



## News

### Blyth Institute Paper Highlighted in *Mathematics Magazine*

The standard notation for higher-order differentials (the Leibniz notation) does not allow differentials to be used in an algebraic manner (multiply, dividing, canceling, etc.). Last year, a Blyth Institute researcher published a new notation for differentials that allow them to be algebraically manipulable (Bartlett and Khurshudyan, 2019).

Recently, this paper was highlighted in *Mathematics Magazine*, a publication of the Mathematics Association of America (Campbell and Rosenthal, 2019), in their “Reviews” section. The review validated the overall the results of the paper, saying, “the authors make a strong case for a clear and honest notation that facilitates working with differentials.” While the reviewers agreed with the fact that the new notation makes working with differentials more straightforward, they thought that, for teaching, it “is probably just as confusing for students as the shorthand expression.”

### Blyth Institute Researcher Publishes Paper on Active Information in Biology

Blyth Institute director Jonathan Bartlett published a new paper earlier this year on using the concept of Active Information in biology. Active Information was originally developed for evolution simulations, such as *Avida* and the *Ev* system, to measure how much information the simulation writers added to the system (Dembski and Marks II, 2009). Essentially, Active Information was developed as a way of measuring “cheating” on the part of programmers trying to demonstrate natural selection with code.

In “Measuring Active Information in Biological Systems,” Bartlett decided to turn the metric onto living organisms, to provide a mechanism to see how much their evolution was actually governed by Darwinian mechanisms and how much of it was guided by mechanisms of variation built in to the organisms themselves (Bartlett, 2020). While it has

been known for a while that there are mutational mechanisms within genomes, it takes a lot of time and money to tease them out. Essentially, this measurement can be used to determine whether a mutational mechanism is worth investigating, or if it should be just considered “spontaneous.” If an organism’s mutations displays significant active information for a selection pressure, this is good evidence that there is a mechanism worth discovering that is producing those mutations.

A followup note on this paper by the author is available in this issue.

### New Era of Research in Active Information

In addition to the applications of active information to biology in the previous news item, there has been a renewed interest in active information from other parties as well. So far, two other active information papers by Daniel Andrés Díaz-Pachón and Robert J Marks II have been published in the journal *BIO-Complexity*. The first one extends active information into unbounded domains (Díaz-Pachón and Marks II, 2020b). The second one uses active information to compare neutral and selective evolution (Díaz-Pachón and Marks II, 2020a).

Additionally, active information has shown to be a useful concept generally in statistical investigations. A trio of authors from the biostatistics and engineering departments of University of Miami published a paper describing the usage of active information in hypothesis testing and its relationship to type-I errors (Díaz-Pachón, Sáenz, and Rao, 2020). The same group also developed a general method of statistical mode-hunting using active information (Díaz-Pachón, Sáenz, Rao, and Dazard, 2019) which has been utilized in data mining software such as PRIMsrc (Dazard et al., 2015).

## Blyth Institute Assists with N95 Mask Shortage

Most people are aware that the COVID-19 pandemic has caused a shortage in N95 masks. Private citizens have stepped into the breach by 3D printing various types of PPE equipment on home 3D printers. The Blyth Institute has been helping out by helping individuals who are printing masks increase their printing capacity.

We would like to thank everyone who is doing the printing for their hard work and efforts in this time. We would especially like to thank the front-line medical workers for whom this equipment is made. Thank you for standing in the gap for us all.

Díaz-Pachón, D A, J P Sáenz, and J S Rao (2020). “Hypothesis testing with active information”. In: *Statistics and Probability Letters* 161. DOI: 10.1016/j.spl.2020.108742.

Díaz-Pachón, D A, J P Sáenz, J S Rao, and J Dazard (2019). In: *Applied Stochastic Models in Business and Industry* 35.2, pp. 1–18. DOI: 10.1002/asmb.2430.

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## References

Bartlett, J (2020). “Measuring Active Information in Biological Systems”. In: *Communications of the Blyth Institute* 2020.2, pp. 1–11. DOI: doi:10.5048/BIO-C.2020.2.

Bartlett, J and A Zh Khurshudyan (2019). “Extending the Algebraic Manipulability of Differentials”. In: *Dynamics of Continuous, Discrete and Impulsive Systems, Series A: Mathematical Analysis* 26.3, pp. 217–230.

Campbell, P J and E S Rosenthal (2019). “Reviews”. In: *Mathematics Magazine* 92.5, pp. 396–397. DOI: 10.1080/0025570X.2019.1673628.

Dazard, J et al. (2015). “R package PRIMsrc: Bump Hunting by Patient Rule Induction Method for Survival, Regression, and Classification”. In: *JSM Proceedings, Section for Statistical Programmers and Analysts*, pp. 650–664.

Dembski, W A and R J Marks II (2009). “Conservation of Information in Search: Measuring the Cost of Success”. In: *IEEE Transactions on Systems, Man and Cybernetics A, Systems & Humans* 5.5, pp. 1051–1061. DOI: 10.1109/TSMCA.2009.2025027.

Díaz-Pachón, D A and R J Marks II (2020a). “Active Information Requirements for Fixation on the Wright-Fisher Model of Population Genetics”. In: *BIO-Complexity* 2020.4, pp. 1–6.

Díaz-Pachón, D A and R J Marks II (2020b). “Generalized Active Information: Extensions to Unbounded Domains”. In: *BIO-Complexity* 2020.3, pp. 1–6.