

CORRECTION

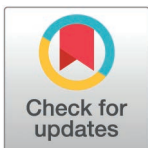
Correction: Bayesian network models to assess antimicrobial resistance patterns of *Streptococcus suis* isolated from swine production systems in the United States between 2014–2021

Ruwini Rupasinghe, Brittany L. Morgan Bustamante, Rebecca C. Robbins, Maria J. Clavijo, Beatriz Martínez-López

The last two authors, Maria J. Clavijo and Beatriz Martínez-López, should be noted as shared co-corresponding authors on this work. Maria J. Clavijo's email address is: mclavijo@iastate.edu.

Reference

1. Rupasinghe R, Morgan Bustamante BL, Robbins RC, Clavijo MJ, Martínez-López B. Bayesian network models to assess antimicrobial resistance patterns of *Streptococcus suis* isolated from swine production systems in the United States between 2014–2021. PLoS Comput Biol. 2026;22(3):e1014117. <https://doi.org/10.1371/journal.pcbi.1014117> PMID: [41886440](https://pubmed.ncbi.nlm.nih.gov/41886440/)



OPEN ACCESS

Citation: Rupasinghe R, Morgan Bustamante BL, Robbins RC, Clavijo MJ, Martínez-López B (2026) Correction: Bayesian network models to assess antimicrobial resistance patterns of *Streptococcus suis* isolated from swine production systems in the United States between 2014–2021. PLoS Comput Biol 22(5): e1014345. <https://doi.org/10.1371/journal.pcbi.1014345>

Published: May 28, 2026

Copyright: © 2026 Rupasinghe et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.