



CoCo Seminar Series Spring 2022

[Extra CoCo Seminar]

A Complexity Science Approach Towards Improving Human Health

Dr. Rion Brattig Correia

**Visiting Research Scientist, Instituto Gulbenkian
de Ciência, Portugal / SSIE Department,
Binghamton University**



Friday April 22, 2022 10:00-11:00am EDT
Hybrid (EB-T1 & Zoom; meeting link available on
<http://coco.binghamton.edu/>)

Human health is a multi-level complex adaptive system of interacting chemical components at the micro, and whole individuals at the macro level. In this talk, I will provide an overlook of my research agenda towards understanding this system, all the way from biochemical regulation and systems biology, to individual, social, and population-level behaviors. I study this system primarily with methods from complexity science and its subfields of data and network science; supported by inherently heterogeneous data, including Boolean networks, genomics, electronic health records, and even social media. I will detail this agenda focusing on two of our latest projects. First, on the use of electronic health records to study the drug interaction prescription phenomenon. Analyzing electronic health records from Blumenau (Brazil), Indianapolis (USA), and Catalonia (Spain), accounting for more than 6M patients followed for over a decade, we found that roughly in every eight patients administered at least one drug interaction, reaching up to 20% of Catalonian patients. Worrysome we also found gender and age biases, such as elderly patients with a worst-than-random chance of administering a drug interaction. Second, I will detail our group's translational and transdisciplinary approach to human diseases. Using comparative transcriptomics and network science we have uncovered an ancient gene expression program shared between male germ cells from evolutionarily-distant animal species. Disrupting this program, via the silencing of 920 conserved germ cell identity genes in *Drosophila*, we demonstrate its functional requirement for a broad set of cellular processes that are essential for male fertility. Among these, we identified 164 new genes never before shown to be required for spermatogenesis in any species. Most importantly, we found 3 new genetic causes of human male infertility, shared by species that have diverged more than 600 million years ago. Our method represents the first application of cross-species network biology to medical genetics and can be easily leveraged in the context of other human diseases.

Rion Brattig Correia is an interdisciplinary complexity scientist who has a Ph.D. in the Complex Network & Systems track of Informatics from the School of Informatics, Computing, & Engineering at Indiana University; and a M.Sc. in Business Management, and a B.Sc. in Management Information Systems, from Universidade Regional de Blumenau, Brazil. He held a postdoctoral position at Instituto Gulbenkian de Ciência (IGC), a life sciences institute in Oeiras, Portugal. He is currently the CEO of a data science tech startup and a visiting research scientist at both IGC and Binghamton University. His research interests include complex systems, network science, computational biology, computational intelligence and digital medicine.

For more information, contact Hiroki Sayama (sayama@binghamton.edu).

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