**Human Genomics**

---

## CORRECTION                                                                 Open Access

# Correction to: An application of slow feature analysis to the genetic sequences of coronaviruses and influenza viruses

Anastasios A. Tsonis[1,2*], Geli Wang[3], Lvyi Zhang[3], Wenxu Lu[3], Aristotle Kayafas[4] and Katia Del Rio-Tsonis[4*]

**Correction to: Hum Genomics 15, 26 (2021)**
**https://doi.org/10.1186/s40246-021-00327-2**

Following publication of the original article [1], the authors would like to change all the word DNA to nucleotide or genetic.

The viruses that we analysed have an RNA genome, however the sequences obtained from the repository (NCBI) are reported as DNA. In this manuscript a neutral term "nucleotide" sequence(s) or "genetic" structure should be used instead of DNA sequences or DNA structure

The original article [1] has been updated.

**Author details**
[1]Department of Mathematical Sciences, Atmospheric Sciences Group, University of Wisconsin-Milwaukee, Milwaukee, WI 53201, USA. [2]Hydrologic Research Center, San Diego, CA 92127, USA. [3]Key Laboratory of Middle Atmosphere and Global Environment Observation (LAGEO), Institute of Atmospheric Physics, Chinese Academy of Sciences, Beijing 100029, China. [4]Department of Biology and Center for Visual Sciences, Miami University, Oxford, OH 45056, USA.

**Reference**
1.   Tsonis AA, et al. An application of slow feature analysis to the genetic sequences of coronaviruses and influenza viruses. Hum Genomics. 2021;15: 26.

---

* Correspondence: aatsonis@uwm.edu; delriok@miamioh.edu
[1]Department of Mathematical Sciences, Atmospheric Sciences Group, University of Wisconsin-Milwaukee, Milwaukee, WI 53201, USA
[4]Department of Biology and Center for Visual Sciences, Miami University, Oxford, OH 45056, USA
Full list of author information is available at the end of the article