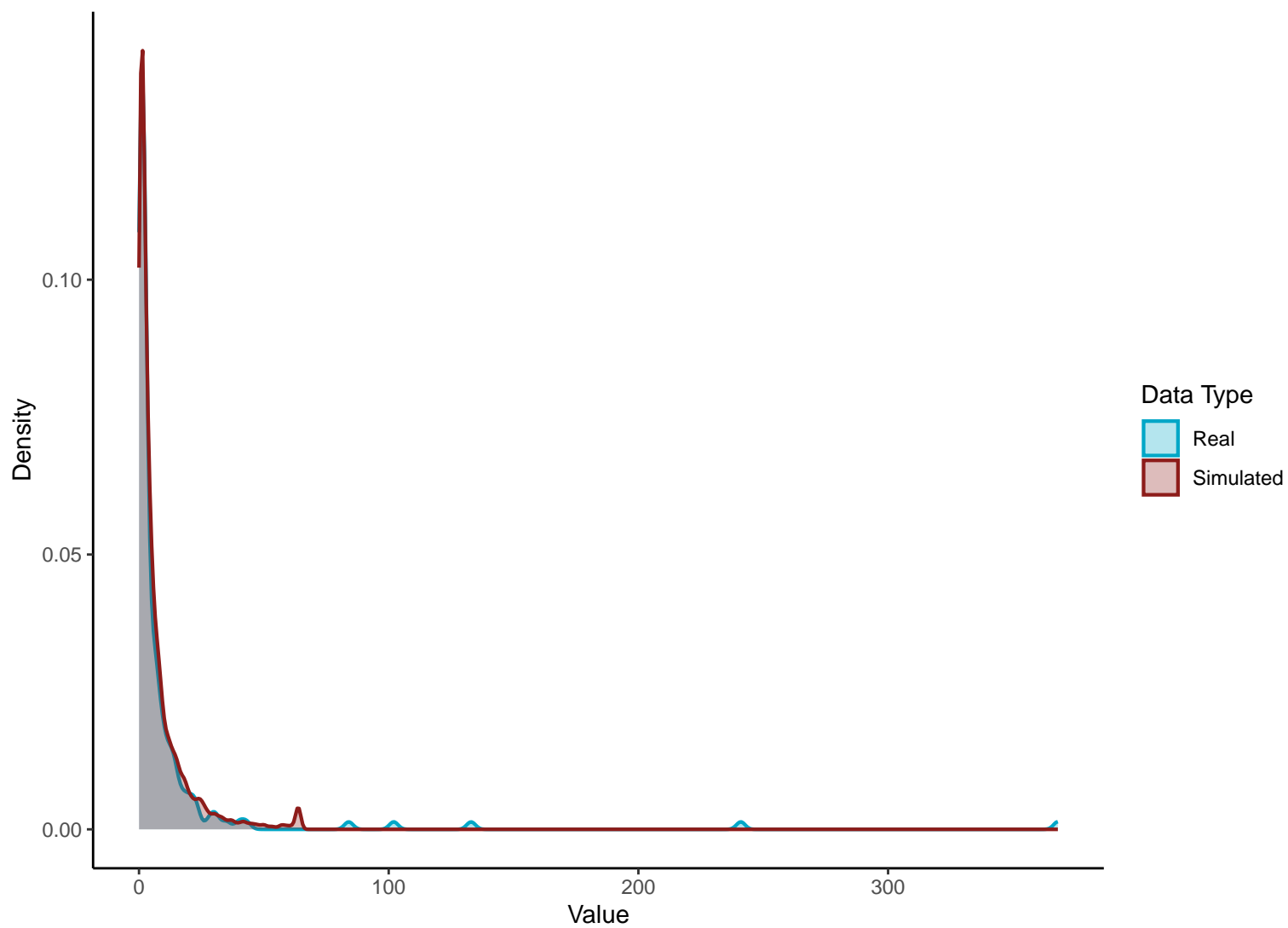
# Oscillospira



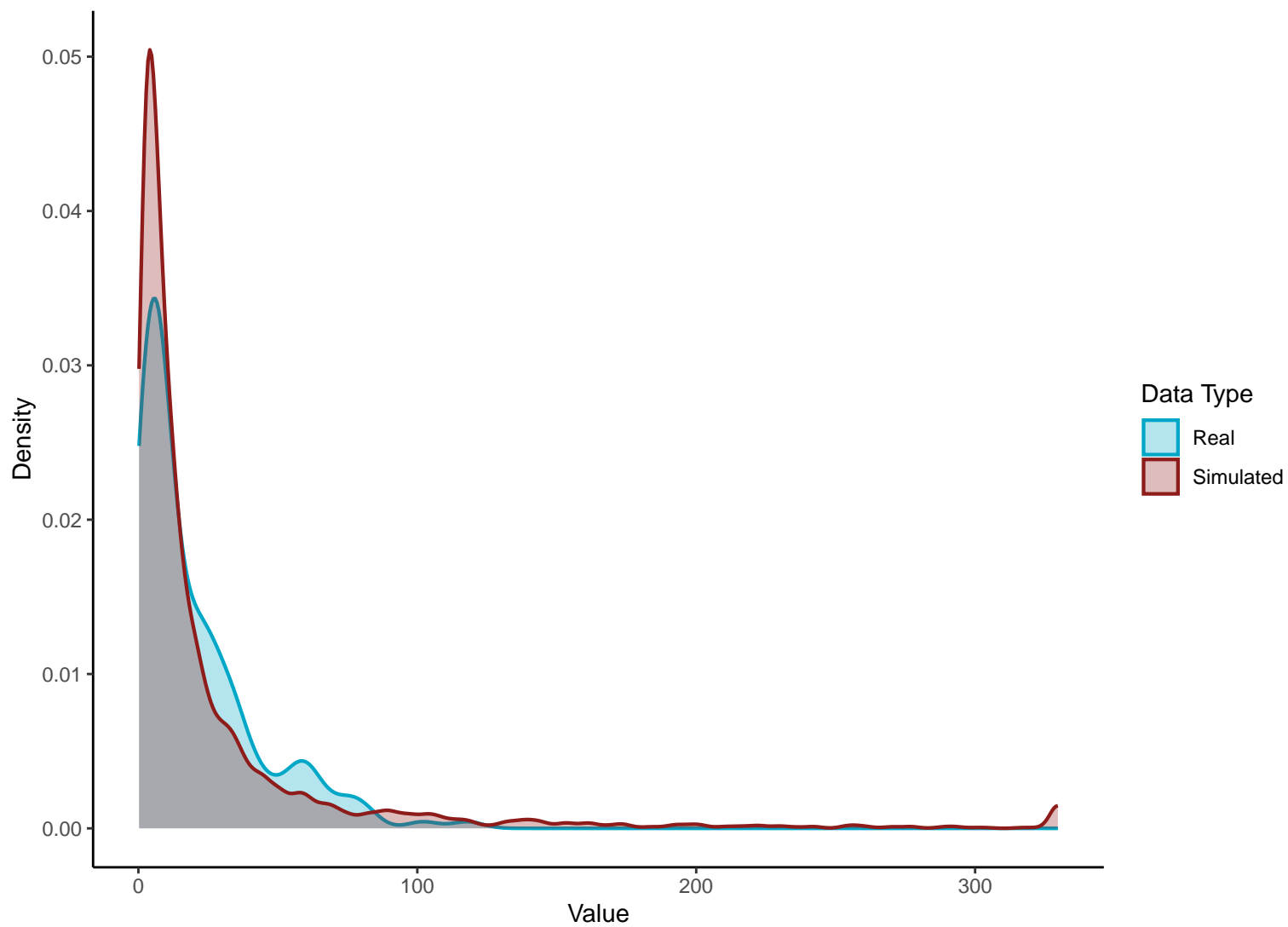
# Mailhella



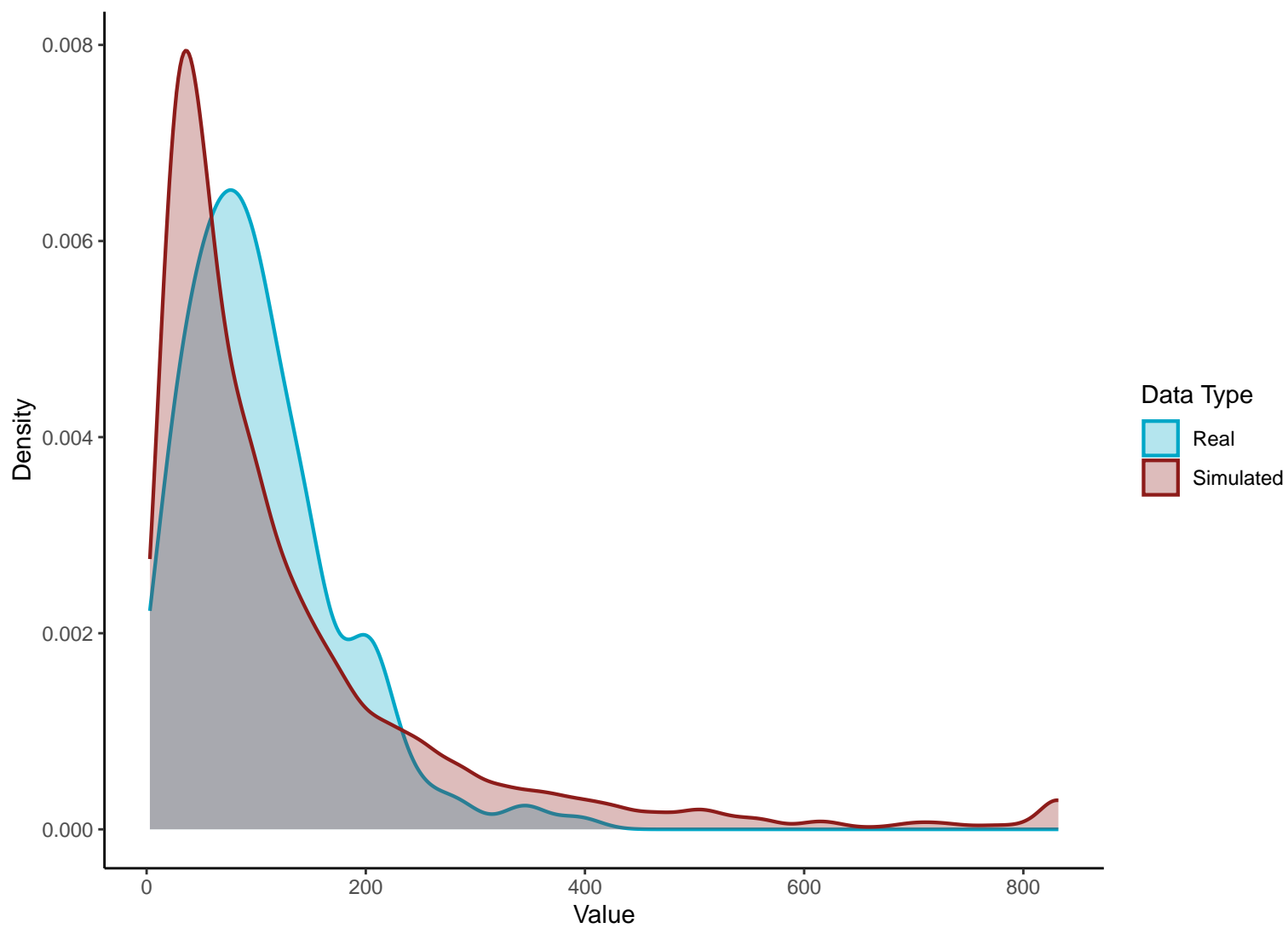
# Negativibacillus



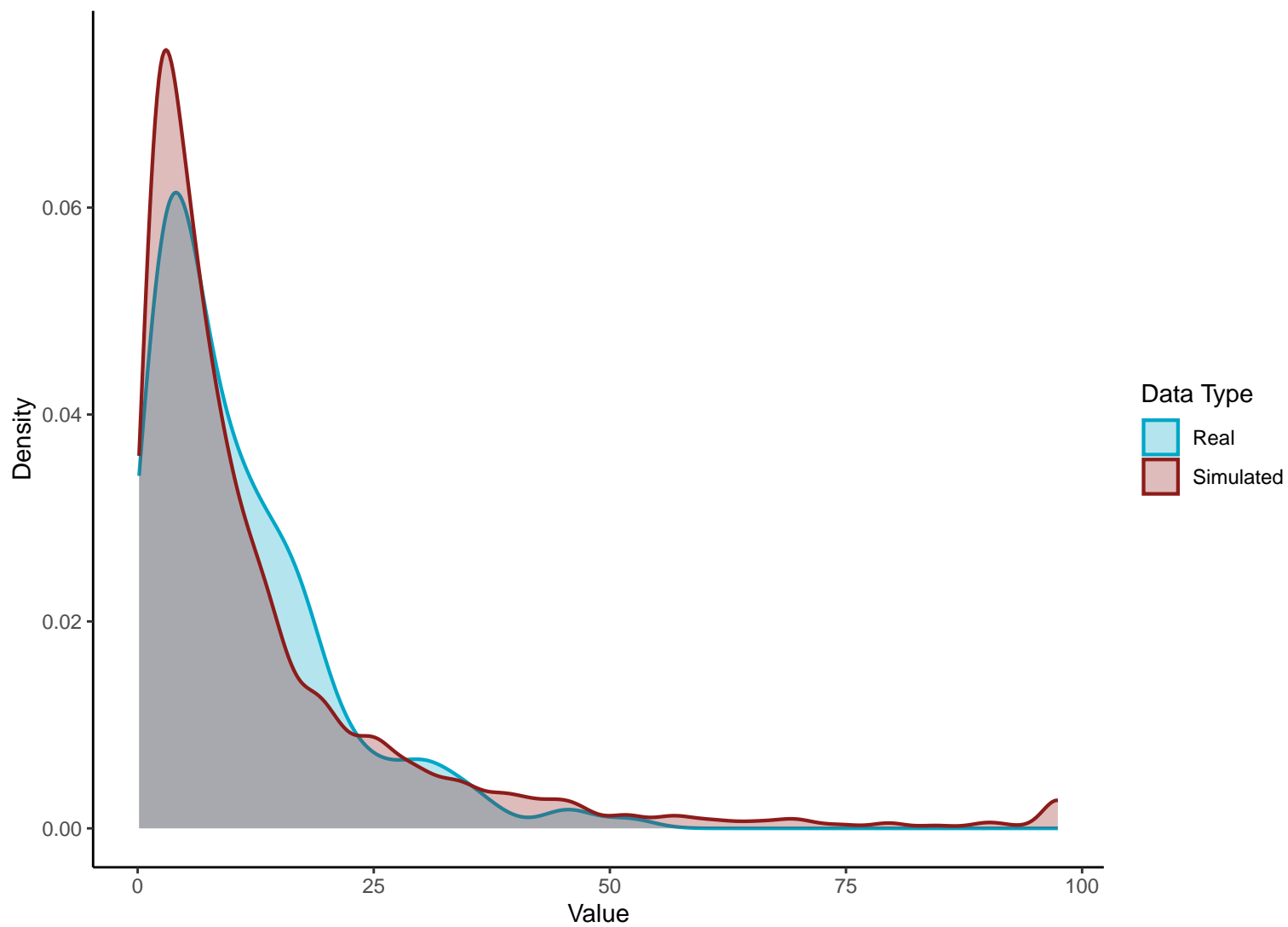
# Succinivibrio



# Peptococcus

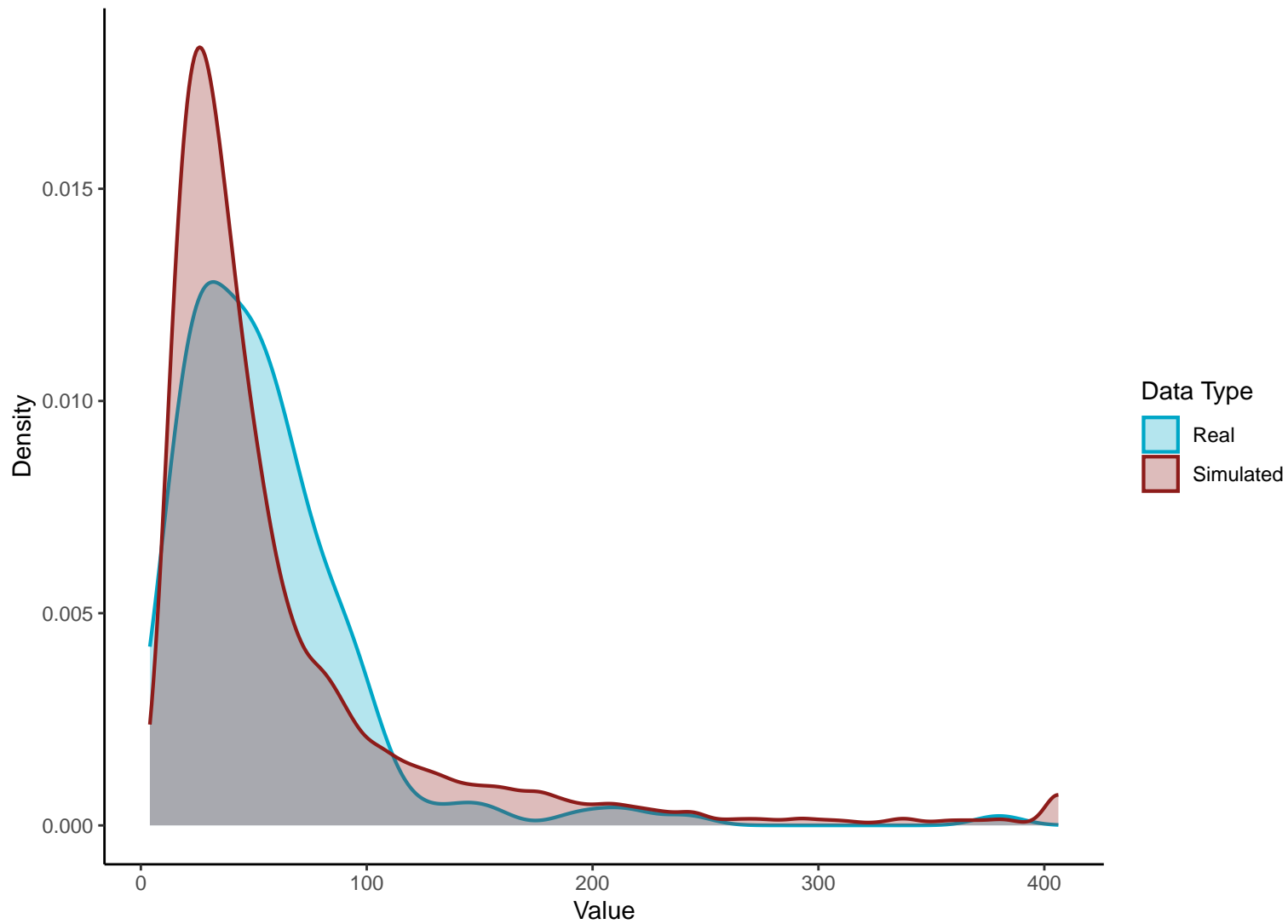


UCG.003

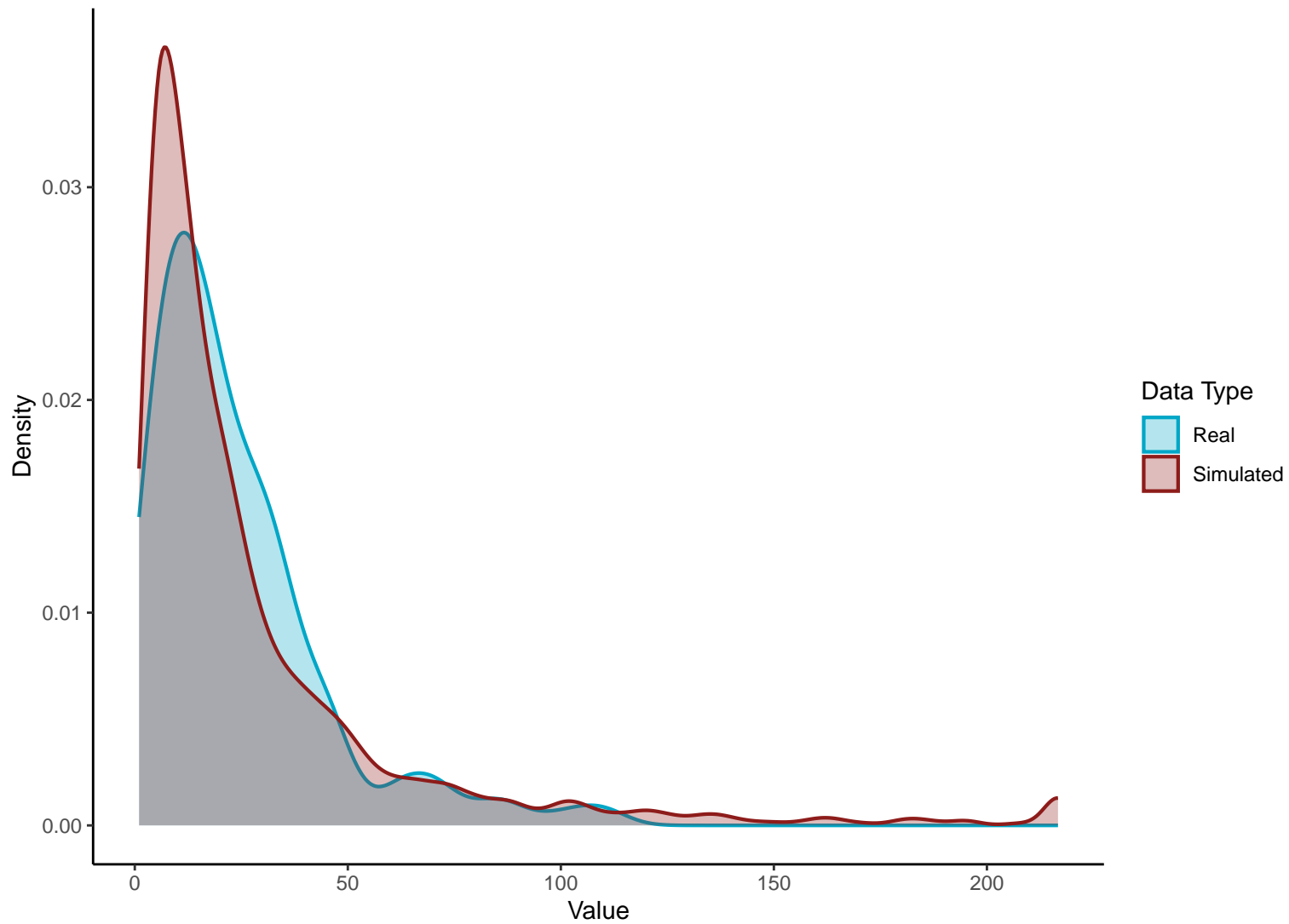




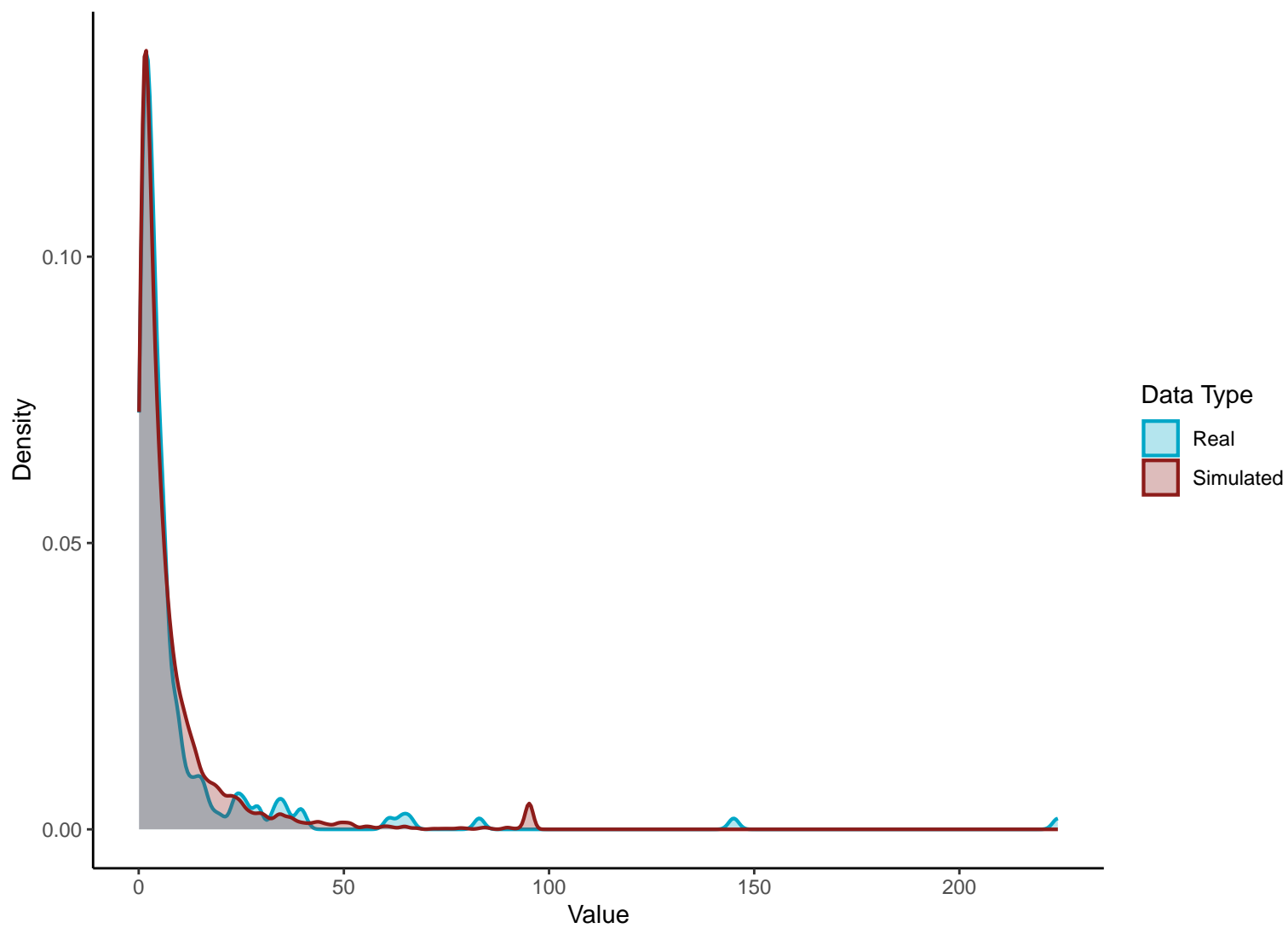
# Lachnoclostridium



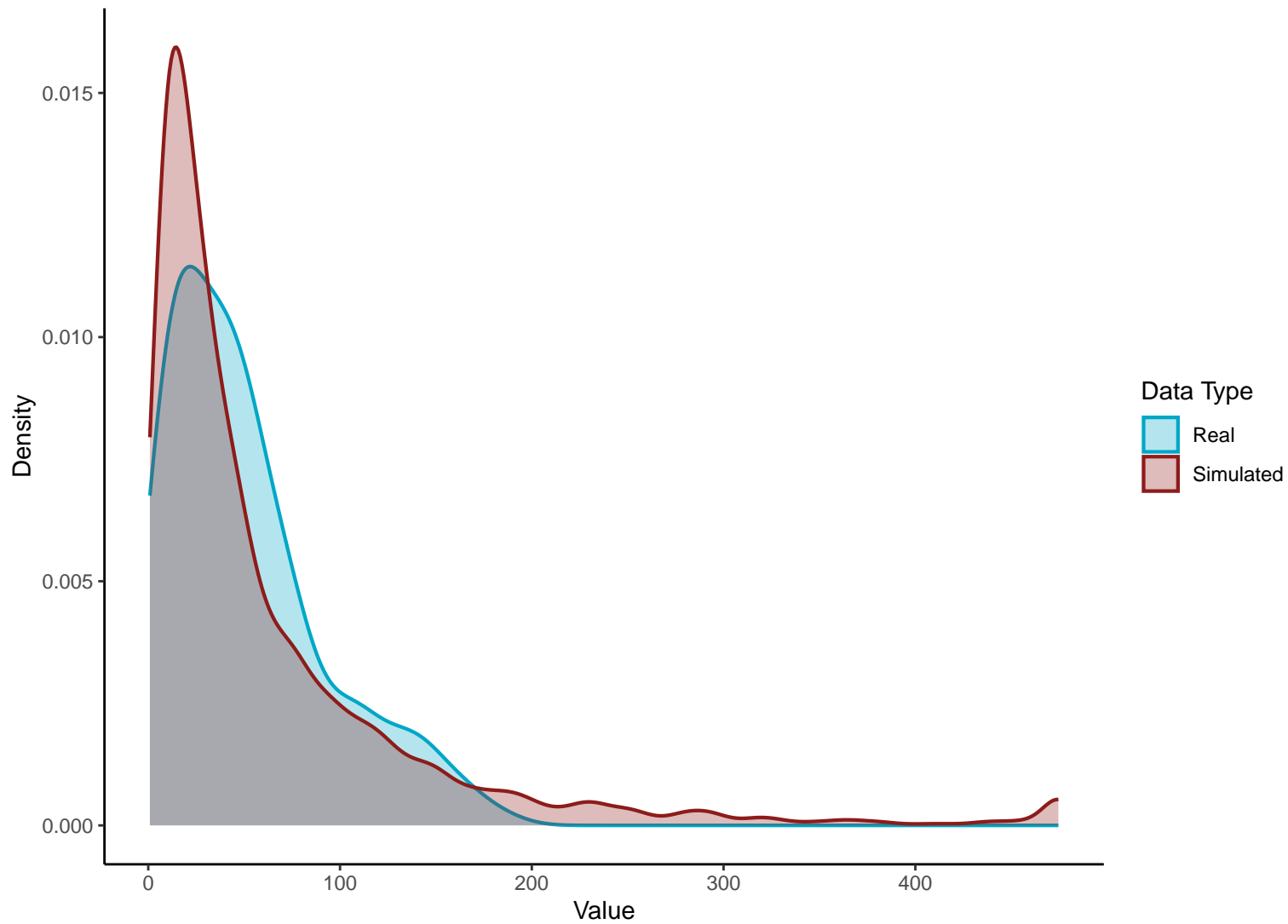
# X.Eubacterium..ventriosum.group



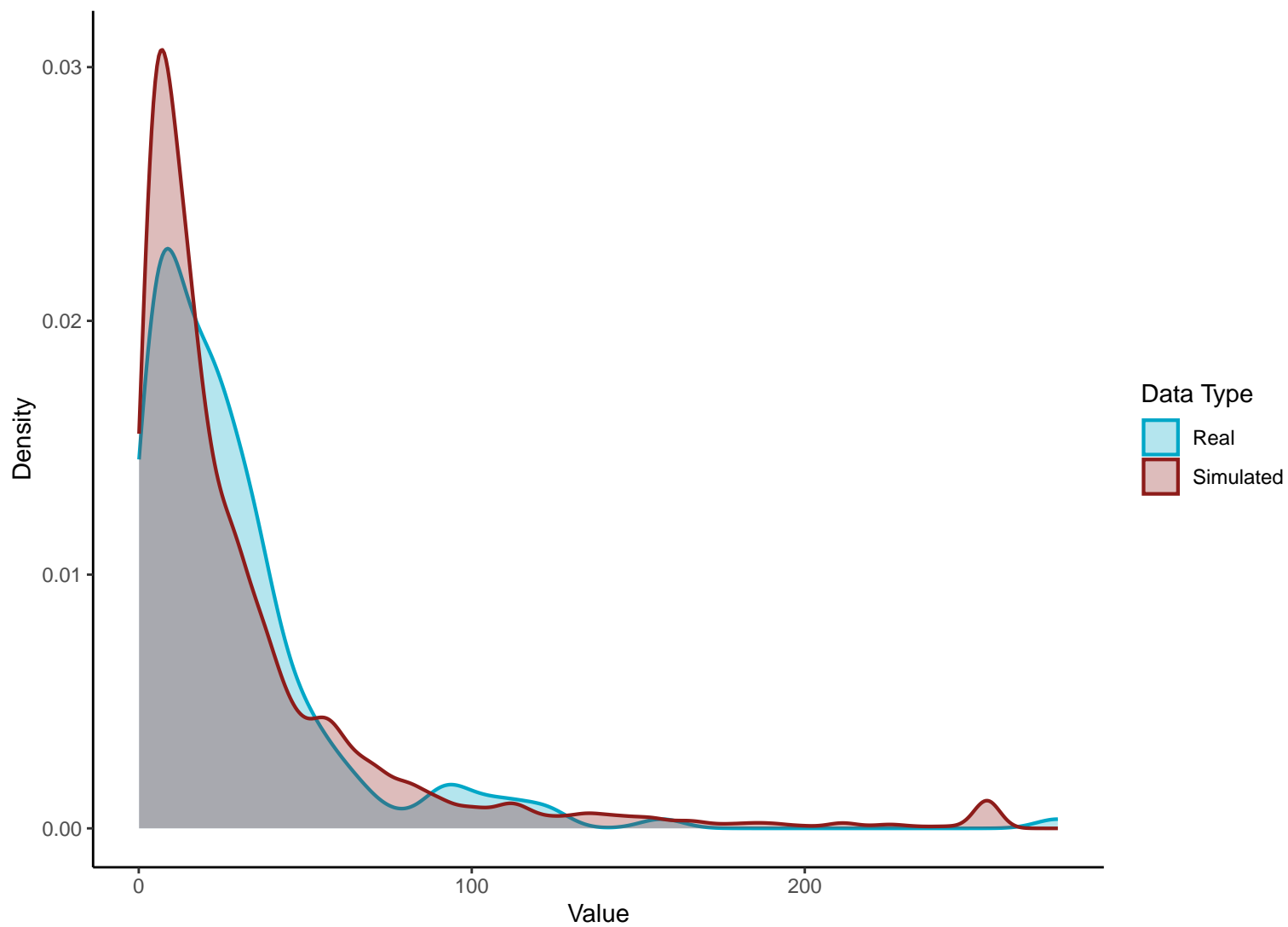
# Anaerococcus



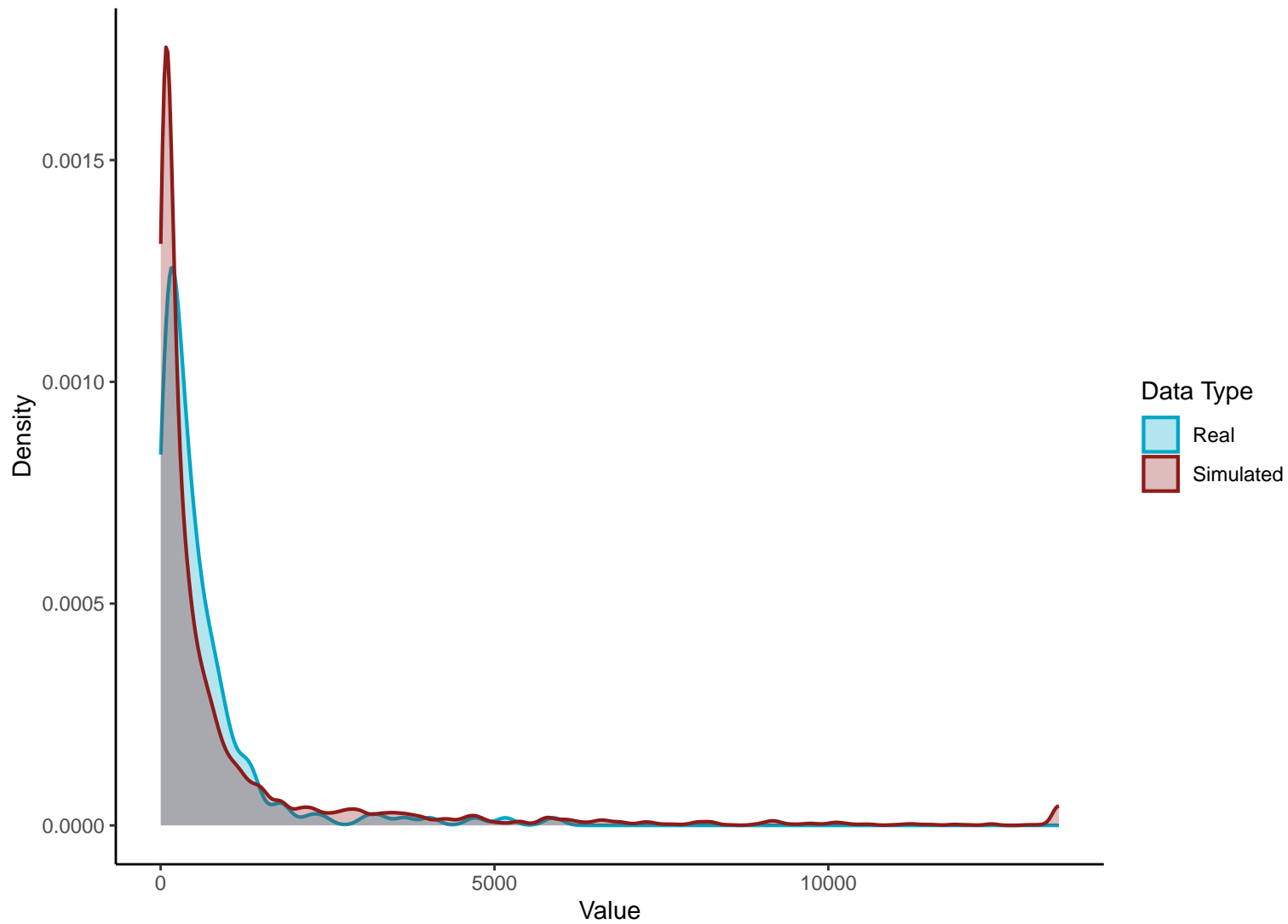
# Enterorhabdus



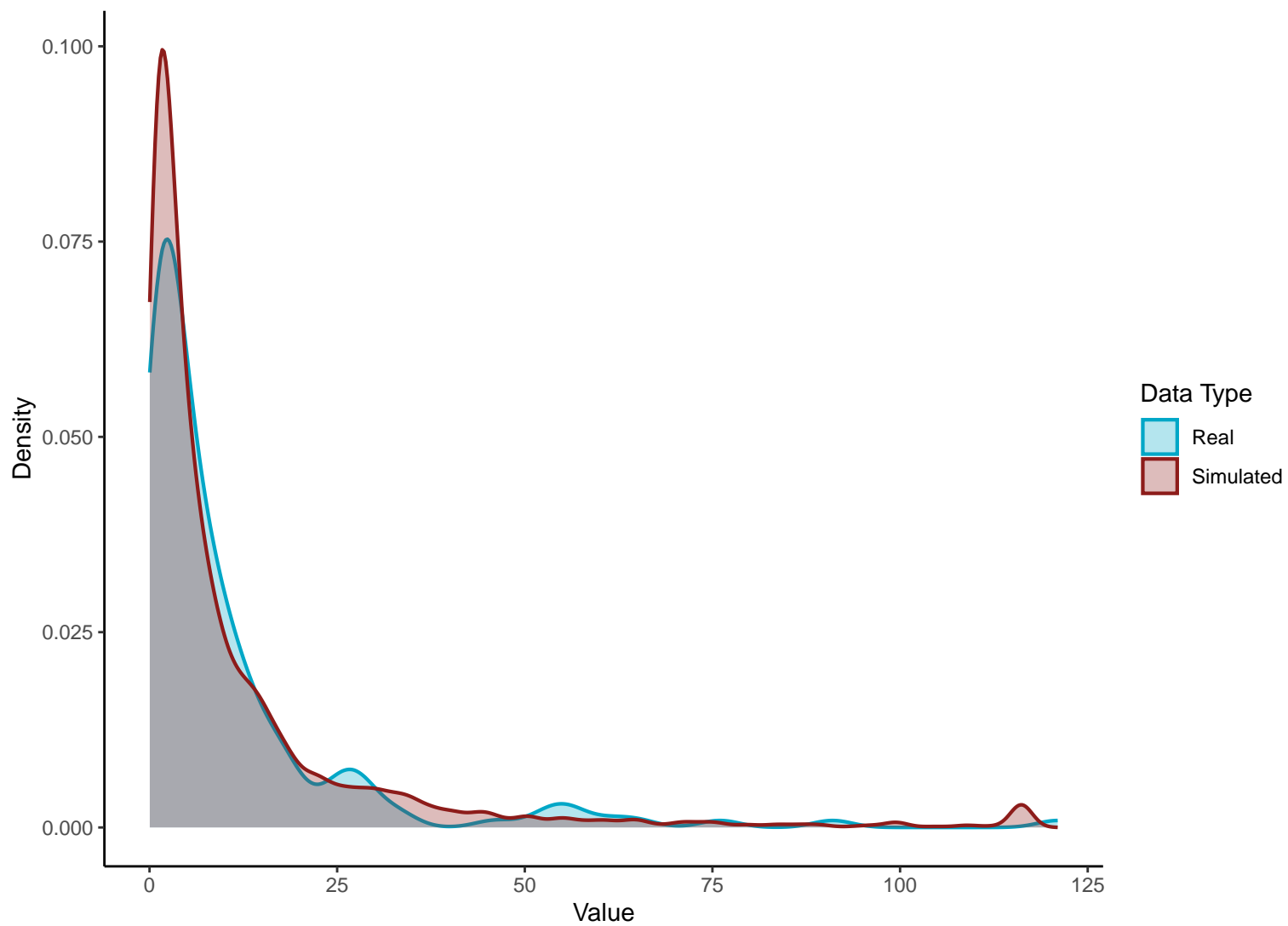
# Libanicoccus



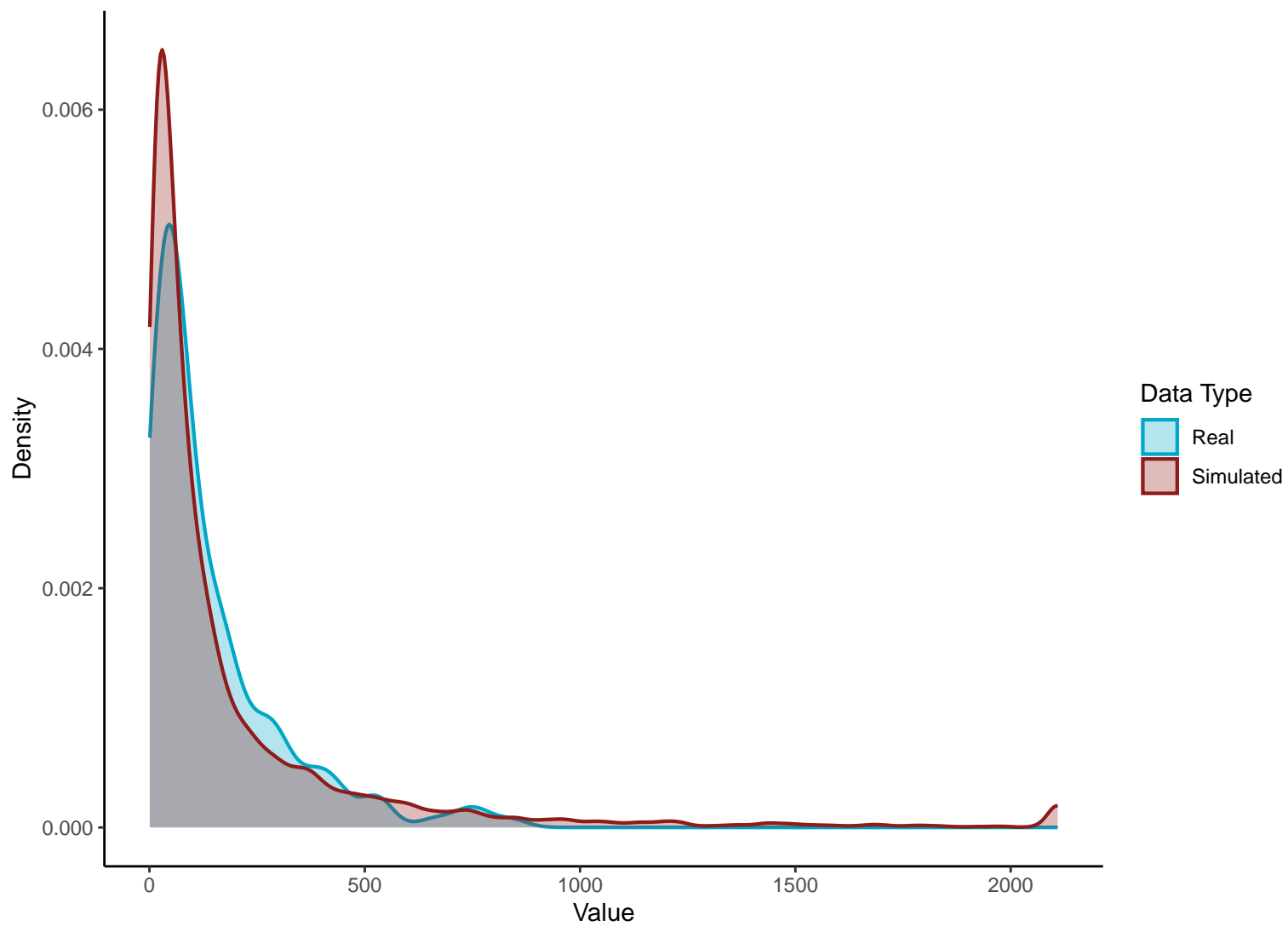
# Turicibacter



XBB1006

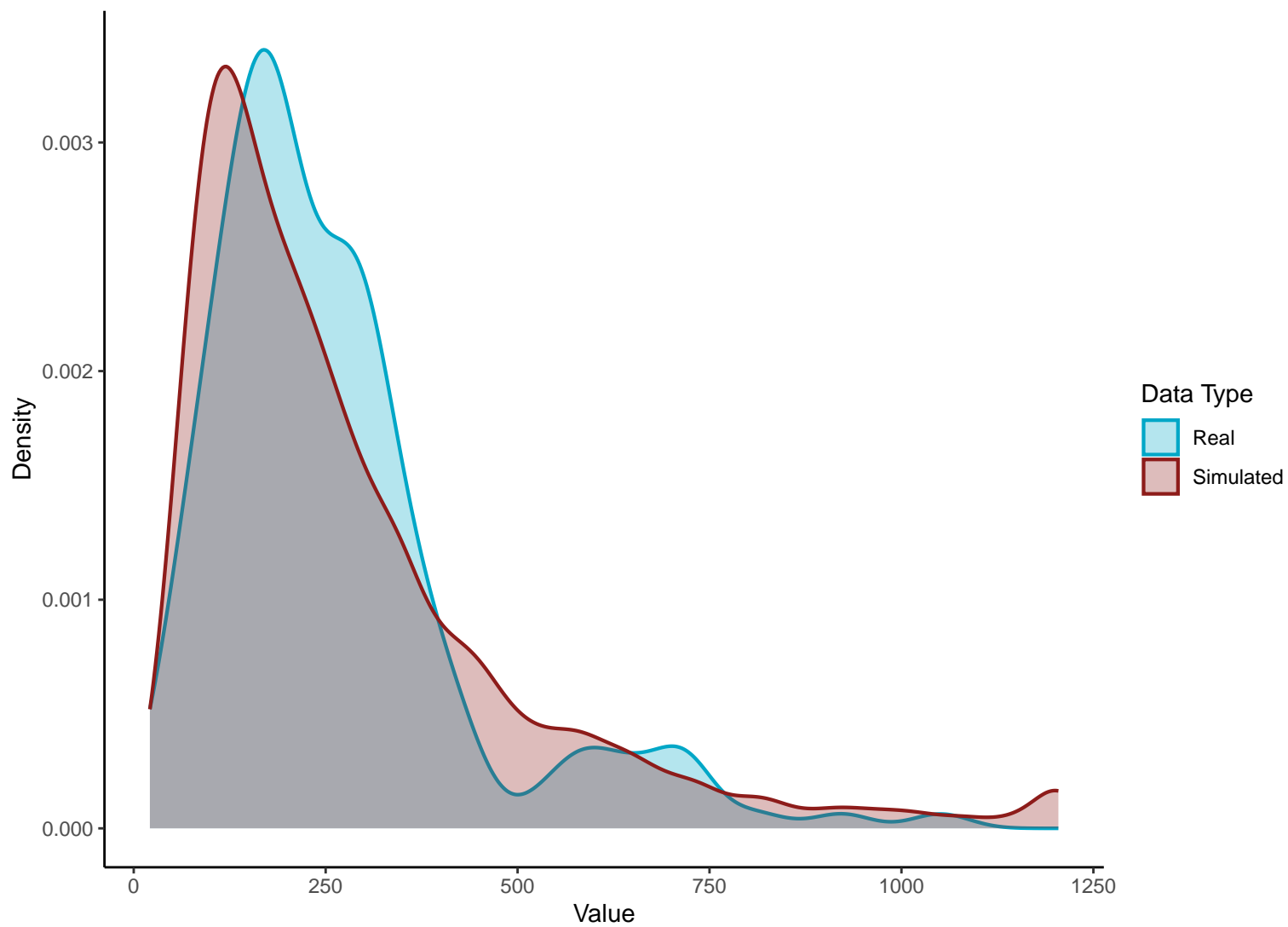


UCG.008

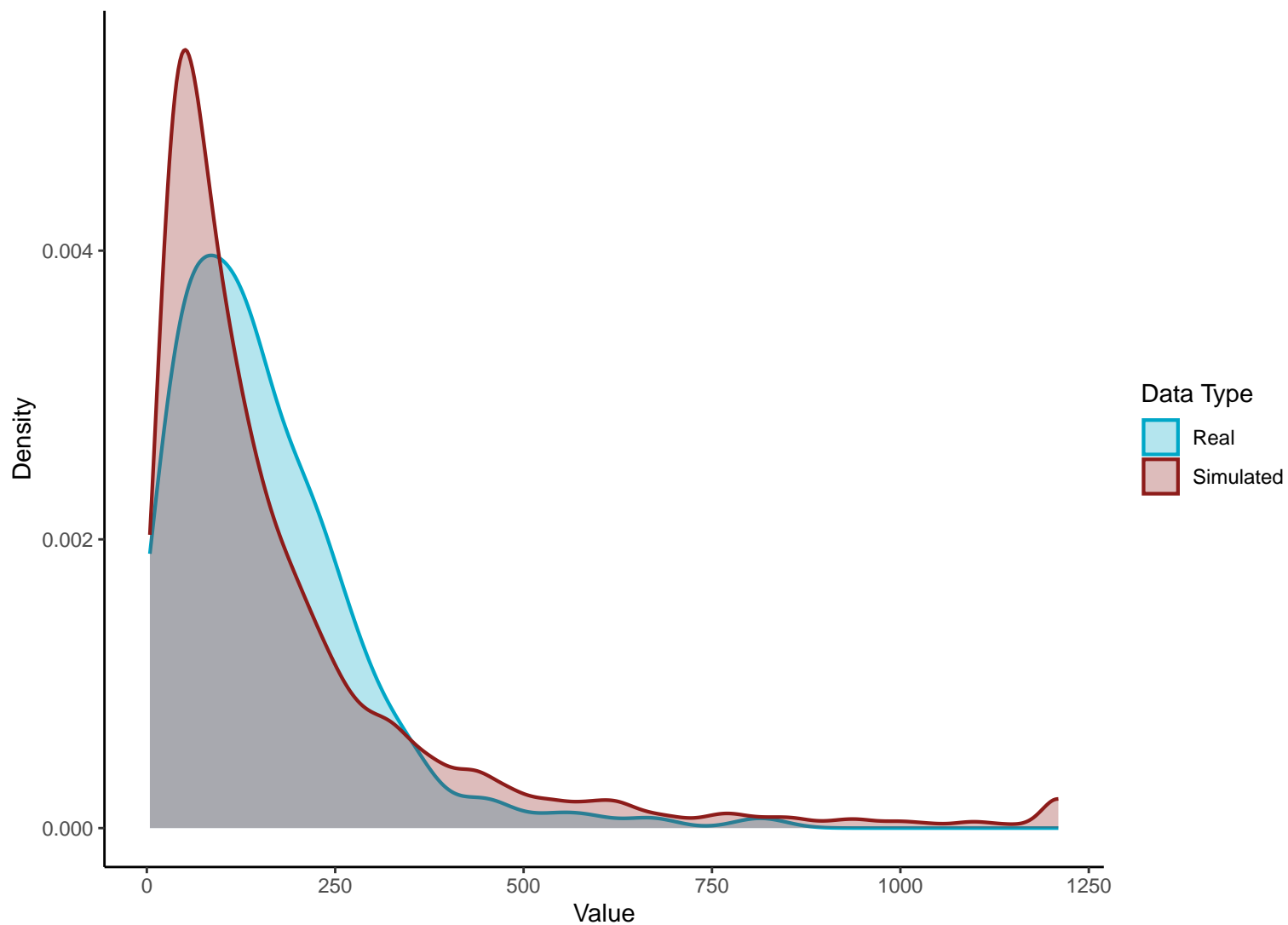




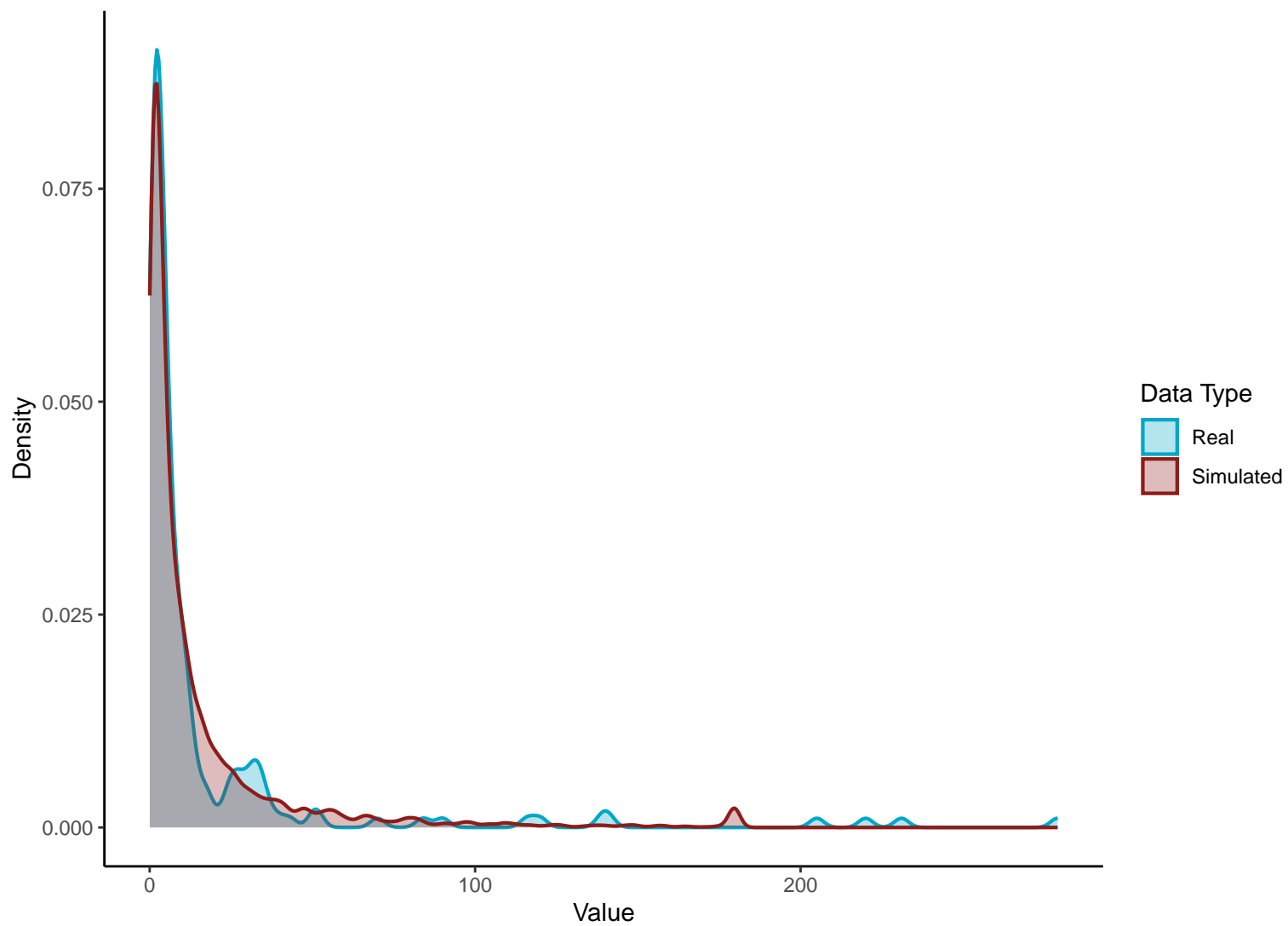
# Intestinibacter



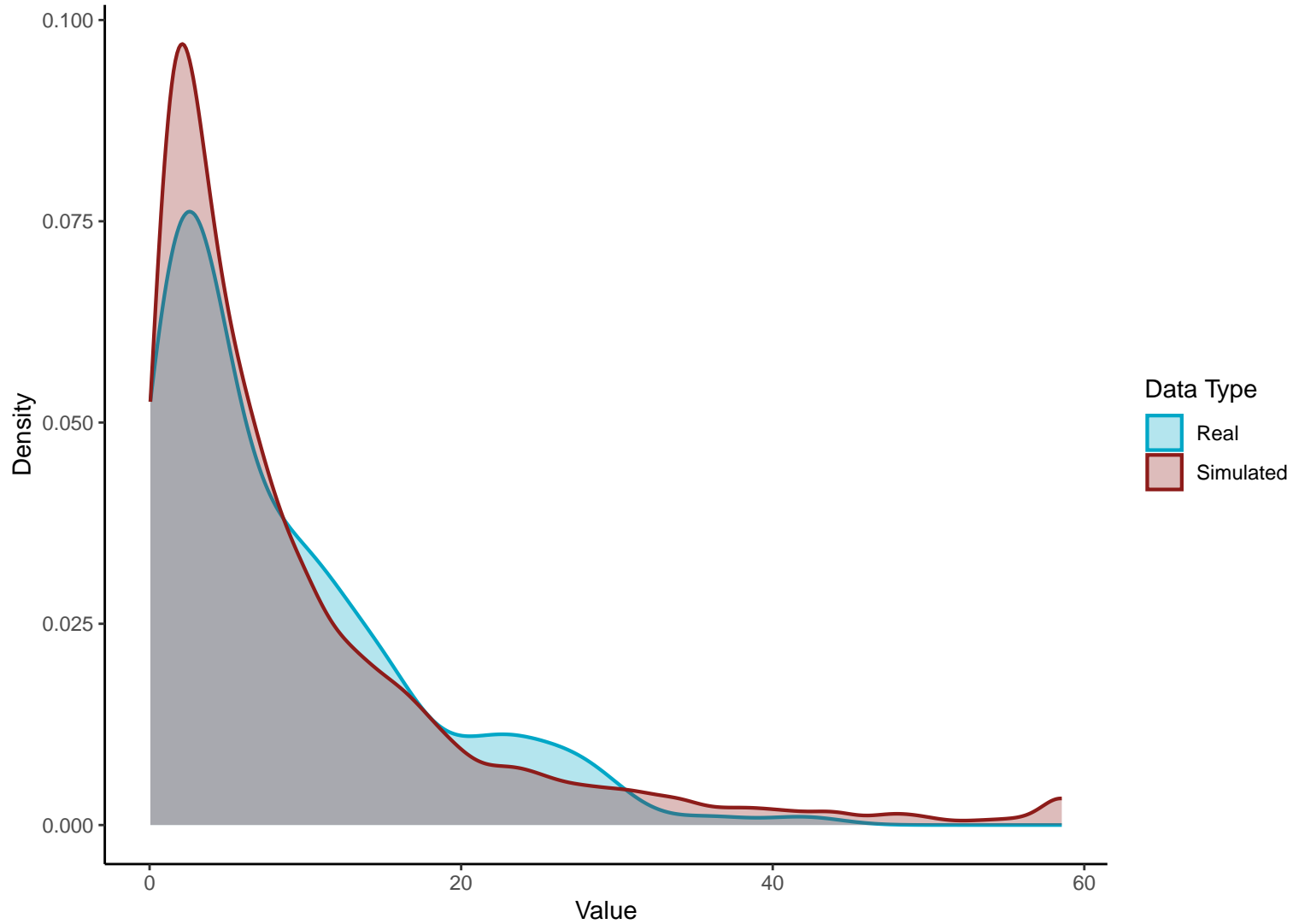
# Fusicatenibacter



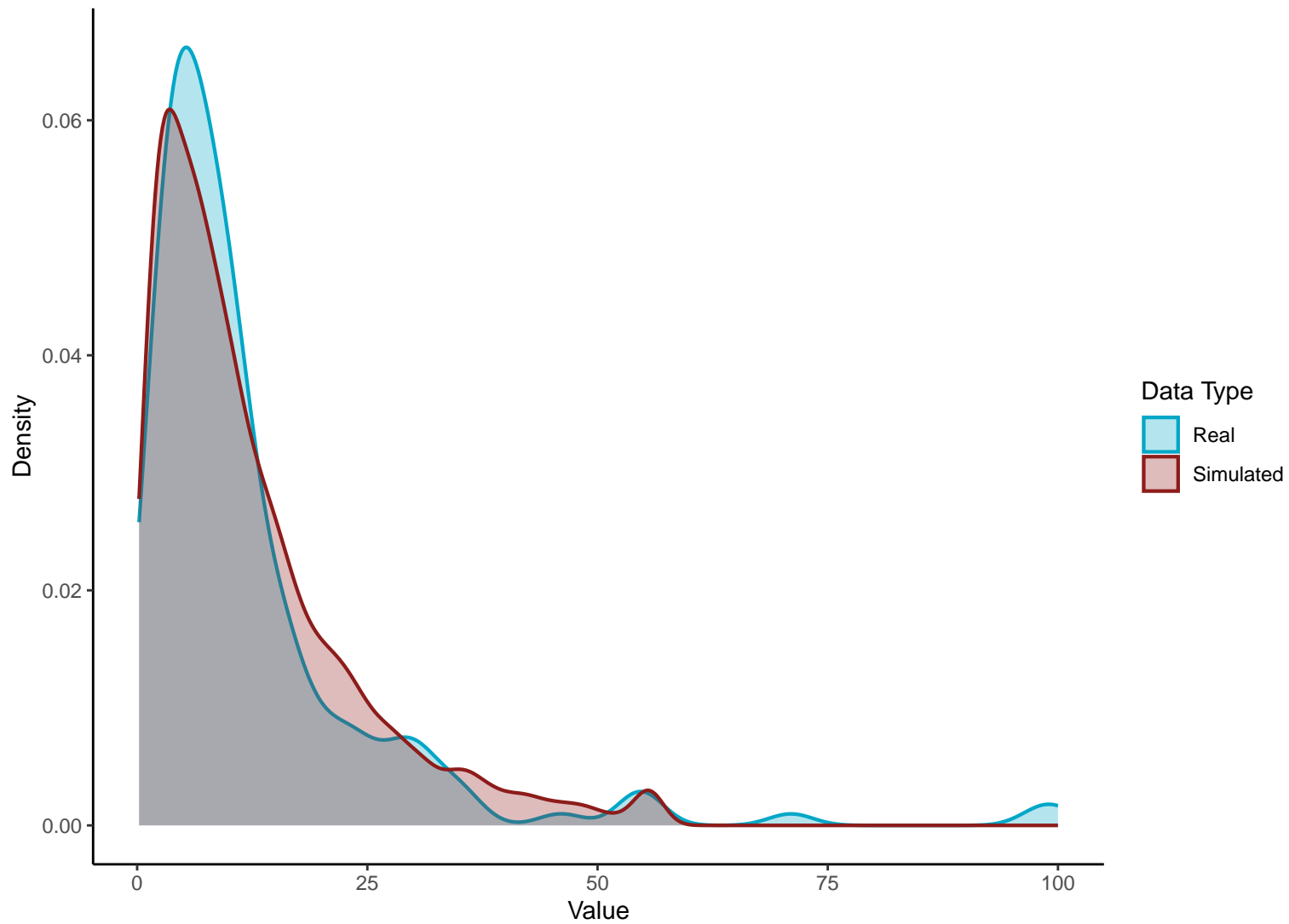
X28.4



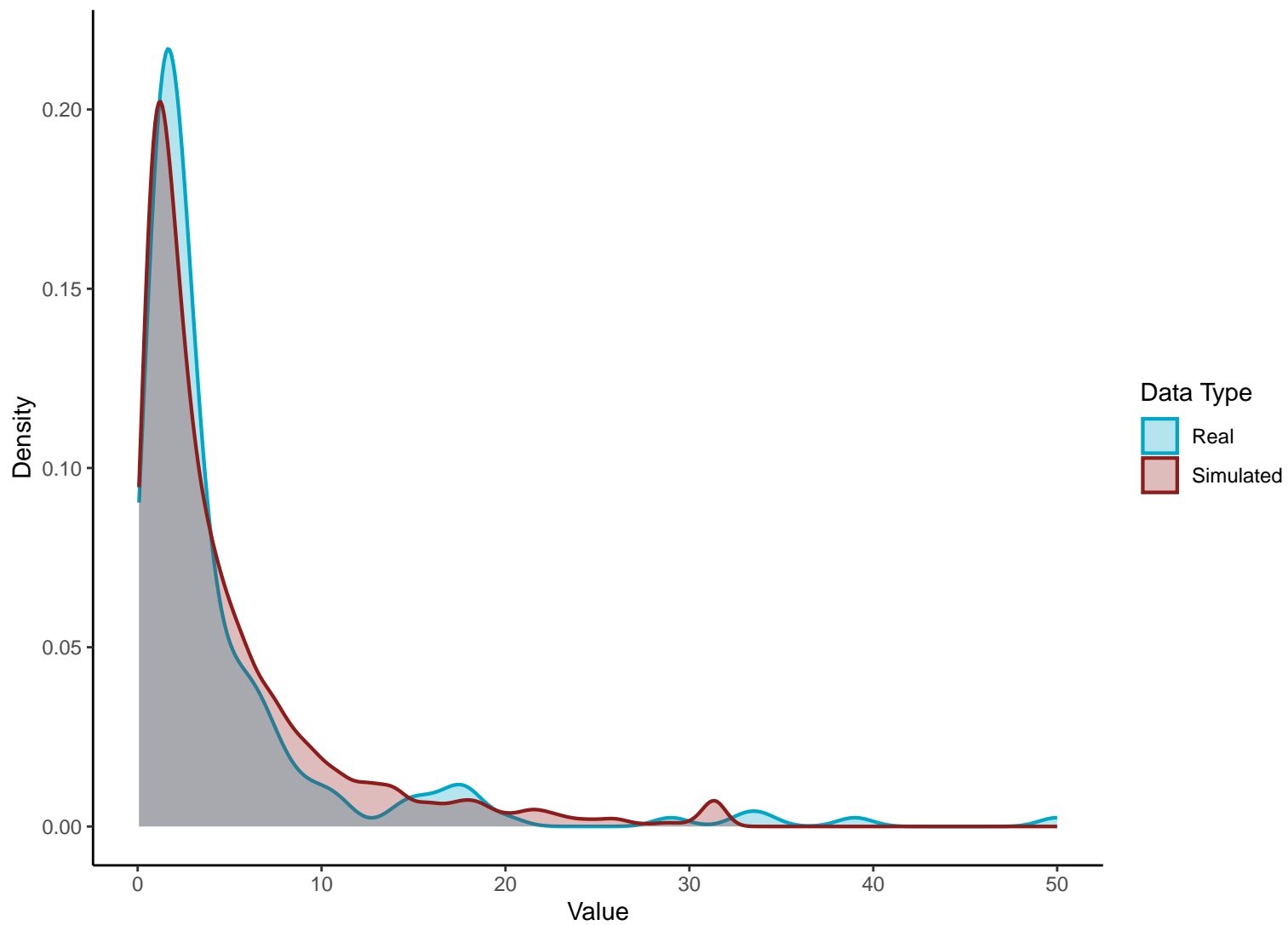
# Howardella



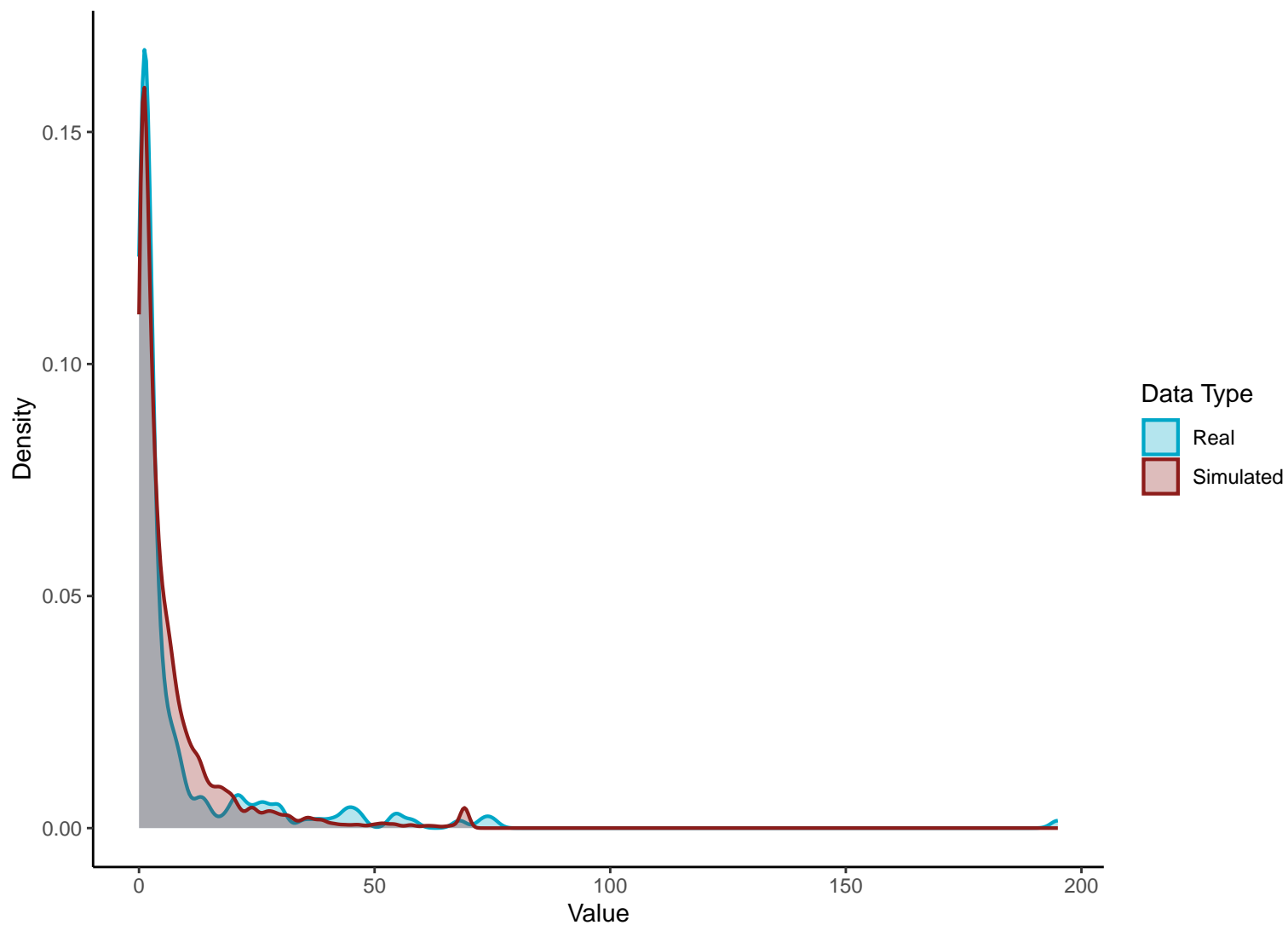
# Paludicola



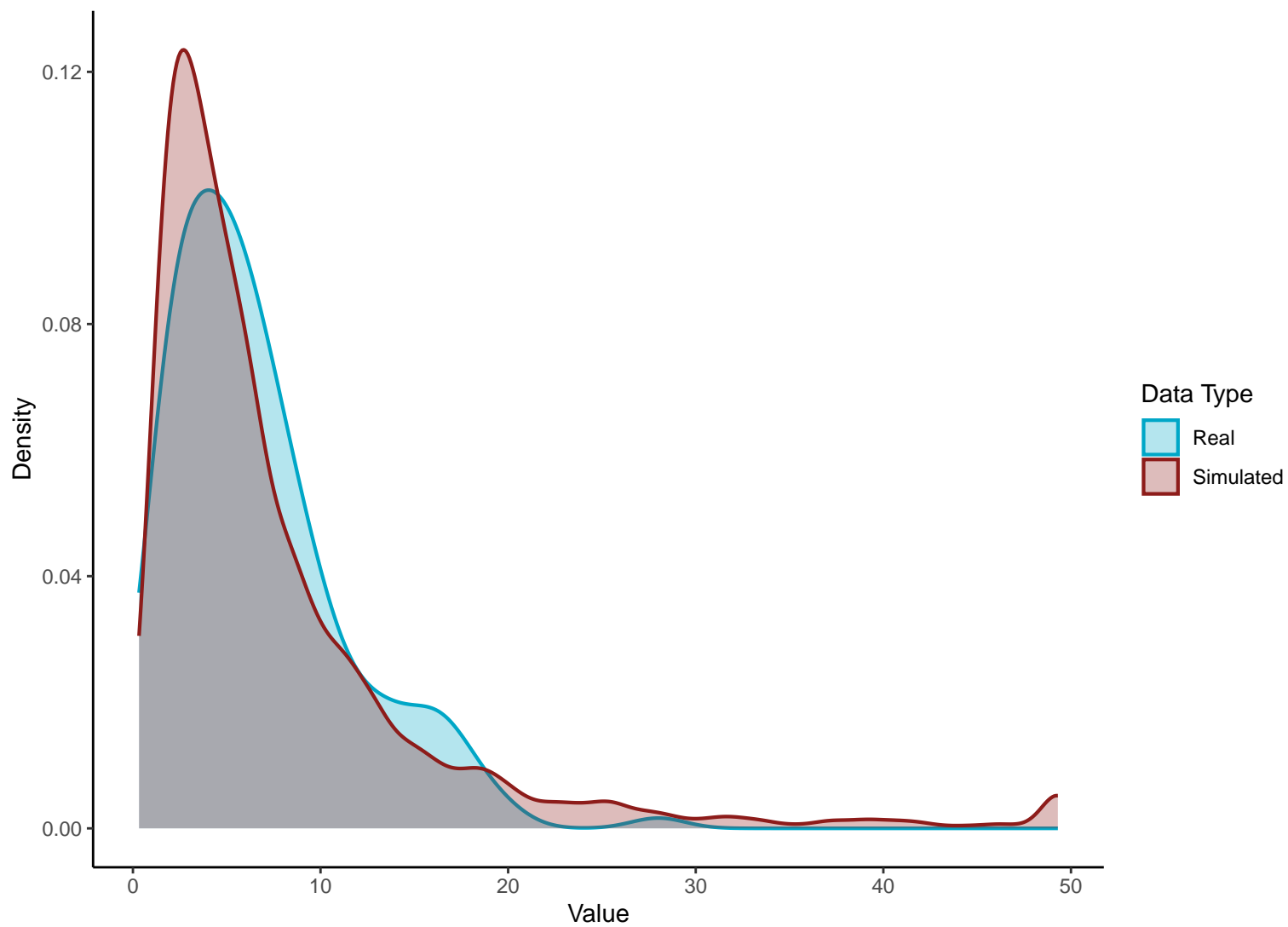
# Tyzzerella



UCG.001

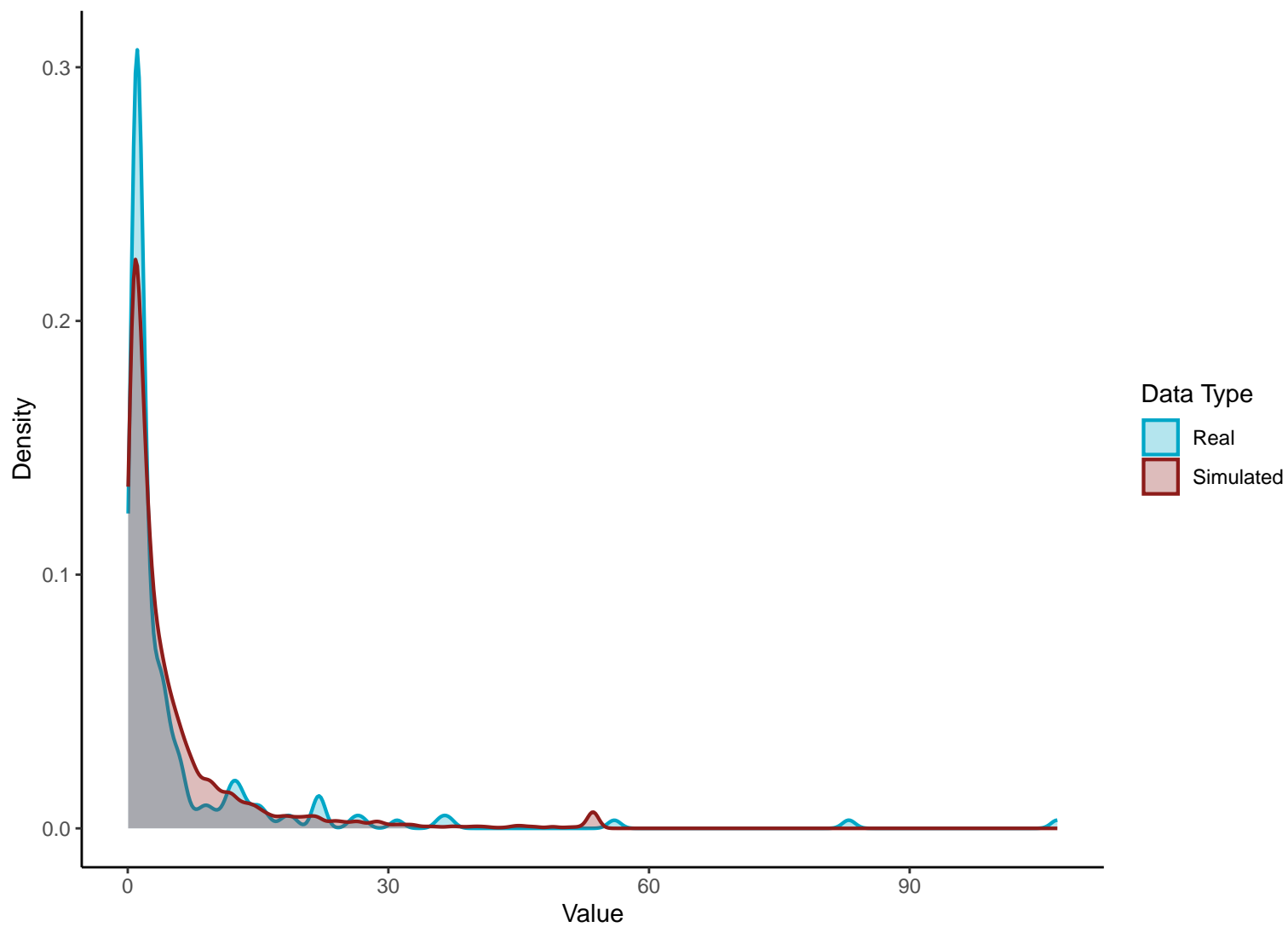


# Lachnospiraceae.UGC.002

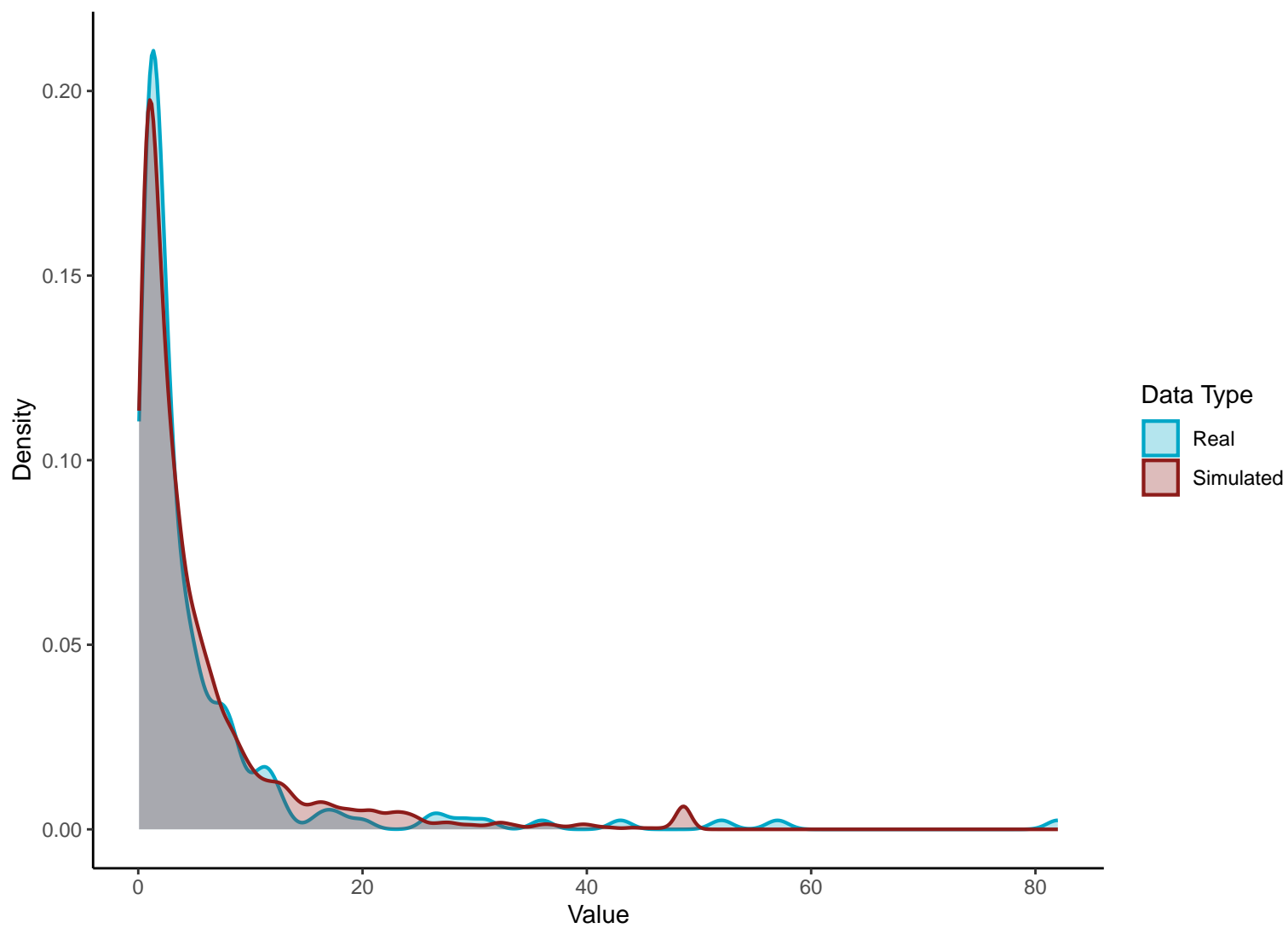




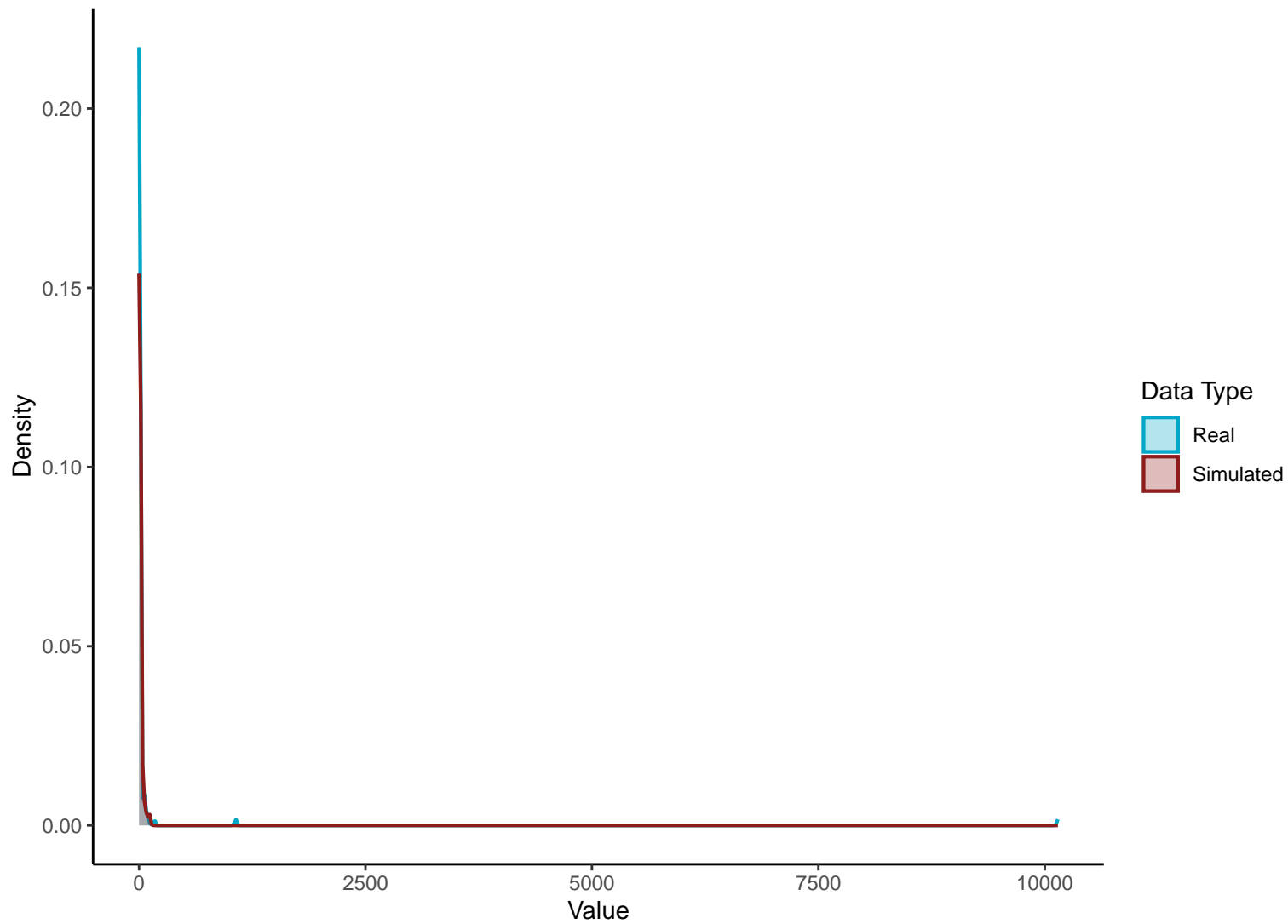
# Lachnospiraceae.UGC.007



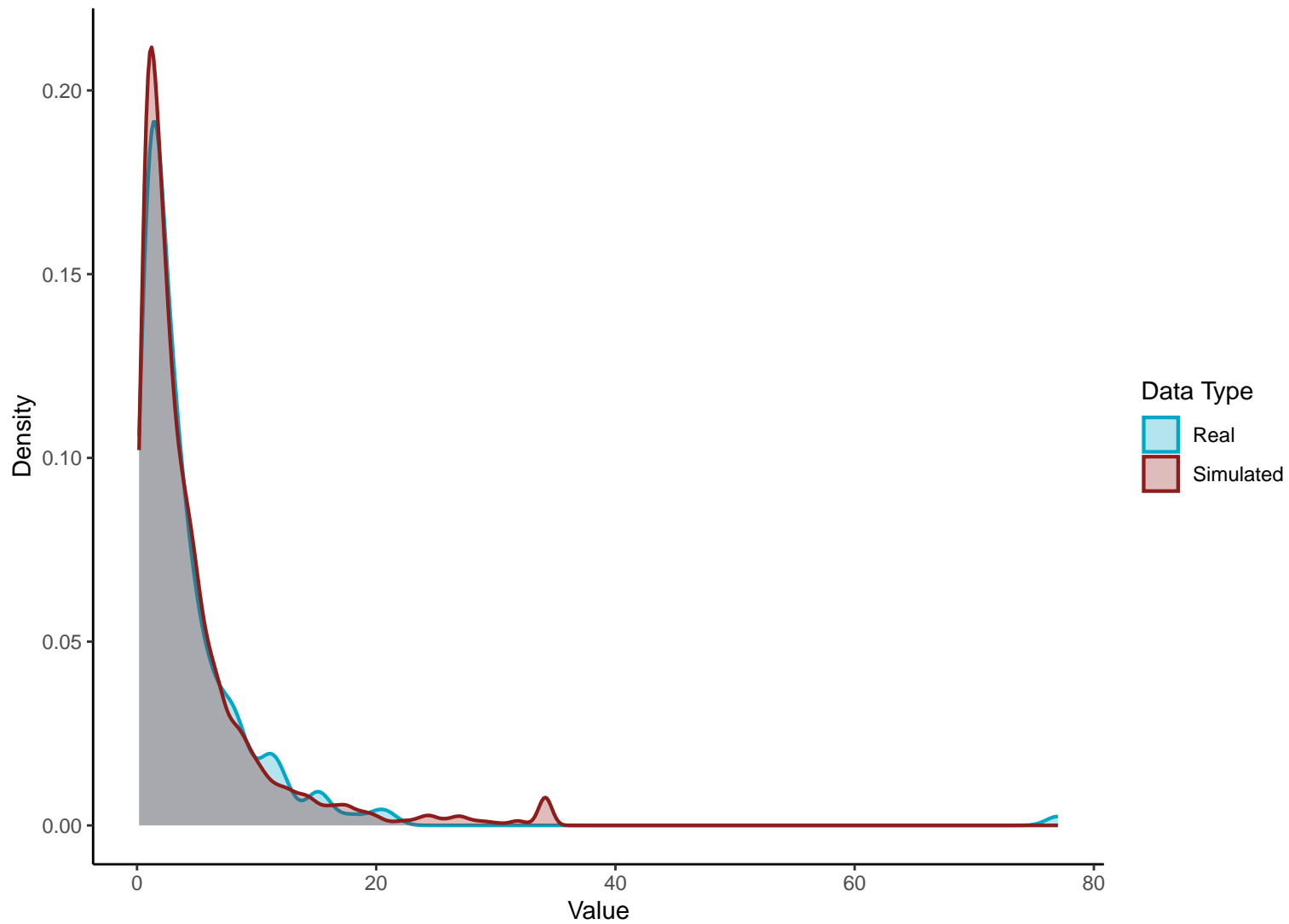
# Lachnospiraceae.UGC.003



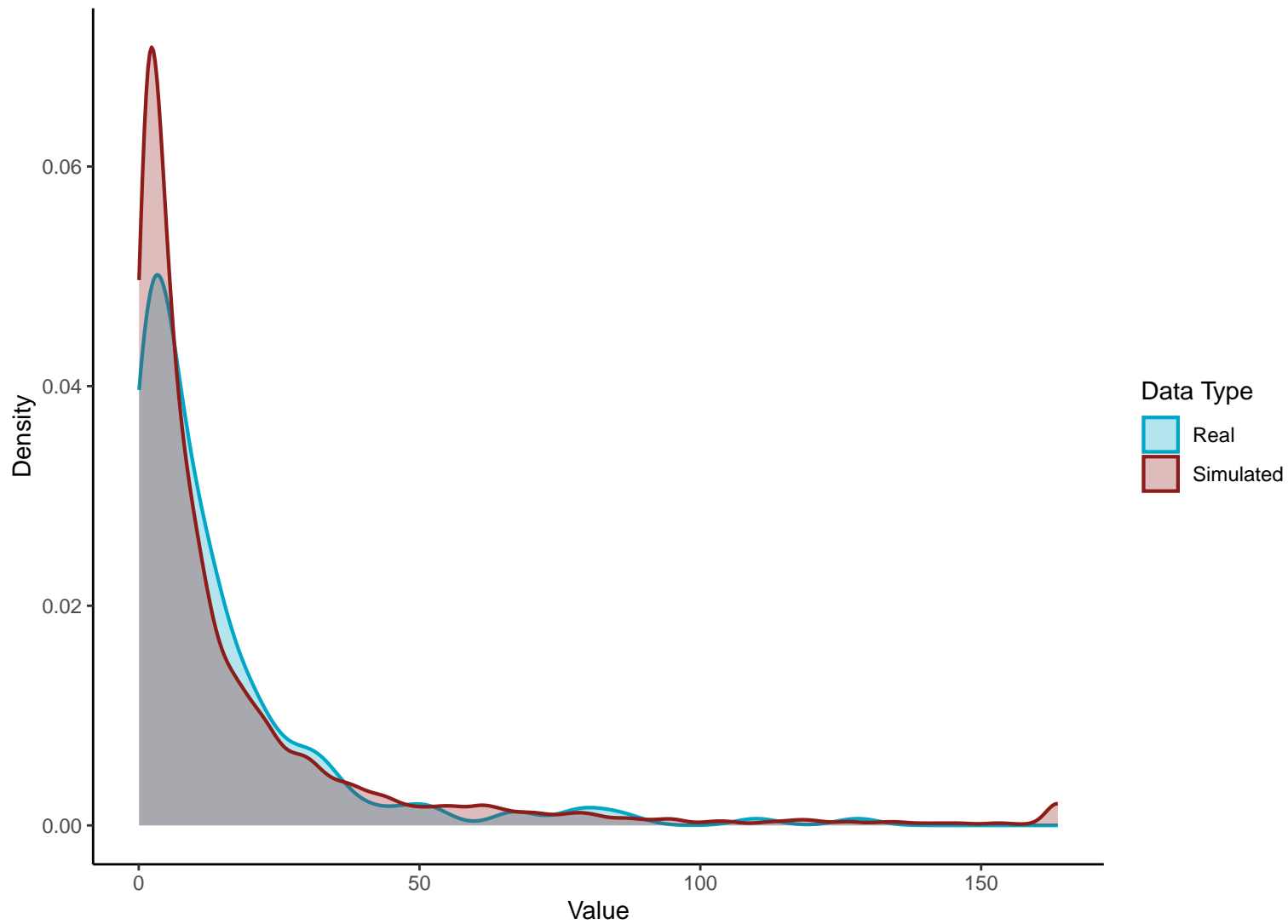
# Bifidobacterium



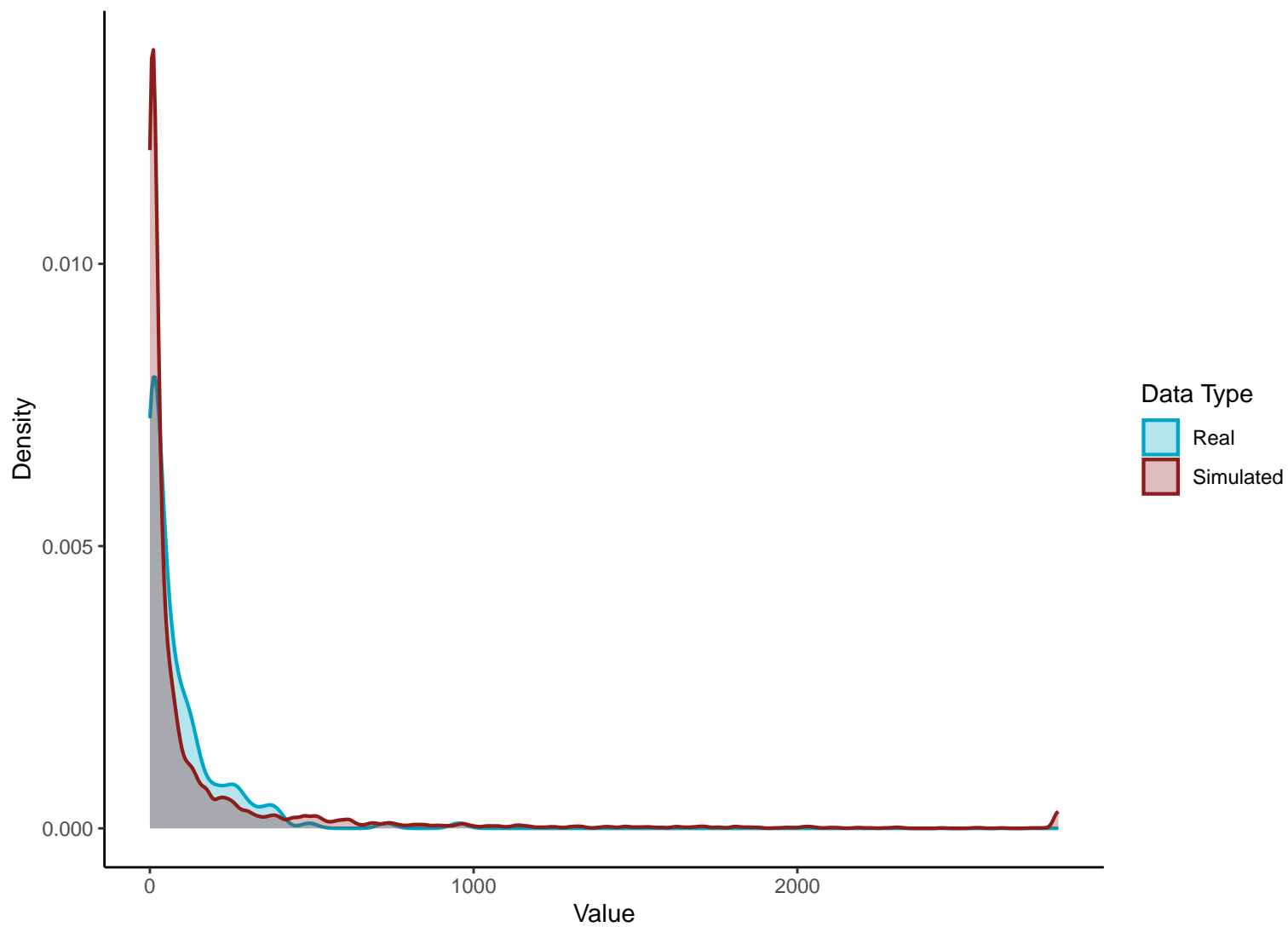
# Butyrivibrio



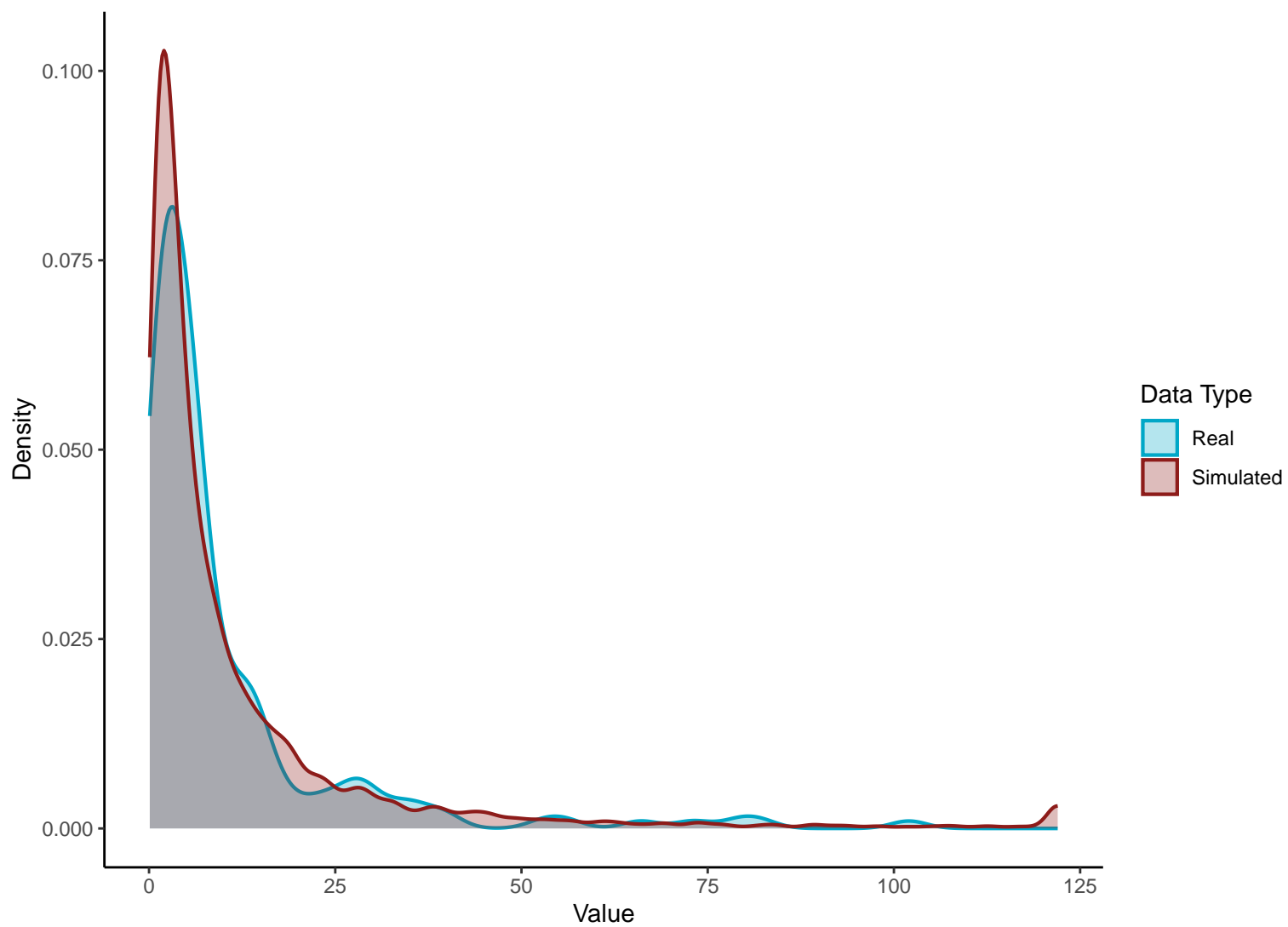
# Pseudobutyrvibrio



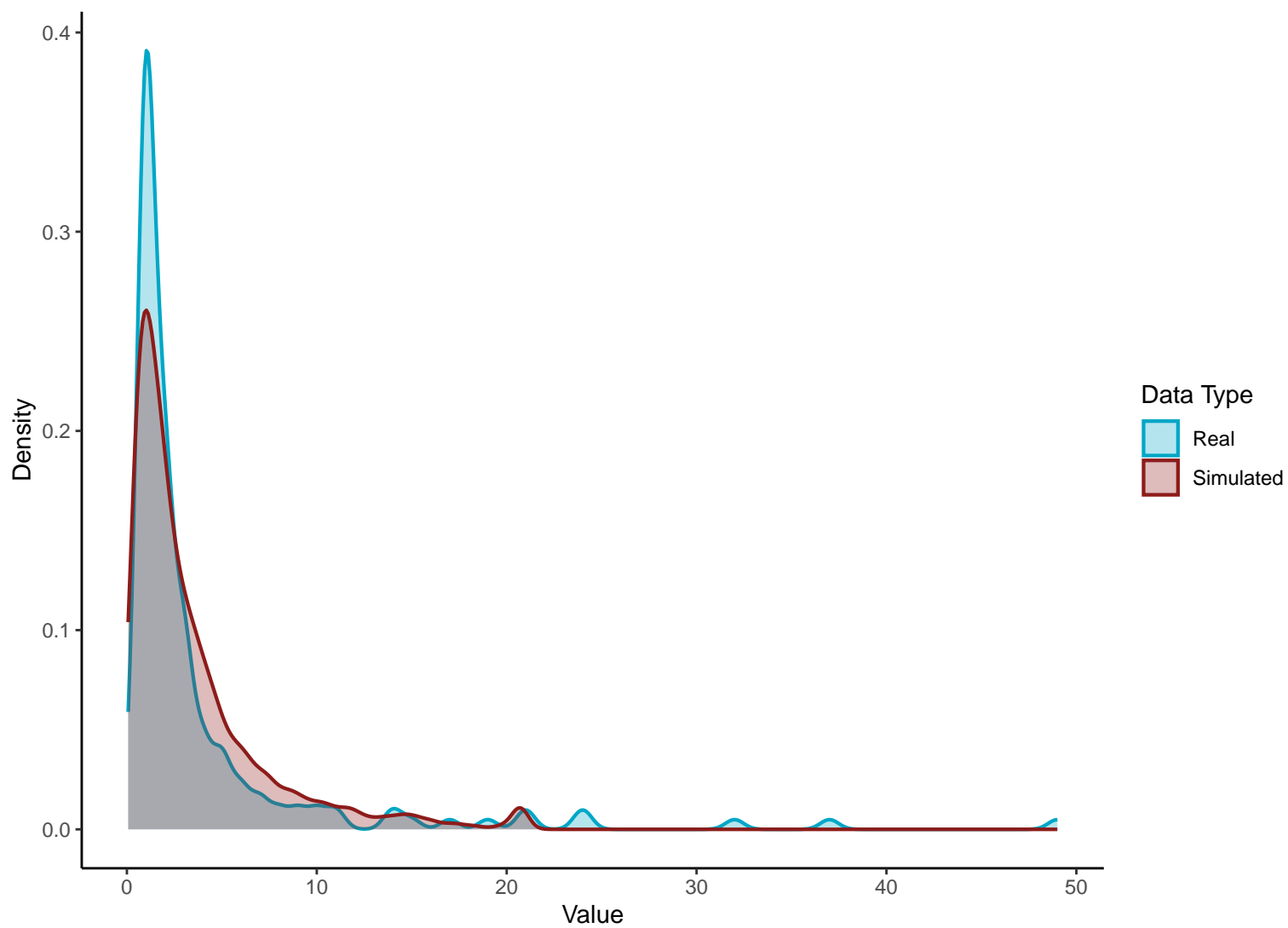
# Catenisphaera



# Prevotellaceae.UGC.004

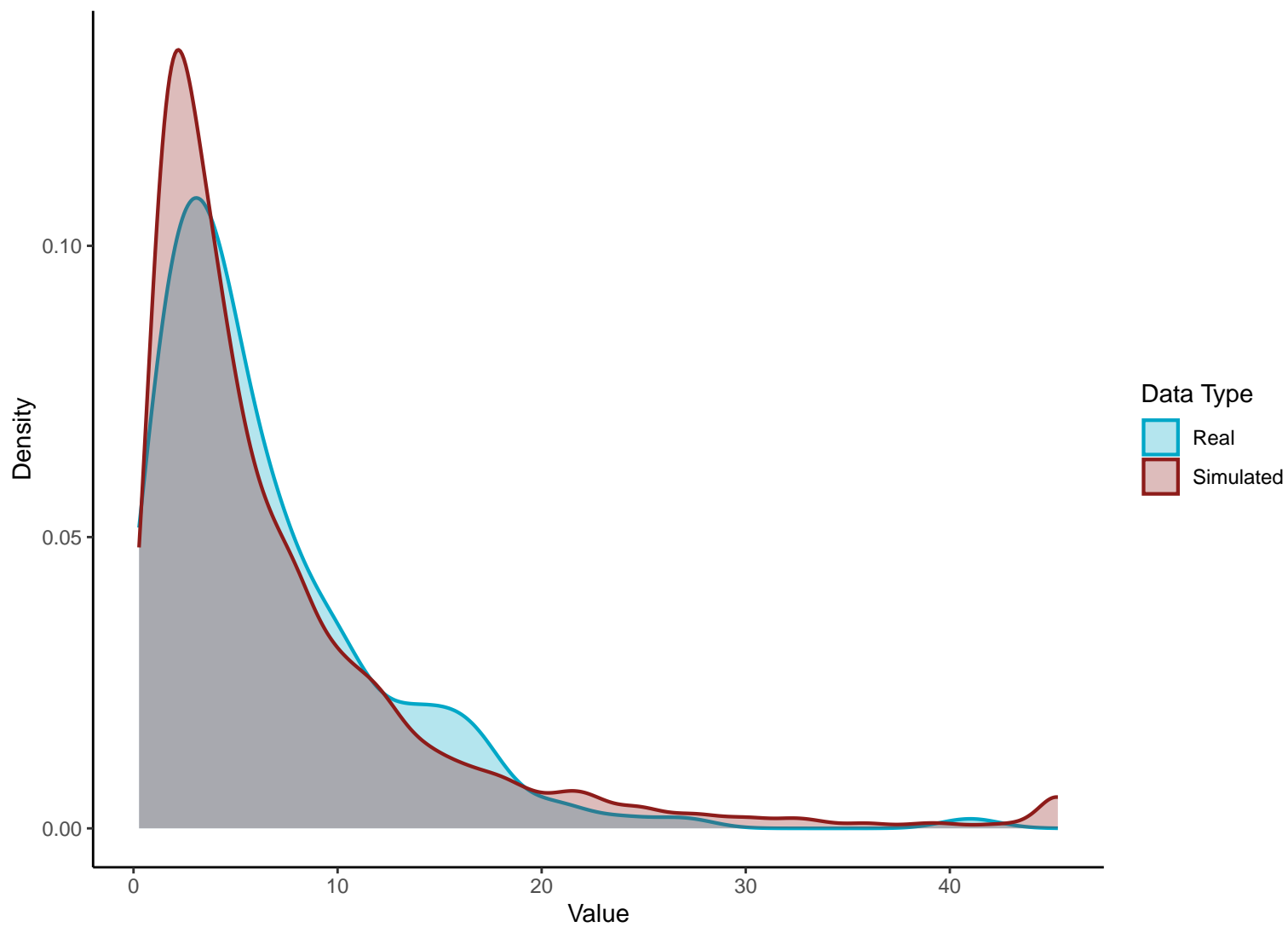


# X.Eubacterium..brachy.group

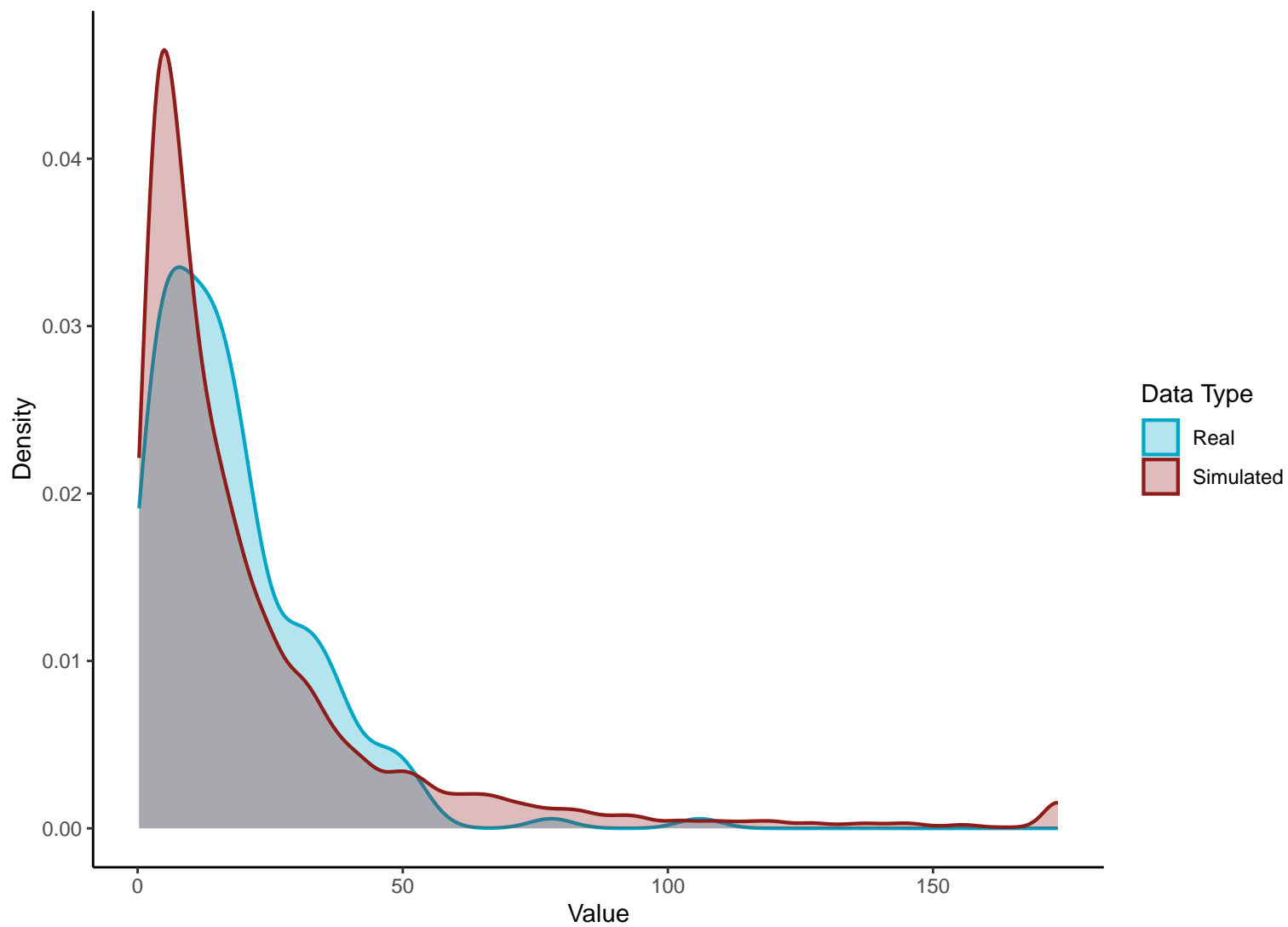




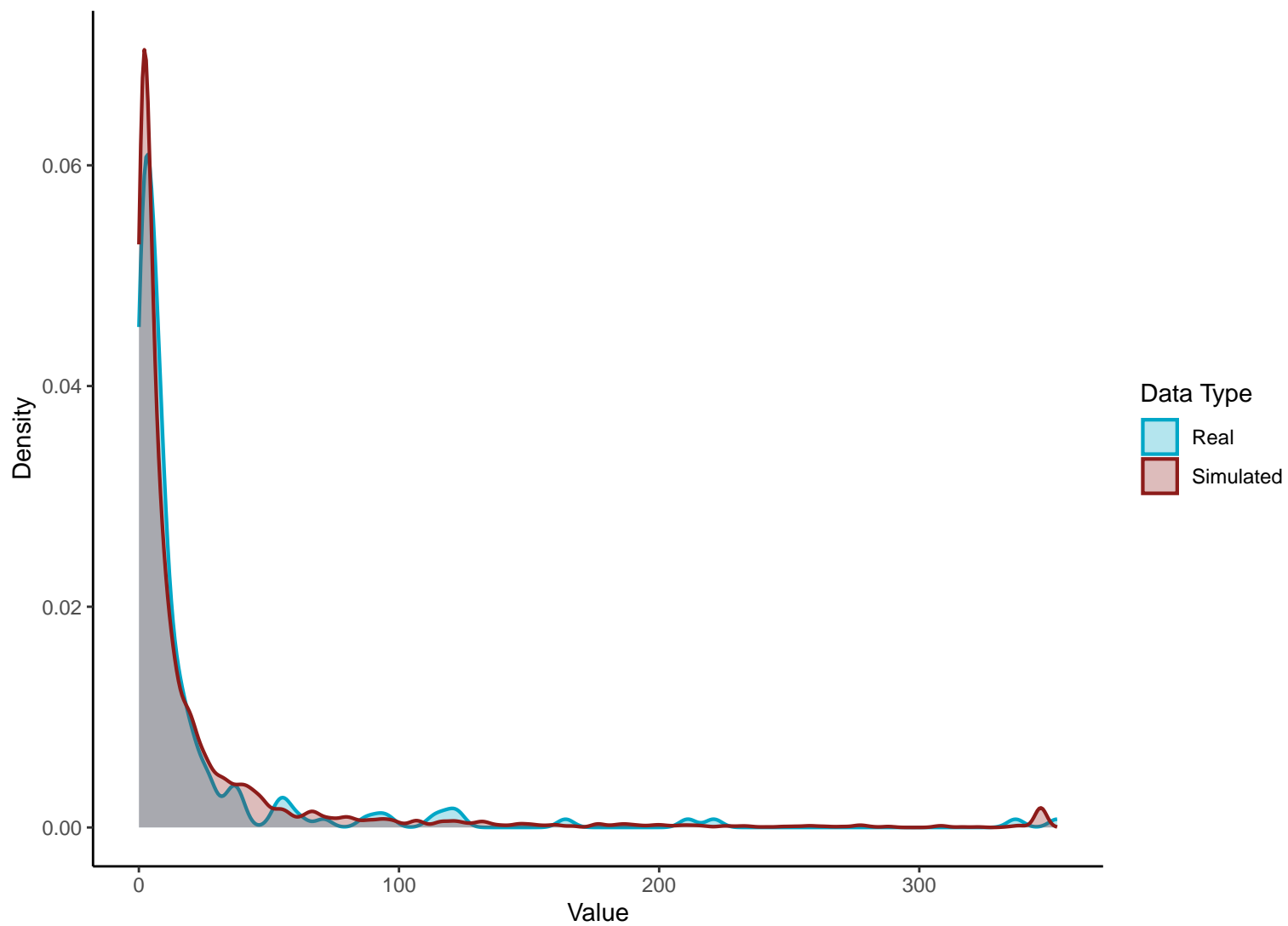
GCA.900066575



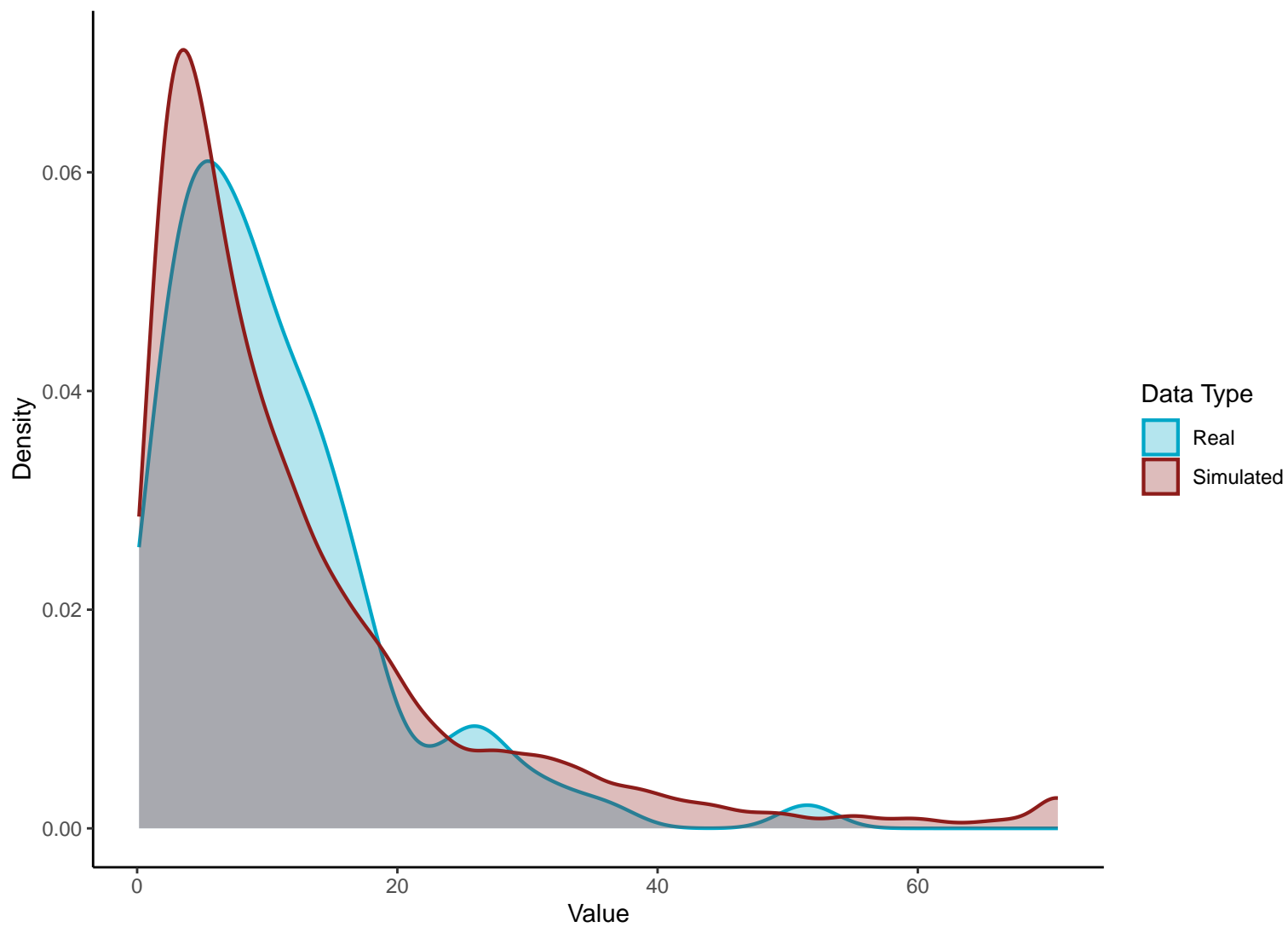
# Lachnospiraceae.UCG.004



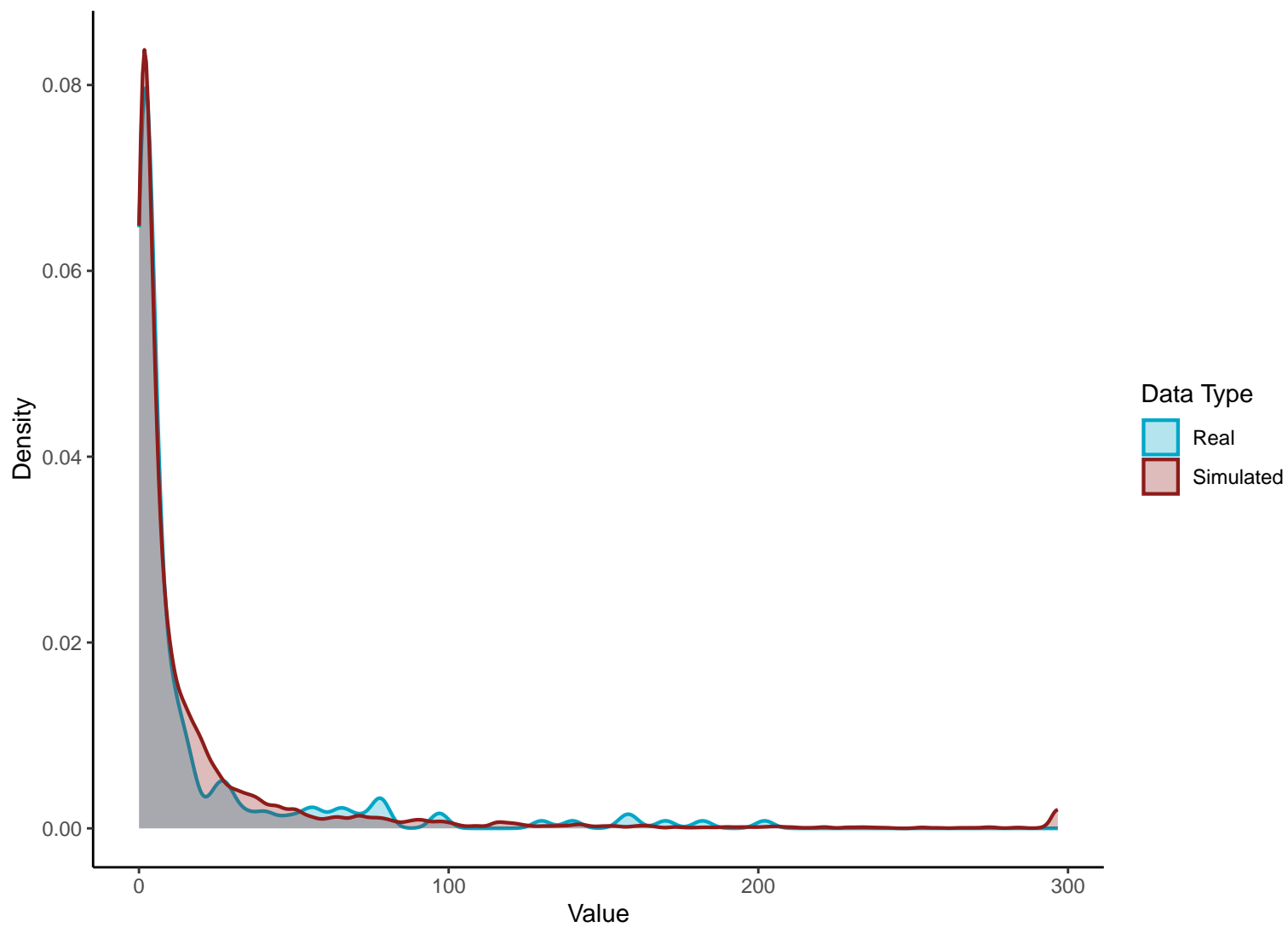
dgA.11.gut.group



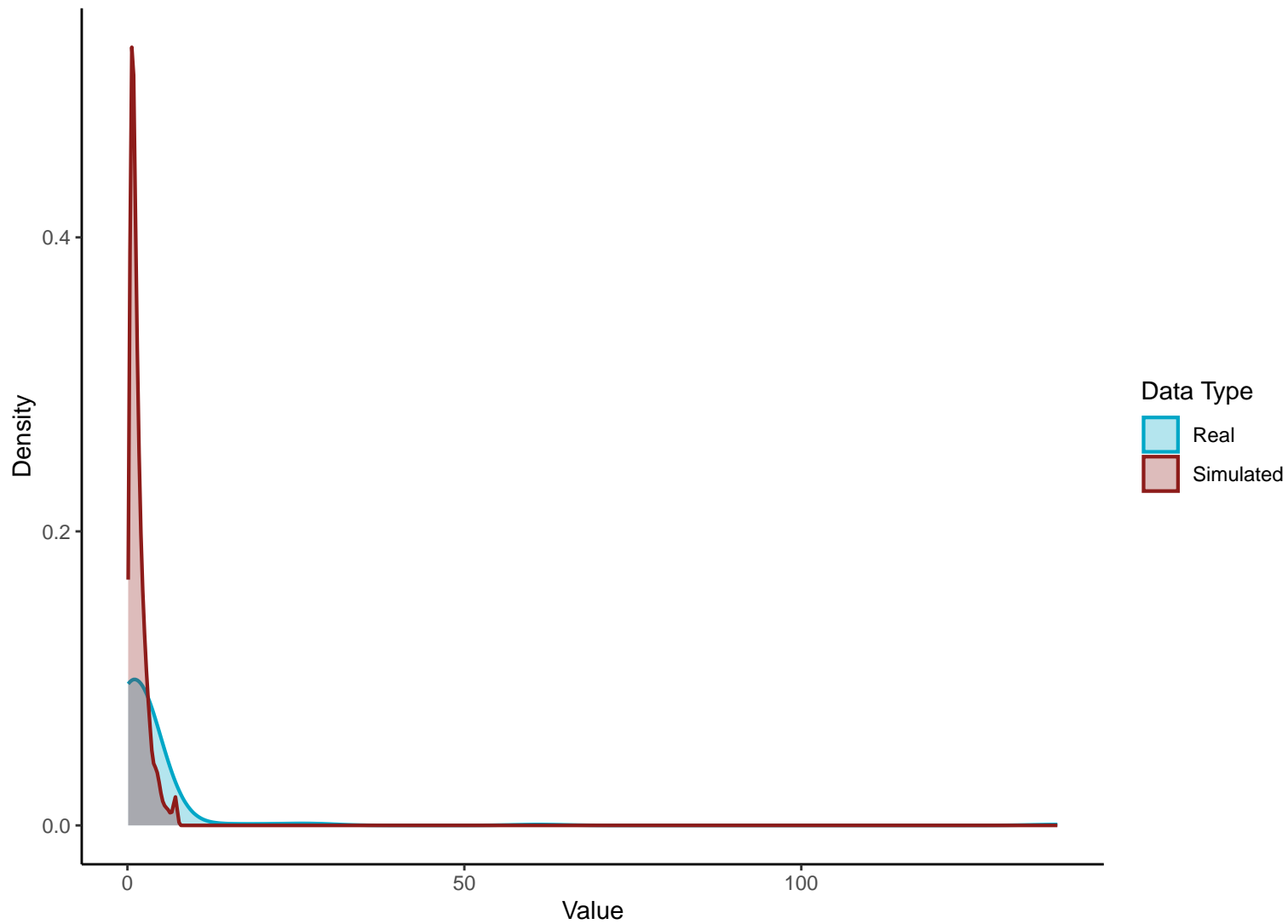
# Erysipelotrichaceae.UGC.006



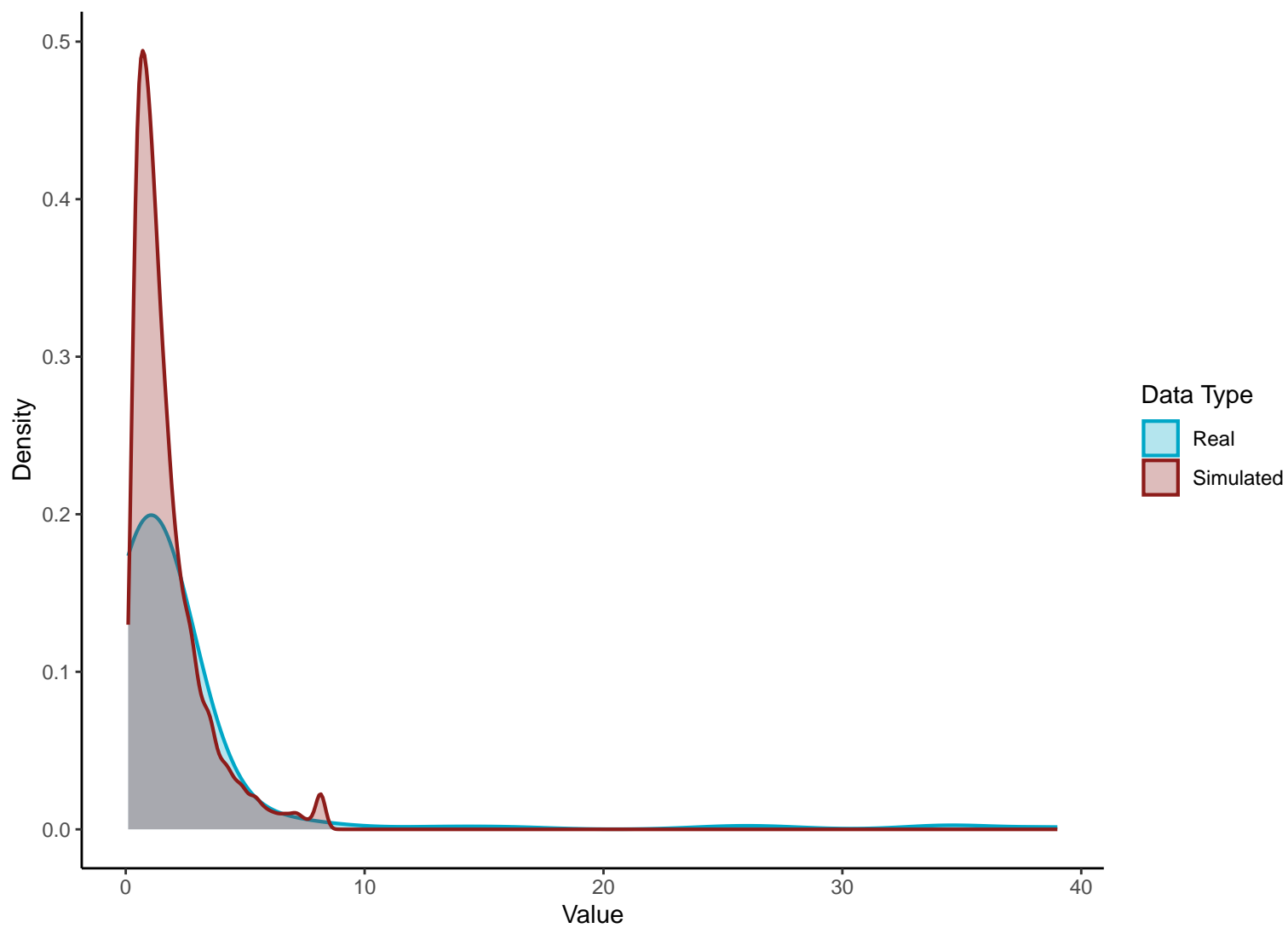
# Erysipelotrichaceae.UGC.003



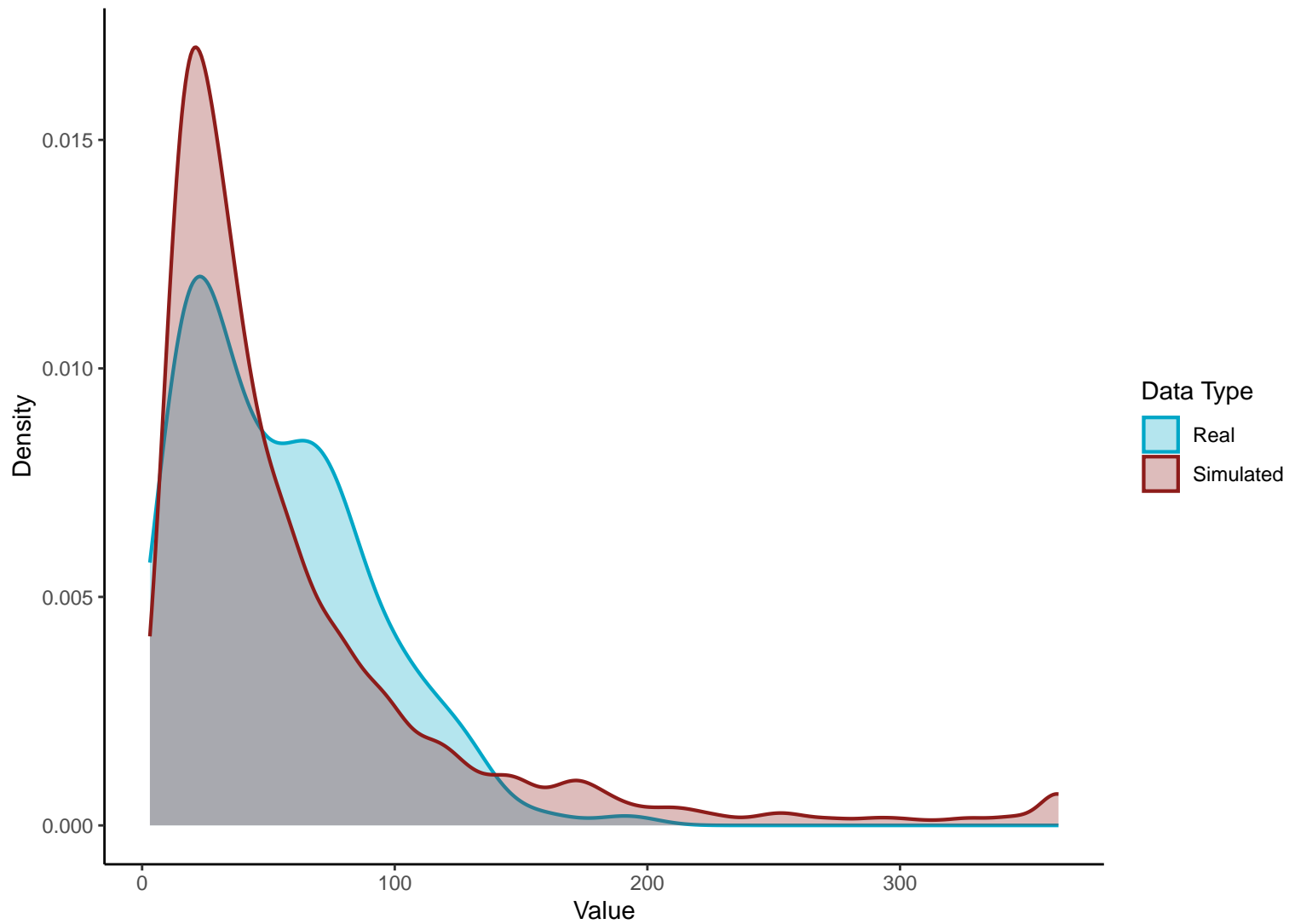
# X.Eubacterium..saphenum.group



# X.Ruminococcus..gnavus.group

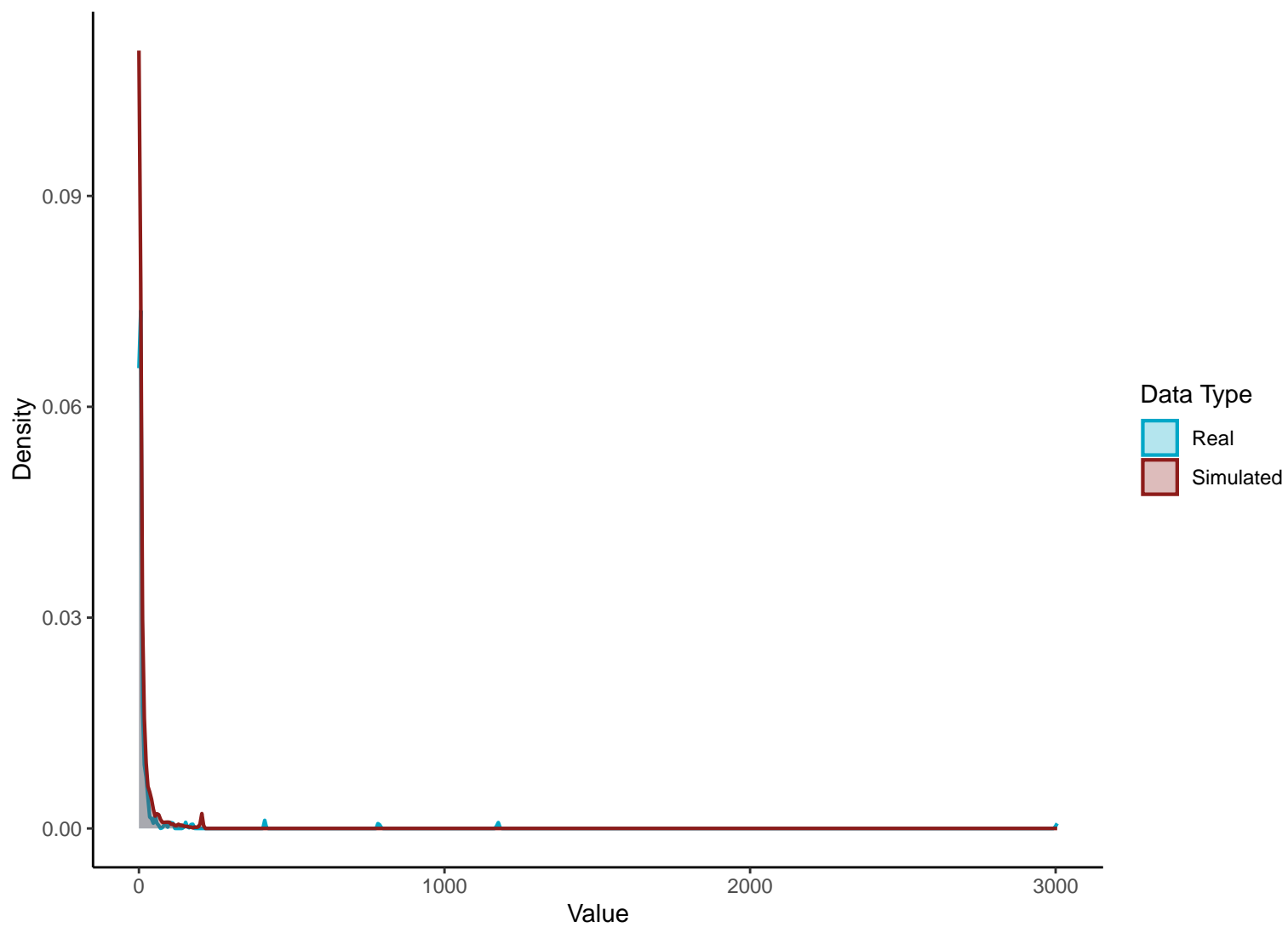


# Fournierella

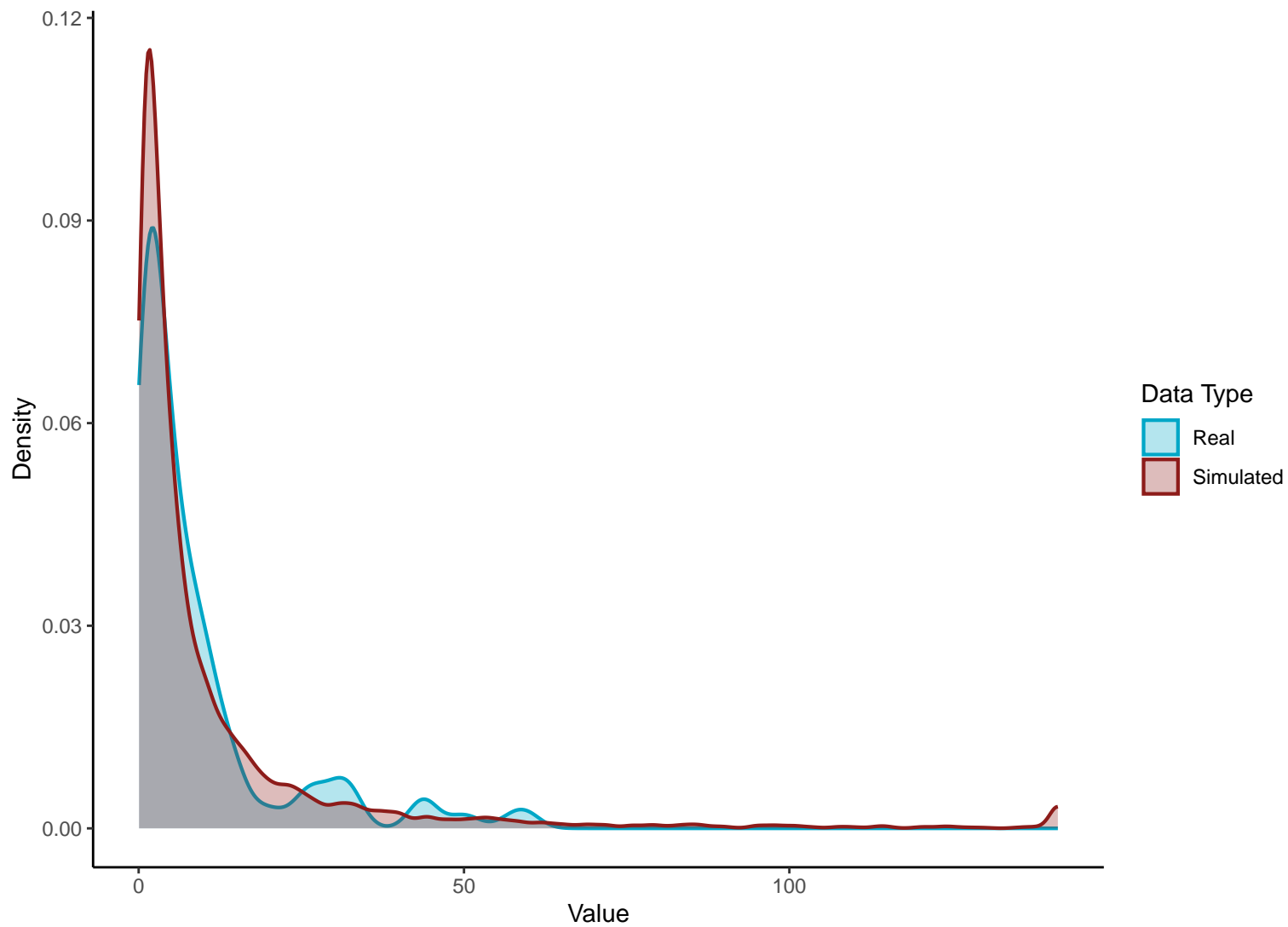




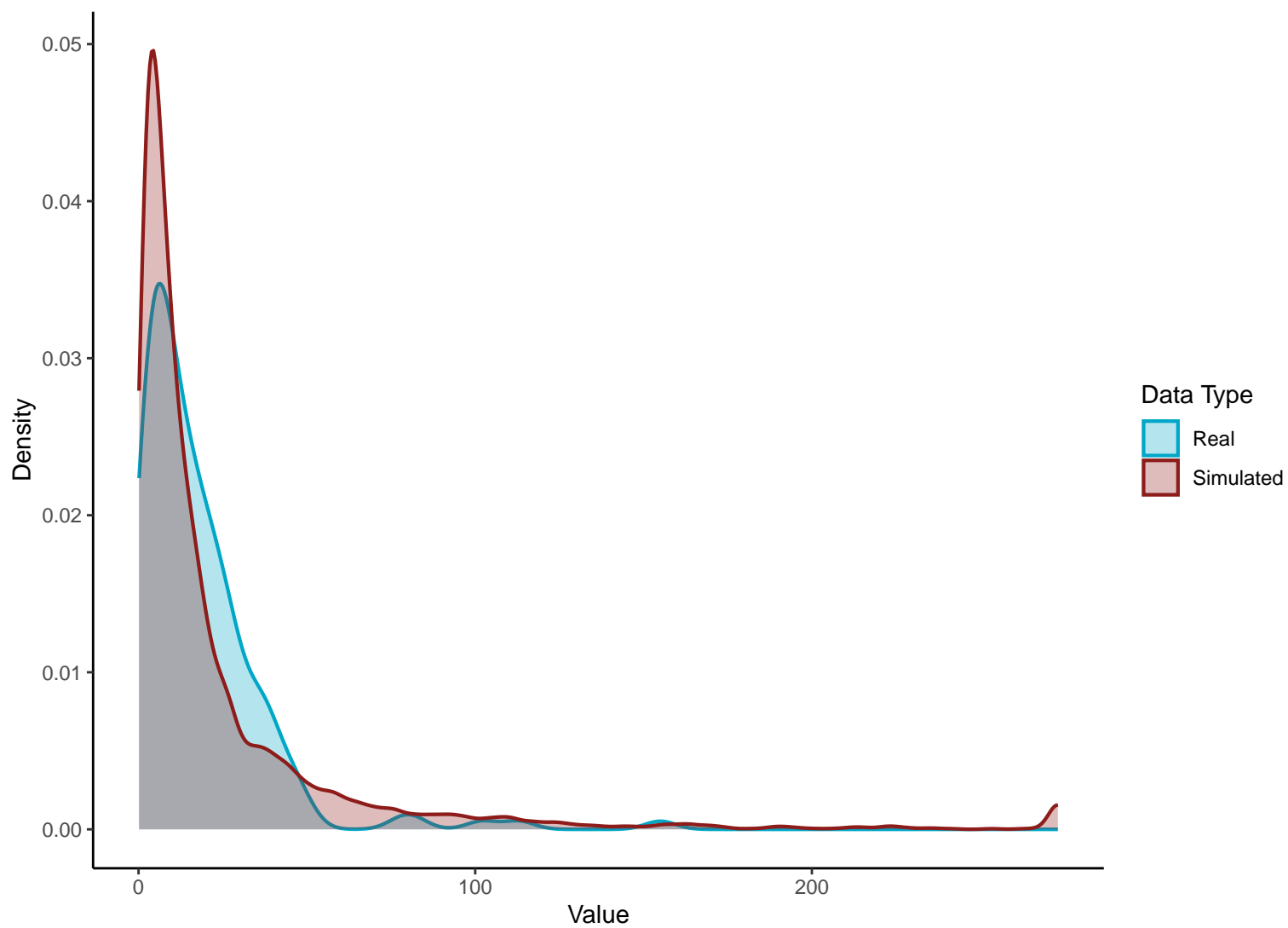
# Escherichia.Shigella



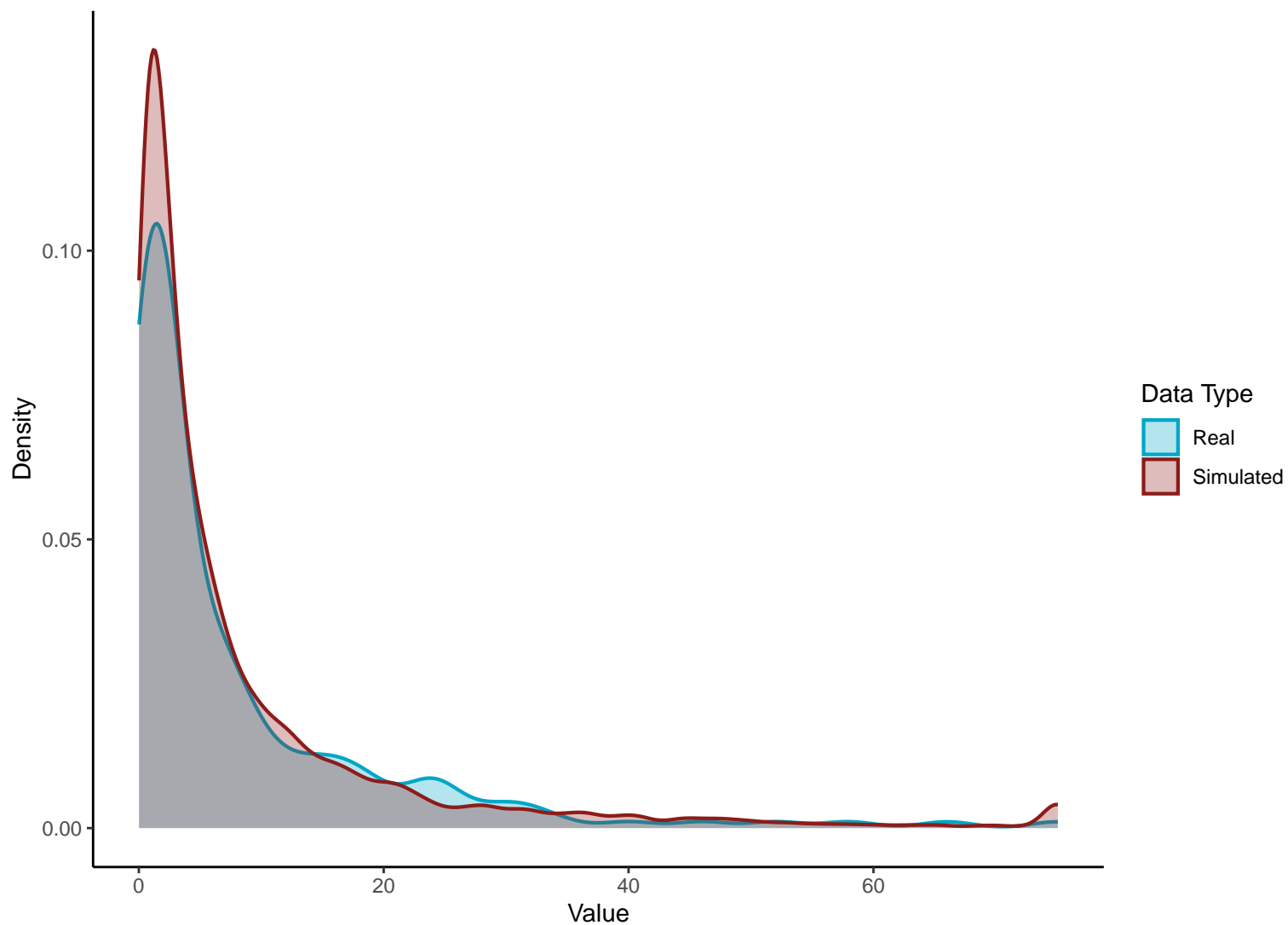
# X.Eubacterium..fissicatena.group



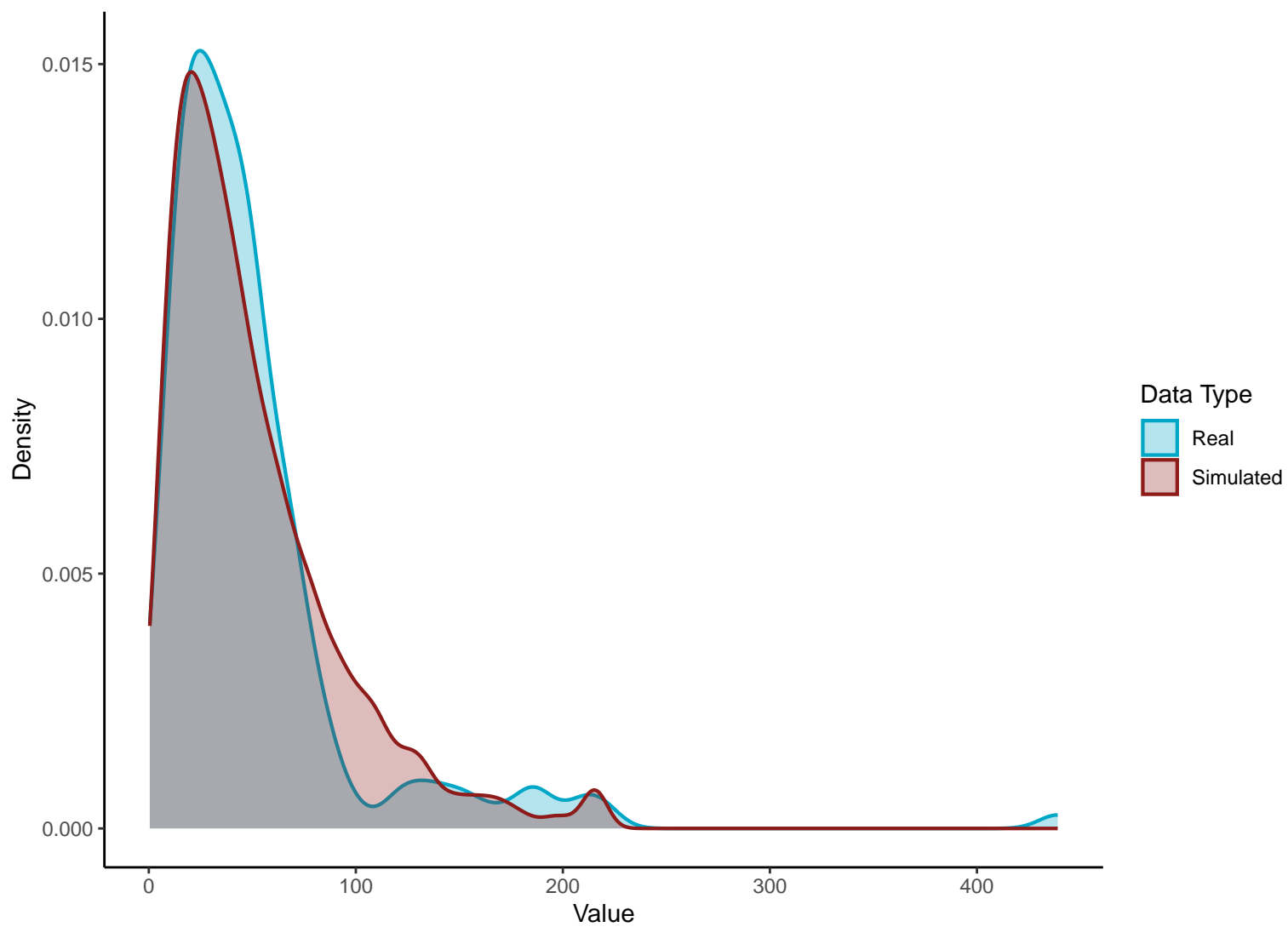
# X.Anaerorhabdus.furcosa.group



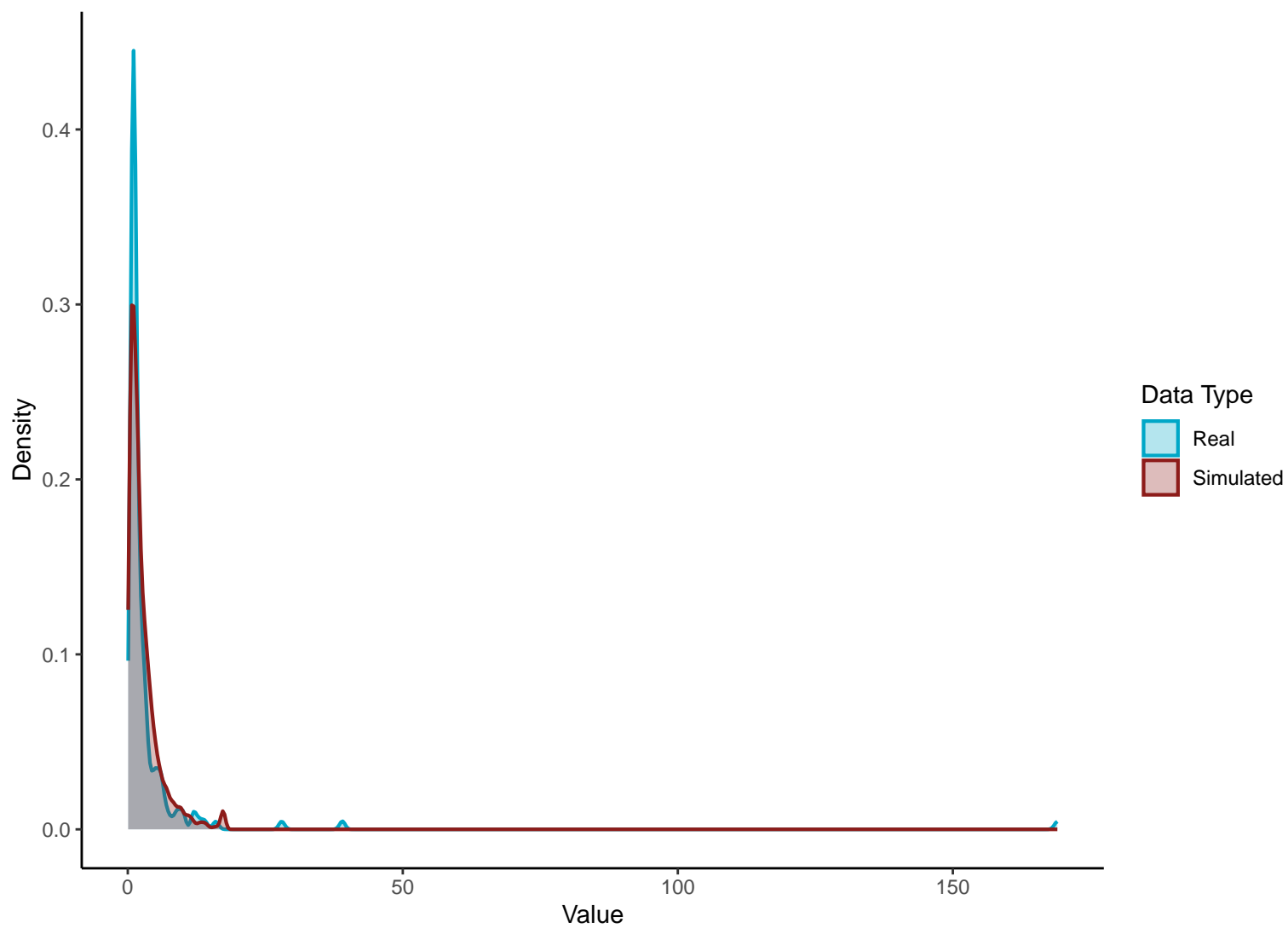
# Lachnospiraceae. UCG.009



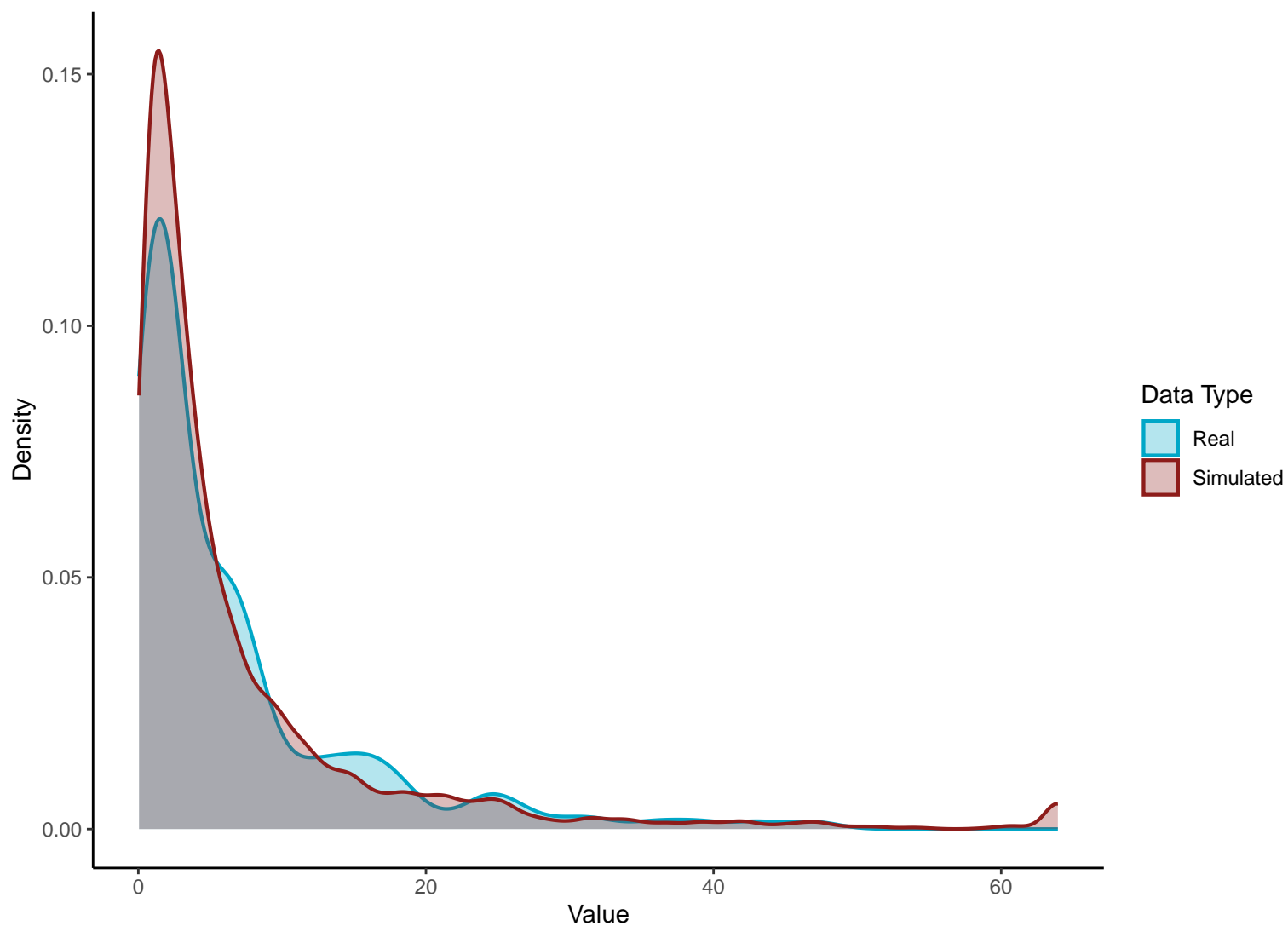
# Paraeggerthella



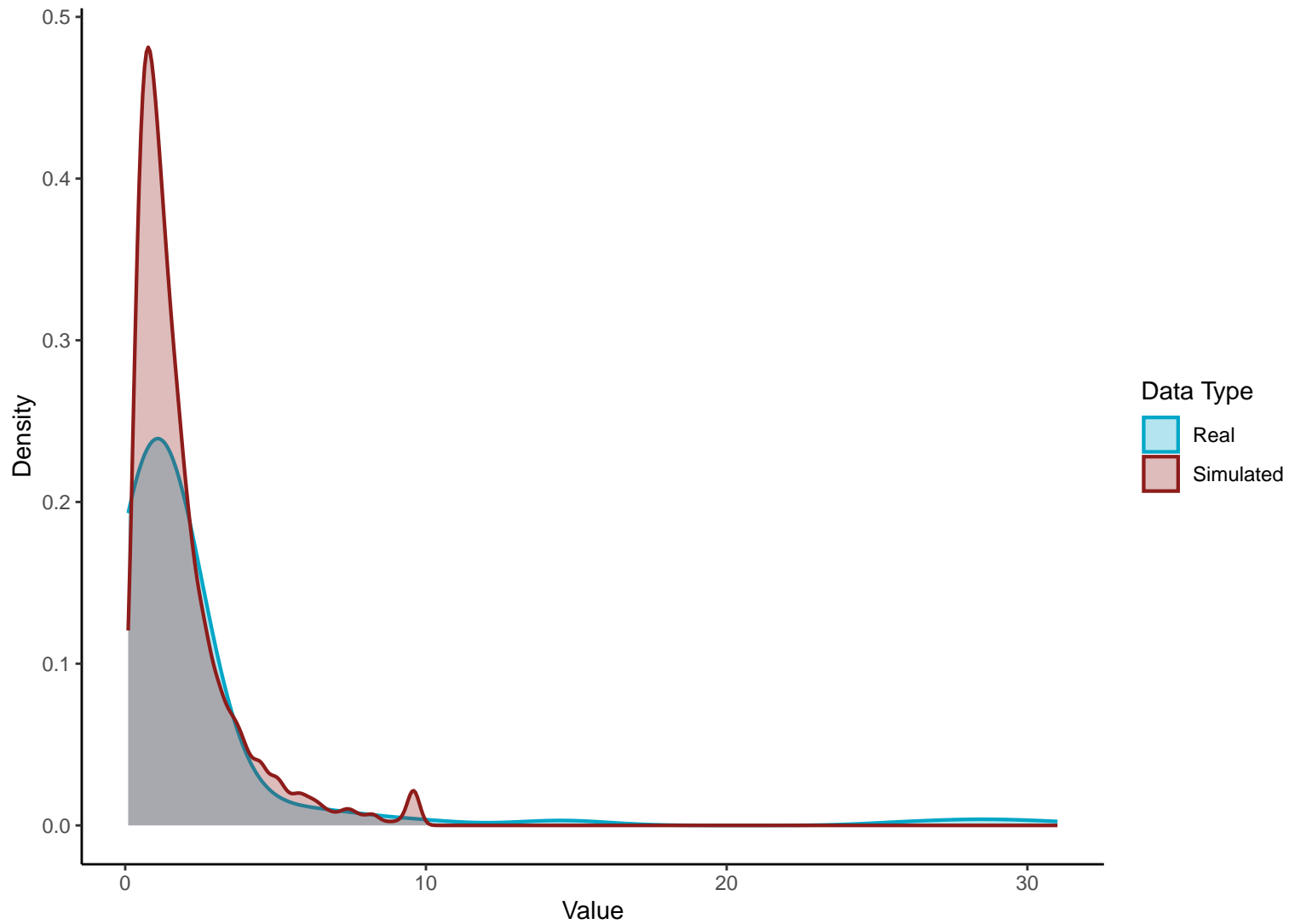
# Selenomonas



# Senegalimassilia

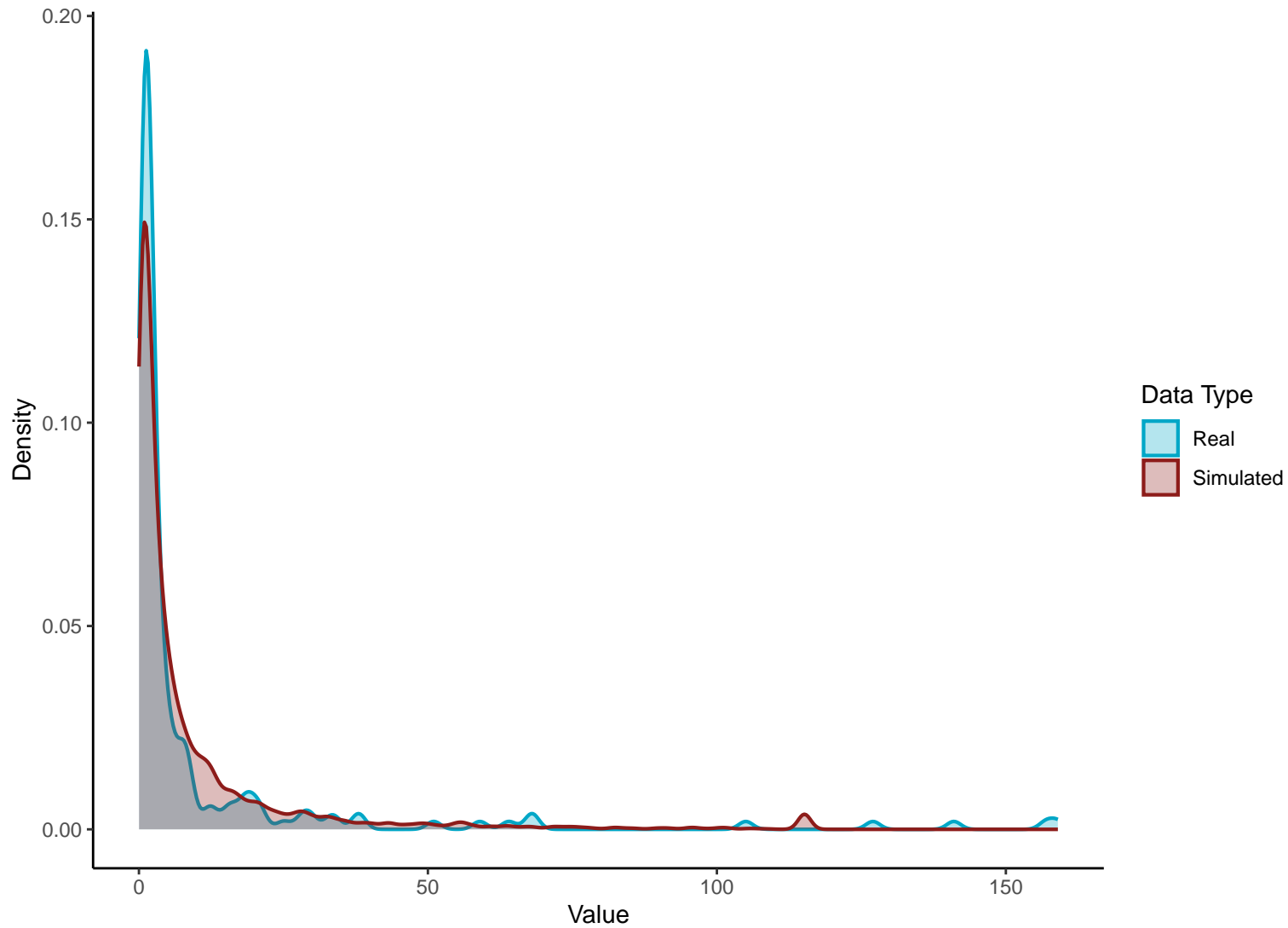


FD2005

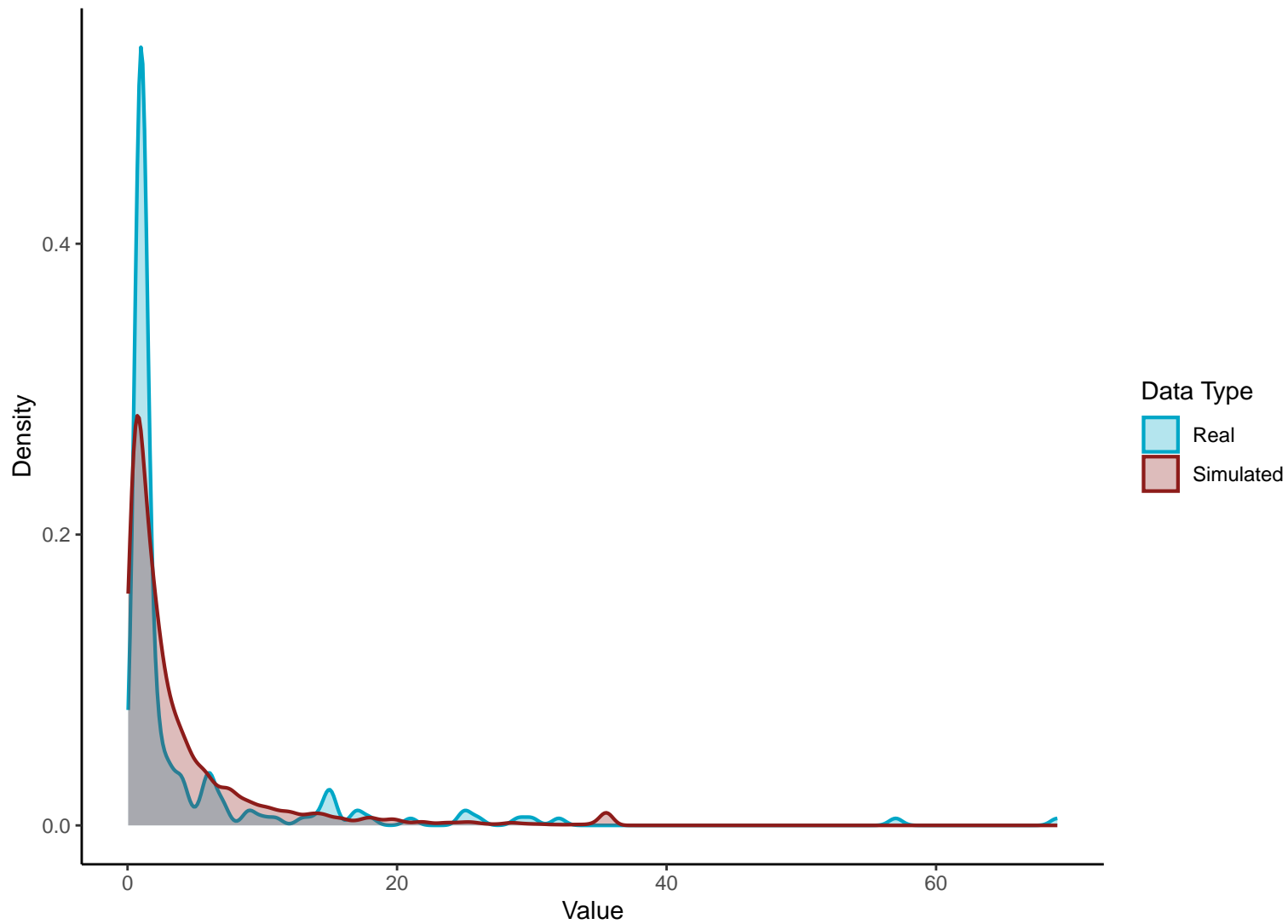




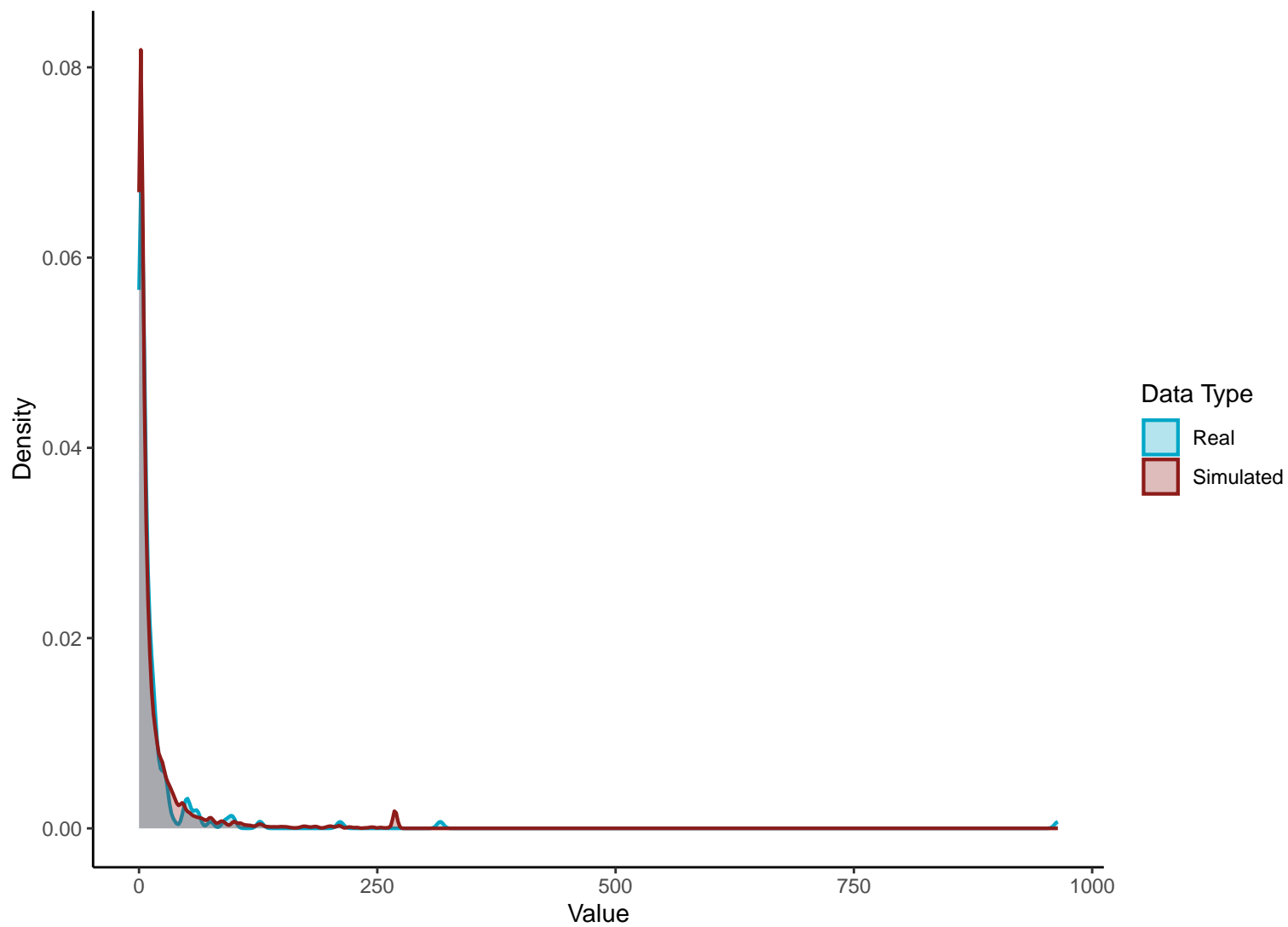
# Veillonella



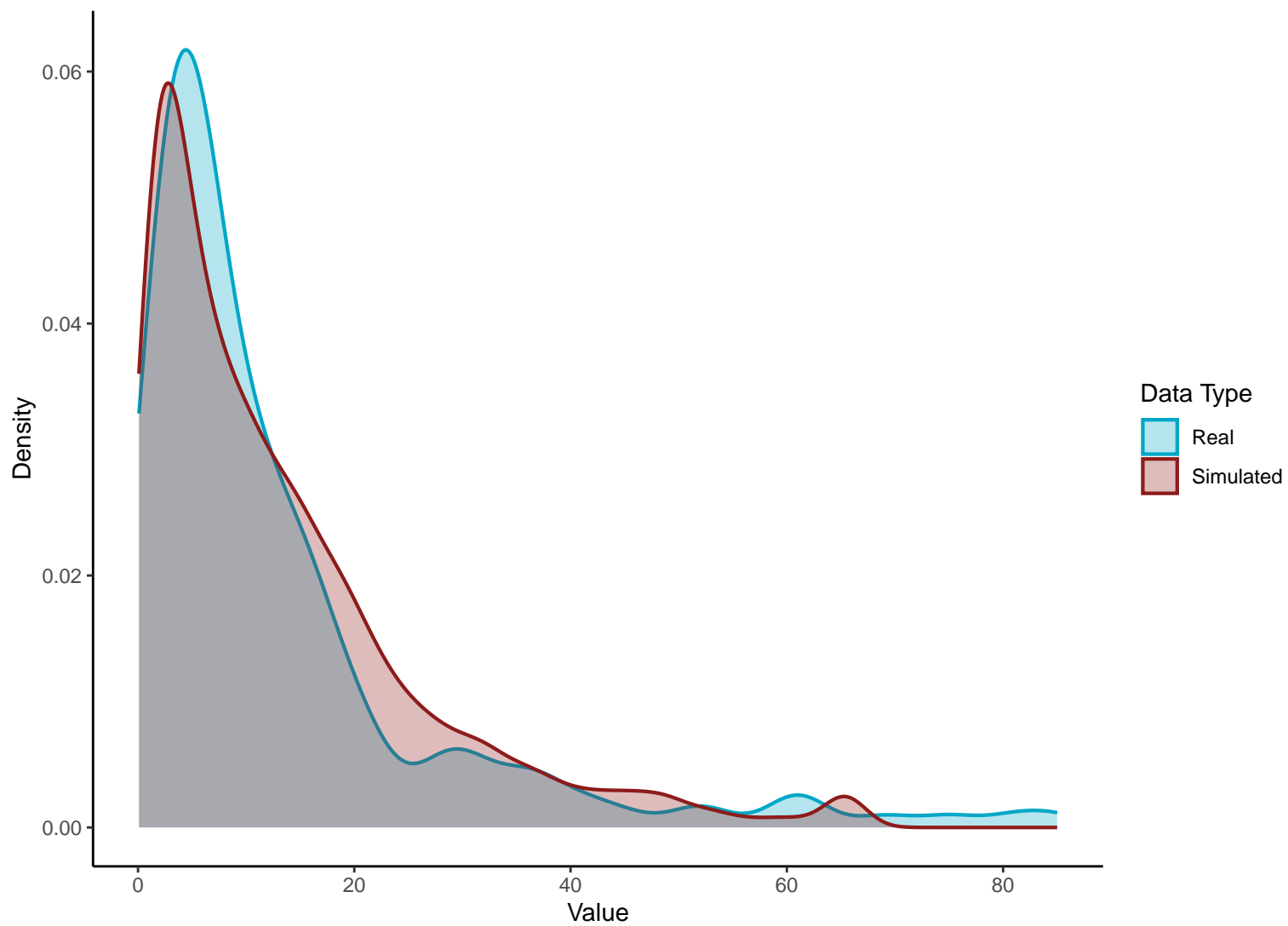
# Clostridium.sensu.stricto.6



CAG.352



CAG.56



# Candidatus.Stoquefichus

