



University of Dundee

Erratum

Lupolova, Nadejda; Dallman, Tim J; Holden, Nicola J; Gally, David L

Published in: Microbial Genomics

DOI:

10.1099/mgen.0.000193

Publication date: 2018

Document Version Publisher's PDF, also known as Version of record

Link to publication in Discovery Research Portal

Citation for published version (APA):

Lupolova, N., Dallman, T. J., Holden, N. J., & Gally, D. L. (2018). Erratum: Patchy promiscuity: machine learning applied to predict the host specificity of Salmonella enterica and Escherichia coli. Microbial Genomics, 4(6). https://doi.org/10.1099/mgen.0.000193

General rights

Copyright and moral rights for the publications made accessible in Discovery Research Portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from Discovery Research Portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain.
 You may freely distribute the URL identifying the publication in the public portal.

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Download date: 19. Oct. 2019

ERRATUM

Lupolova *et al.*, *Microbial Genomics* 2018;4
DOI 10.1099/mgen.0.000193





Erratum: Patchy promiscuity: machine learning applied to predict the host specificity of *Salmonella enterica* and *Escherichia coli*

Nadejda Lupolova, ¹ Tim J. Dallman, ² Nicola J. Holden³ and David L. Gally^{4,*}

Microbial Genomics 2017;3, doi: 10.1099/mgen.0.000135

An error occurred during the publishing process of this article.

There was text inserted in the final paragraph of the Discussion, in the following sentence:

'We consider that machine learning has tremendous potential to interrogate complex seqLineColumnRule IDProbe Message-Node TextNode XpathParent Node Textfatal/var/www/html/_default/resources/microbio/__package/144333/144333. xmlf002block-formatting check: Entire content of title should not be formatted (Tagging Guidelines)Salmonella entericauence datasets and identify genes/sequences associated with host specificity.'

The sentence should read as follows:

'We consider that machine learning has tremendous potential to interrogate complex sequence datasets and identify genes/sequences associated with host specificity.'

The Microbiology Society apologizes for any inconvenience caused.

Received 1 June 2018; Accepted 1 June 2018

Author affiliations: ¹University of Edinburgh, Edinburgh, UK; ²Public Health England, England, UK; ³James Hutton Institute, Dundee, UK; ⁴Division of Immunity and Infection, The Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh EH25 9RG, UK. *Correspondence: David L. Gally, dgally@ed.ac.uk