**From the Single Cell Of Origin Prediction (SCOOP) to the**

**Biofilm Data and Information Discovery System (Biofilm-DIDS)**

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**Abstract:**

The Single Cell Of Origin Predictor (SCOOP) framework is an experimental and computational framework for the identification and validation of target molecules for potential therapeutics in oncology. SCOOP development started 2 years ago with a focus on Atypical Teratoid Rhabdoid Tumor (ATRT), a very aggressive central nervous system tumor that comprises 10% of pediatric brain tumors. This aggressive tumor remains a challenge in the field of pediatric neuro-oncology and newer therapeutic approaches are desperately needed to increase survival for the young patients. At the current stage, SCOOP consist into 3 wet lab and protocols (3D spheroid, FACs, PCR), and 4 computational modules (Systems Biology, Machine Learning, Bioinformatics workflow). This framework will allow in the near future the prediction of the drug (4sc) response to the ATRT tumor, by integrating spatiotemporal cells information and systems biology using computational tools. Our Bioinformatics Tool Discovery System (Bio-TDS, biotds.org) was developed to assist researches researchers in retrieving the most applicable analytic tools by allowing them to formulate their questions as free text. One of the primary components of the Bio-TDS is the datamining, ontology, and natural language processing workflow for annotation, curation, query processing, and evaluation. We are working with SDSMT on a project that would integrate Bio-TDS and the SCOOP framework into aBiofilms Data and Information Discovery system (Biofilm-DIDS). Biofilm-DIDS will be a Data Driven Material-Biofilm Discovery Framework that will collect and combine disparate big datasets pertinent to biology and material scientist, use artificial intelligence (computer vision and machine learning approaches) to analyze and predict gene responses and biofilm phenotypes impacted by nanoscopic surficial properties.



**Biography:**

Dr. Etienne Z. Gnimpieba is a faculty Research Assistant Professor of bioinformatics in the University of South Dakota (USD) Biomedical Engineering program and Educational Director of the SDBRIN (South Dakota Biomedical Research Infrastructure Network). As faculty, Dr. Gnimpieba is involved in multiple research activities, including computational systems biology, and advanced cyber infrastructure development for data analysis for bioscience and biomedicine knowledge discovery. He has published articles in Nucleic Acid Research, Molecular Cancer Research (AACR), Molecular Biosystems journal (RSC Publishing), Faseb journal, and several conference proceedings related to computer science usage in Bioscience and Biomedicine. Before Dr. Gnimpieba joined USD, he received a PhD in biotechnology and bioinformatics, an MS in computational engineering in Informatics and Mathematics for Integrative Biology, and an MS in computer science specialized on systems modeling, artificial intelligence, and human-machine interface. He is currently a data science Advisor at INANOVATE Inc., a biotechnology company specializing in therapy and diagnosis systems development, where he is developing new predictive systems for cancer and related disease diagnoses, using data science tools.

**When: Tuesday, February 19, 2019 at 4:00 pm**

**Where: EP252**