



ALEX GILSON **RE: Assembly Problems** 1 month ago

Tandem repeat regions present sequence assembly obstacles in most systems, due to the nature of their sequences. Should a region be full of tandem repeats, with shorter read length, differentiating which parts are from the same read/a different part of the same sequence becomes challenging. I found an article from Ole K Torresen et al (2019) that discusses this issue. The authors's main concern for these repeat regions was how they can affect multiple levels of analysis for the regions they reside in, and when not accounted for correctly, can lead to multiple low confidence reads/sequences that yield low confidence proteins in an area that may simply have a few repeats within it.

Tørresen, O. K., Star, B., Mier, P., Andrade-Navarro, M. A., Bateman, A., Jarnot, P., Gruca, A., Grynberg, M., Kajava, A. V., Promponas, V. J., Anisimova, M., Jakobsen, K. S., & Linke, D. (2019). Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. Nucleic acids research, 47(21), 10994-11006. https://doi.org/10.1093/nar/gkz841

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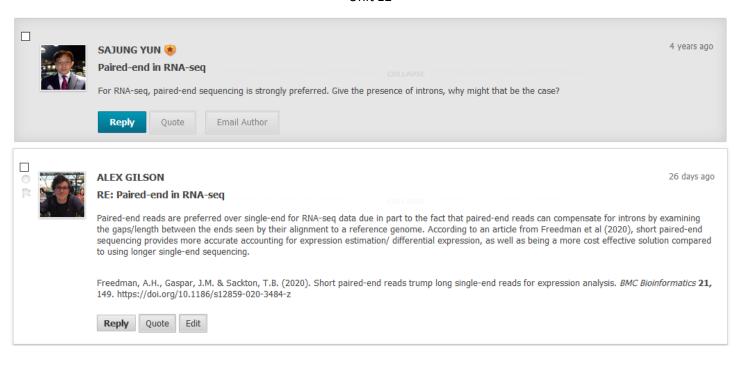


ALEX GILSON RE: Epigenetics 1 month ago

Epigenetics is the study of biological mechanisms of inheritance, involving the control of gene expression that does is not directly associated with the underlying DNA sequences of the genome, and these actions that are also reversible (Kovalchuk and Kovalchuk, 2012). Comparatively, geneitcs is a more broad category that is the study of the mechanism of inheritance in general and particularly interested in genes (Kovalchuk and Kovalchuk, 2012). The difference between the two areas of study lie in the fact that epigenetics is concerned with things such as histone modifications and chemical associations with DNA, rather than looking at its sequence.

Igor Kobalchuk & Olga Kovalchuk. (2012). "Epigenetics in Health and Disease". Pearson Education, Inc. Upper Saddle Rive, NJ 07458. ISBN 978-0-13-259708-1.

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