The central dogma of molecular biology: Investigating student conceptions about transcription


Genetics is fundamental for biology literacy, yet it is one of the biology disciplines most challenging for students. The central dogma explains how genetic information flows in biological systems and is necessary to understand gene expression and regulation; but evidence shows that first-year biology students do not have a clear model of what genes are and how they are expressed. Multiple-choice tests are a commonly used assessment instruments to evaluate student knowledge at the beginning of a biology course. However, multiple choice tests do not provide information about reasoning flaws or reveal the heterogeneity of student thinking, which can be revealed by students writing. The Automated Analysis of Constructed Response (AACR) Research Group combines linguistic and statistical analyses to build models that allow the computerized analysis of students’ writing to predict expert scoring. Our research group created a series of three constructed response (CR) questions based on one item from the Genetic Concept Assessment to explore students’ understanding of the central dogma. Our results, after analyzing over 3,000 written responses, not only corroborate that students struggle to understand the Central Dogma but also provide greater insight into their reasoning and misconceptions than do multiple choice assessments. A noteworthy result in our study is that of the three processes involved in the central dogma -- replication, transcription, and translation -- transcription seems to be the most challenging for students to understand. After conducting interviews with 19 students about these questions, we hypothesized that the conceptual difficulty students have with this process is because they do not understand why transcription of DNA into mRNA is necessary for protein synthesis. To investigate this hypothesis, we designed a CR question where students were asked to explain why they thought transcription was necessary. In this talk we will discuss two main topics: 1) how text analysis enhances our understanding of students learning difficulties by highlighting students’ alternative conceptions; and 2) how the lack of understanding of the role of mRNA in protein synthesis represents a learning obstacle to students’ understanding transcription.

This is a proposed paper to the 7th Annual Biology Education Research Symposium, during the 2015 NABT Professional Development Conference. The talk follows the traditional format of 15 minutes for presentation and 5-10 minutes for questions. The proposal submission deadline is on June 15, 2015 and acceptance or denial will be notified in early July, 2015. Because all presenters are required to provide an electronic manuscript for distribution through the Proceedings, this presentation will also result in a publication.
**Postdoc overall research plan:** I have been a research Associate at the Automated Analysis of Constructed Response (AACR) research group for 9 months. In our research group we investigate computerized analysis of students’ written responses to constructed response (CR) questions in STEM, particularly in Biology. Our questions focus on big ideas that are important and/or challenging for students to learn. Using CR assessments allows students to express their knowledge in their own words, which provides instructors greater insight into their students’ understanding. The tools developed by AACR make feasible the use of written assessments in large enrollment classes, which are a necessary step in the process of reforming instruction, especially in introductory classes. I am broadly interested in better understanding learning difficulties in Genetics, and in particular in creating a learning progression scheme for teaching gene expression and regulation at the college level, which is not currently available. To this end, I am investigating students’ responses to the same questions at different levels (science vs non-science majors, introductory vs. upper division courses) on different topics in Genetics related to gene expression and regulation.

**Technology behind the work (if new or unusual in the field):** The AACR Research Group combines linguistic and statistical analyses to build models that allow the computerized analysis of students’ writing to predict expert scoring. Our innovative approach was recognized by SPPS Inc. in 2007, when our research group received the SPSS Insight Awards in Academic and Scientific Research. More recently, the National Science Foundation has awarded the AACR project over $6M in research grants for creating a national network for automated analysis of constructed response assessments to support our contributions towards improving STEM education research.

**Impact for the participant:** As biology is the main focus of our research, the National Association of Biology Teacher Conference is the best audience to present and discuss our finding, disseminate our work, and create future collaborations. Our research has not been previously presented in this Conference. At an individual level, NABT is an ideal place for professional development and networking, to meet with colleagues not only from the US but also from around the world, and share experiences and expertise in biology and life science education. This will also allow me to network with potential employers who may hire me after I have completed my post-doctoral research.

**Travel plan:** The travel award will be used to help cover the expenses to attend the 2015 Professional Development Conference of the National Association of Biology Teachers and give an oral presentation in the Biology Research Education Symposium. This Conference will take place in Providence, RI, between November 11-14 2015. (http://www.nabt.org/websites/institution/index.php?p=10 ). The cost of registration is $274 before July 31st. Lodging will be circa $170/night plus taxes (~$850 plus taxes).