

## Learning Genetics on the Fly: Interrelating Three Conceptual Models in Genetics (Poster)

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### Abstract

Rapid advance in the field of genetics and development of new genetic tools led to understanding of the molecular mechanisms underlying genetic phenomena. This new understanding changes the nature and complexity of the domain of modern genetics. Many indications point out difficulties students have in understanding this field (Freidenreich et al., 2011; Lewis and Kattmann, 2004; Marbach-Ad and Stav, 2000; Thörne and Gericke, 2014). According to Stewart, Cartier, and Passmore (2005) genetic literacy is characterized as understanding of three interrelated conceptual models. The first model is the genetic model, which focuses mostly on classical genetics. The second model is the meiotic model which explains the cellular basis for the transfer of genetic information from one generation to the next. The third model is the molecular model which explains the molecular mechanisms by which genes affect traits. As Stewart et al. (2005) noted, genetic literacy involves not only understanding each of the three models, but also integrating them to generate coherent and comprehensive explanations of genetic phenomena. Prior research has shown that even with instruction, students have difficulty connecting the three models (Freidenreich et al., 2011; Stewart and Dale, 1990). In this study we present the design principles of a computational learning and teaching environment that we developed towards this end and the learning outcomes of 10th grade students who learned modern genetics using this environment.

We designed a computational learning and teaching environment, entitled "Learning genetics on the fly" (<https://stwww1.weizmann.ac.il/fly/>, Haskel-Ittah and Yarden, 2017). This environment presents genetic phenomena as the combination of all three conceptual models. This environment stresses molecular and meiotic aspects of genes, such as protein function and chromosomal location, in the context of a given genetic phenomenon. Since the involvement of invisible particles in the mechanisms leading to genetic phenomena was suggested by Marbach-Ad (2001) to raise difficulties, we made use of authentic visualizations. The learning environment is based on multiple external representations (Ainsworth, 2006) and scaffolds movement between the three models allowing students to potentially develop more connected understandings of genetic concepts and phenomena.

By analyzing students' concept maps we show that following the use of this environment student could form more connections between concepts that are related to classical genetics and those related to modern genetics. Our results suggest that activities that target both classical and modern genetics may assist students in forming these connections.

**Keywords:** Genetics, protein, computational learning environment, visualizations.

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