

Errata for Population Genomics with R

Page xiv: (fifth line from bottom) opportunity \rightsquigarrow opportunity

Page 14: (row describing psmcr) sequantially \rightsquigarrow sequentially

Page 15: (end of caption of Fig. 1.9) selection of on loci. \rightsquigarrow selection on other loci.

Page 17: (fifth line of Sect. 2.1.1) it will be to to extract DNA

Page 28: (in footnote 2) Illumna \rightsquigarrow Illumina (Note: the purchase of PacBio by Illumina has been canceled.)

Page 56: (before the last bloc of R code) the file names \rightsquigarrow the file named

Page 70: (third item in the list near the bottom of the page)
the operation can reversed \rightsquigarrow the operation can be reversed

Page 176: (in the paragraph after the first block of R lines) because of the very predicted

Page 233: (line 10) by(xsel) \rightsquigarrow by(x)

Page 245: (near the end of the first paragraph) the \rightsquigarrow then

Page 303: the scales of the axes of Fig. 9.16 are wrong because of several small bugs in psmcr which have been fixed in version 0.1-2 of this package. Mostly, the axis scales were wrongly multiplied by 10^4 . The corrected figure is shown next page (slightly different because the bootstraps were re-run).

Page 355: Reference 40 was badly formatted; it should be:

[40] Choquet, M., I. Smolina, A. K. S. Dhanasiri et al. 2019. Towards population genomics in non-model species with large genomes: a case study of the marine zooplankton *Calanus finmarchicus*. *Royal Society Open Science* 6:180608.

Page 356: The authors' names of reference 62 were badly formatted; they should be:

[62] Dulin, D., T. J. Cui, J. Cnossen et al. 2015...

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