Do Alternative Instructional Approaches Result in Different Learning Progressions?

Moraima Castro-Faix, Rutgers University, moraimac@rutgers.edu
Amber Todd, Wright State University, amber.todd@wright.edu
William Romine, Wright State University, william.romine@wright.edu,
Ravit Golan Duncan, Rutgers University, ravit.duncan@gse.rutgers.edu

Abstract: Learning progressions (LPs) are the hypothetical pathways that students may take as they learn about core ideas in a domain. LPs take a developmental approach to learning and assume that there are constraints that drive the learning paths. The question then is: how strong are the constraints of the learning process? We report on a comparison of two distinct instructional interventions informed by the same genetics progression that were implemented with introductory biology students (10^{th} and 11^{th} grades). The interventions targeted the ideas in the LP but differ in the: (1) sequencing of instruction, (2) focus phenomena, and (3) activities. To determine the learning paths for each instructional intervention we used causal model search and path analyses to explore relationships within and between these ideas. Our findings may indicate that the two instructional contexts result in maps that have both differences and similarities providing further evidence about the strengths of conjectures in LPs.

Introduction

Learning progressions (LPs) are hypothetical pathways that students may take as they develop more sophisticated ways of reasoning about important ideas and practices in a domain (Alonzo and Gotwals, 2012;Duncan & Hmelo-Silver, 2009). LPs begin with a consideration of students' prior knowledge and initial understandings to define the lowest level (lower anchor) of the LP. The uppermost level of the LP explicates target understandings (upper anchor) in the domain and is based on analyses of the domain and societal expectations (what students should know by the end of a specific grade or grade band). Between the lower and upper anchors of the LP are descriptions of intermediate levels of growing sophistication. The intermediate levels are derived from research on student thinking and learning in the domain. Movement along the progression depends on carefully designed instruction (Corcoran, Mosher and Rogat, 2009).

In essence, LPs take a developmental approach to learning with the underlying assumption that there are developmental constraints and affordances that drive the learning path. We use "developmental" in the sense that acquisition of new knowledge depends on existing knowledge (Wiser, Smith, & Doubler, 2012); the developmental constraints in this sense are not necessarily related to age. From a cognitive perspective, the question is: how strong are the constraints of the learning process? It may be that constraints are relatively loose and many different learning paths exist between the same start and end points. Theories of learning that take a more situated, knowledge-in-pieces, perspective (diSessa, 1988; Lave & Wenger, 1991) suggest that this may be the case. Alternatively, it may be that the constraints are strong and that there are very few possible paths that are most effective and efficient in promoting learning. Research on second language acquisition has shown that learning of certain grammatical features follows a "natural order" (Krashen, 1981 p. 10) suggesting that, at least in some domains, there are strong constraints on learning and a predictable path. If the developmental constraints are strong, then LP scholarship can help us identify such constraints and inform curriculum and instruction. However, the constraints are weak, and there are numerous possible paths, it is not clear whether LPs can contribute to the development of a best–practice instructional approach. Understanding the nature of the constraints on learning and how these impact learning paths is a currently unresolved issue of interest in LP research (Duncan & Gotwals, 2015; Sevian & Talanquer, 2014).

One way to explore this issue is to develop different instructional interventions informed by the same progression; that is, both interventions target the same core ideas but differ in how and when (sequence) they are taught. If the developmental constraints are strong one would expect that learning will follow the same path regardless of the specific instructional intervention. However, learning may be less efficient with an instructional intervention that is not well aligned with the hypothesized trajectory (levels of the progression). Learning under the conditions of an intervention that is better aligned with the LP will be more efficient. This is akin to building a complex Lego structure using one of two sets of instructions. One set, the "aligned" set provides instructions that call for the pieces in the "right" order; the other "non-aligned" set calls for the same pieces but in an order that is not ideal. In both cases the Lego structures will eventually be built, but it will be a much more troubled and cumbersome process with the non-aligned instructions. Note that both sets of instructions involve the same

building blocks and the final structure is the same, but the order of assembling the blocks is different. A radically different conceptualization is the assumption that the learning constraints are very soft or non-existent, and in that case the two instructional interventions will lead to very different outcomes. In our analogy this means that the despite having the same building blocks the final Lego structures themselves will be entirely different. Therefore, having an experimental design with two different instructional approaches can potentially provide evidence that can differentially support one of the two hypotheses (strong versus weak constraints).

Here we report on such a comparison in the context of two distinct instructional interventions informed by the same genetic progression that was developed and revised by the authors (Shea & Duncan, 2013; Duncan, Rogat & Yarden, 2009; Todd & Kenyon, 2015). Both interventions were implemented with students learning introductory biology at the high school level (10^{th} and 11^{th} grades). The interventions targeted the same core ideas in the LP but the order of addressing these ideas, the focus phenomena, and the specific instructional activities were different. Students learning in both instructional conditions were assessed with written assessments that used ordered multiple-choice items (Briggs & Alonzo, 2009; Briggs et al., 2006).

To determine the learning paths in each condition we used causal model search and path analysis to explore relationships within and between these ideas, and how the modeled relationships fit with the data. The following two research questions guided our analyses: 1) How do two different instructional interventions developed using the same progression influence high school students' core ideas and the connections between ideas in an LP? 2) What do the progression maps suggest about the nature of the constraints on learning? We next describe the genetics learning progression that informed the design of the instructional interventions in the two conditions and then describe the two interventions.

Theoretical framework: The genetics LP

The genetics progression was developed using the framework of genetics literacy by Stewart, Cartier and Passmore (2005) to identify core genetics ideas. The framework for genetics literacy depicts three interrelated conceptual models: (a) the inheritance model, which explains the probabilistic patterns of correlation between genes and traits; (b) the meiotic model, which explains the cellular processes that allow for the transfer of genetic information from one generation to the next; and (c) the molecular model, which explains the cellular and molecular mechanisms by which genes bring about their physical effects within an individual. The genetics LP describes learning for grades 5-10 and includes eight core ideas, or constructs, grounded in the three conceptual models described above (Duncan et al., 2009). In this paper we focused our analyses on two constructs that capture ideas from the molecular model—constructs B and C; and two constructs that capture ideas from the inheritance and meiotic models—constructs E and F, respectively.

To simplify matters, we refer to constructs B and C as the molecular genetics constructs. Construct B is about the nature of the genetic information. It embodies the idea that genes are instructions that encode the structure of proteins. Construct C, in turn, deals with the roles of proteins in genetic phenomena. Proteins are essentially the mediating mechanism between genes and traits; they carry out a variety biological functions such as: channels, structural support, sending messages within the cell, etc. Protein function impacts the structure and function of cells and those in turn impact the structure and functions of tissues and organs. When proteins malfunction (due to a mutation in the genetic instructions for them) this may alter the function of the cells, tissue, organ, and whole organism.

We refer to constructs E and F as the classical genetics constructs. Construct E describes how genes are passed from one generation to the next though sex cells (sperm and egg). It involves understanding the equal contribution of genetic material from both parents, the random distribution of genes in sex cells, and the process of meiosis. Construct F involves the patterns of correlations between the gene variants (alleles) and the physical characteristics (traits). Examples of these patterns include: recessive, dominant, sex linked, etc. Individuals have two alleles for each gene (one from each parent) that can vary in terms of their DNA sequence. The higher levels of construct F also involve understanding patterns of inheritance at the molecular level.

While we anticipate that the constructs are all related to each other, both within and across the genetics models, the progression as developed (Duncan et al., 2009) did not include any conjectures about how the constructs relate to each other. There was simply not enough research to merit making such assertions. Later work using data from empirical studies of the progression has begun to characterize relationships between constructs (Shea & Duncan, 2013; Todd & Romine, 2017). The analyses we conducted for this paper also provide valuable information about potential dependencies and relationships between constructs and how these relationships develop under different instructional conditions.

Methods

Study contexts and instructional interventions

We report data from two research groups that developed instructional materials using the same genetics LP. The instructional interventions developed were implemented with HS students. In the next section we discuss each implementation context and the different instructional interventions.

Research Group 1 context

The Research Group 1 implementation study was carried out with 285 students in the classes of five 11th grade biology teachers in a suburban eastern United States high school. The school's students come from diverse backgrounds: 47% African-American, 23.7% Caucasian, 17% Hispanic and 12% Asian with 44% of the students considered economically disadvantaged. In collaboration with the participating teachers we developed a 10-week instructional unit in genetics that consisted of three modules focusing on concepts in molecular (4 weeks), classical genetics (4 weeks), and a bridging unit (1 week) that connected ideas in molecular and classical genetics. The molecular module addressed constructs B and C of the progression while the classical genetics module addressed constructs E and F (Duncan et al., 2017). The bridging module connected the molecular and classical genetics models by helping students develop molecular-based explanations of inheritance patterns.

For the purposes of a larger project we had two instructional conditions. About half of the students learned with the molecular genetics module first followed by the classical genetics module and then the bridging module- this is the MC condition. The other half of the students learned with the classical genetics module first followed by the molecular module- this is the CM condition. Each teacher taught classes in both conditions (within teacher assignment). Thus even within Research Group 1 we have two instructional interventions that vary in sequence, but not in content. Table 1 illustrates the MC condition in the first column.

All modules focused on model-based inquiry and students developed and evaluated models of genetic mechanisms using evidence. The modeling activities were followed by benchmark lessons that synthesized what was learned in the modeling activities, introduced relevant terminology, and provided opportunities to practice using the newly learned ideas. More information can be found in: Todd, Romine, and Cook-Whitt, 2017 (See Table 1).

Table 1: Instructional interventions

Research Group 1 Instructional Design	**Research Group 2 Instructional Design**
Molecular Module (M)	**Molecular and Classical Modules**
Does HIV resistance exist? (1 week, modeling) Use evidence to develop models of the molecular basis of genetic HIV resistance- **Constructs addressed:** B,C	**How Do Cells Become Cancerous** (2.5 weeks, intervention lesson set, problem-based). Examine cell types, structure/function relationships, cellular differentiation. **Constructs Addressed**: B, C
What is the link between genes and proteins in genetic disorders? (1.5 week, modeling) Jigsaw activity in which: students construct models, using evidence, for DMD, Albinism, or Diabetes. **Constructs addressed:** B,C	**Why Are Siamese Cats Colored The Way They Are?** (2.5 weeks, intervention lesson set, problem-based) Examine enzymes and proteins, structure/function relationships, protein denaturation. Construct and revise models of how activity of proteins can lead to visible traits. **Constructs Addressed**: C
Genetically Modified Organisms: (1.5 week, modeling) Use evidence to evaluate 3 competing models about taking a gene from one species and putting it into another. **Constructs addressed:** B, C	**How Can *Hyla chrysoscelis*, A Native Frog, Tolerate Being Frozen?** (1.5 weeks, problem-based) Examine protein functions. **Constructs Addressed**: C
Classical Module (C)	**How Can We Reduce the Risk of Obesity in Our Community?** (2.5 weeks, problem-based) Examine protein structure/function, nutrients in body. **Constructs Addressed**: B, C
Introduction to Pedigrees and Punnet squares (1.5 weeks, modeling) Rules of Inheritance using pedigrees from 3 Families. Build models of inheritance for dominant and recessive disorders. **Constructs addressed**: E, F	**How Can There Be A Case of Disputed Maternity?** (2.5 weeks, intervention lesson set, problem-based) Examine DNA structure, chromosomes, karyotypes, meiosis, patterns of inheritance. Use paper models of meiosis and crossing over, collect evidence to solve case of maternity dispute. **Constructs Addressed**: B, C, E, F
How is hair texture inherited? and Why is colorblindness more common in males? (2.5 weeks, modeling)	**Can We Genetically Engineer a Superhuman?** (2.5 weeks, intervention lesson set, problem-based) Examine diseases at gene/protein/cell/trait level, mutations, protein structure/function,

Co-dominance and sex-linked traits. Revise models of inheritance. **Construct addressed:** F	observed traits explained by patterns of inheritance. **Constructs Addressed**: B, C, E, F
Bridge Module (B)	**How Can We Diagnose and Develop a Treatment Plan for a Simulated Patient?** (2 weeks, problem-based) Examine symptoms, proteins, mutations, propose genetic treatment. **Constructs Addressed**: B, C, E, F
What is the link between genes, proteins and the phenotype in a genetic disorder? (1 week, modeling) Students developed models of the molecular basis of inheritance patterns in the following contexts: blood types, cancer, CF, Sickle Cell and Dwarfism. **Constructs addressed:** B,C,E,F	

Research Group 2 context

The Research Group 2 implementation study involved sixty-five students within a 10th grade introductory biology class at a Midwestern United States suburban public grade 6-12 STEM school. Student demographics represent the region with white/non-Hispanic students making up 69.9% of the school population, 12.5% black non-Hispanic, 9.6% multiracial, 5% Asian/Pacific Islander, and 3.4% Hispanic; 24.5% of the school's population is considered economically disadvantaged.

All 10th grade students in this school received the same instruction, designed predominantly by the biology teacher but containing four instructional intervention lesson sets targeted to the upper levels of the constructs of the LP. Consistent with the school's mission to utilize project-based learning and inquiry activities, the intervention lesson sets and other teacher-developed genetics lesson sets were all problem-based and centered on a driving question (see Table 1). The students began the instructional period focused on the molecular constructs (i.e. molecular first), learning about structure/function relationships of proteins and cells, cellular differentiation, and protein denaturation. These lesson sets focused on constructs B and C, among others not discussed in this paper. For example, at the end of the second lesson set, students were able to explain how enzyme denaturation in different parts of a Siamese cat's body leads to the coat pattern seen. Students then learned about the classical constructs, examining DNA structure, chromosomes, karyotypes, meiosis, and patterns of inheritance. Throughout the classical genetics lesson sets, instruction also focused on integrating the molecular model (constructs B and C) with the classical models (E, and F). For example, in the sixth lesson set, students used colored pencils to illustrate how an individual with an allele coding for a light blue pigment and an allele coding for a dark brown pigment would have brown eyes because the darker pigment masks the lighter pigment, although both are expressed. More details about the instruction can be found in Todd, Romine, & Cook-Whitt, 2017 (see Table 1 second column).

Data collection

The assessments used for this study included ordered multiple-choice items (OMC). OMC items are developed to map onto the levels described by the genetics LP (Briggs, 2016). Rather than giving right or wrong scoring to each item response, OMC items allow for giving partial credit to each response. This is helpful for allowing researchers to obtain more information about students' level of reasoning about a particular construct using the same item and reduces the number of items needed in an assessment.

Research Group 1: The assessment instrument (described in Duncan et al., 2017) consisted of 56 ordered multiple-choice (OMC) items. These items were selected from a pool of 85 OMC items that we developed, piloted and validated in previous research (Duncan et al., 2017). The 56 items were selected included about 4–5 items per construct and each item included response options that mapped onto 2-4 levels of the relevant construct.

Research Group 2: The assessment instrument is a previously validated Learning Progression-based Assessment of Modern Genetics (LPA-MG, Todd, Romine, & Cook-Whitt, 2017; Todd & Romine, 2017). The LPA-MG also consists of OMC items mapping on to the levels described in our modified version of the genetics LP (Todd, Romine, & Cook-Whitt, 2017). The 36-item LPA-MG assesses all progression levels with each construct containing three items; the item response options mapped onto the 4-6 levels of the relevant construct.

Data analysis

Coding of the data

Both research groups used a Guttman coding scheme to translate students' responses into a location along each construct, using the assumption that if students' understandings corresponded to a higher level of the construct

(say B4), then they had previously mastered and surpassed the lower levels of the construct (i.e. B1, B2, and B3). Assuming a four-level construct, a student with a mastery level of B2 would receive a score of "1100," indicating non-mastery of the two upper levels. We elicited this coding for each item, and then averaged the scores across the construct. For example, a score of "0.83 0.78 0.63 0.57" for "F1 F2 F3 F4" indicates that this student held relatively high mastery of F1 and F2, and lower mastery of F3 and F4. After the data were coded and averaged across the construct, we employed the techniques of causal model search and path analysis to explore relationships between these discrete ideas, and how the modeled relationships fit with the data.

Model search

Relational structure in the data was sought using the fast greedy search (FGS) algorithm implemented in TETRAD (Glymour et al. 2016). This score-based algorithm was implemented in previous work with genetics learning progressions (Todd, Romine, & Correa-Menendez, 2017), and is described in detail in Madigan and Raftery (1994). Briefly, score-based algorithms like FGS search the data for probable relationships and then combine these relationships into a more complex structure in a way which maximizes the likelihood of the model given the data (Raftery, 1995). We used the Bayesian Information Criterion (BIC) approximation to this likelihood, which carries with it the prior assumption that in the absence of data, all models are equally probable (Raftery, 1995).

After searching the space of probable models, a model is selected which minimizes the BIC score as it is specified by Raftery. In order to constrain the model search space, which is hyperexponential with an increasing number of parameters (Madigan & Raftery, 1994) and given the extensive research on validation of these progressions (Todd & Romine, 2017), we added the constraint that the progression levels within each construct were related and sequential, and required those links to exist in the model before searching for additional links.

We applied the above process to three datasets: (1) Research Group 1, MC Intervention (2) Research Group 1, CM Intervention, and (3) Research Group 2 MC Intervention. This resulted in a best-fitting directed acyclic graph (DAG) describing links within individual constructs as well as links between related constructs. Fit of these graphical structures with the data were then confirmed using path analysis.

A model being the "best model" does not mean it actually explains the data as all models in the set may be poor-fitting (Link & Barker, 2006). Fit of the resultant relational structure derived from the model search process with the data was confirmed using path analysis. We evaluated fit of each structure with the data from which it was derived using Mplus7 by comparing the covariance matrix inferred by the model to the actual covariance structure in the data. We used three fit indices: the comparative fit index (CFI), the Tucker-Lewis Index (TLI), and the Root Mean Square Error of Approximation (RMSEA). Values of 0.9 or above for the CFI and TLI indices indicate a good-fitting model (Hu & Bentler, 1995). An RMSEA of 0.06 or below indicates a good fitting model (Hu & Bentler, 1995).

Results

We compared three instructional interventions developed with the genetics LP to determine the role of instruction. The progress maps suggest more similarities than differences across the instructional interventions. We first provide evidence for fit of the path models with the data and then discuss the patterns we noticed across the implementations.

Fit indices derived from path analysis indicate that all models uncovered by the FGS algorithm fit the data well. The CM model from Research Group 1 had an RMSEA = of 0.058, a CFI of 0.95, and a TLI of 0.93. The MC model from Research Group 1 had an RMSEA of 0.059, a CFI of 0.95, and a TLI of 0.93. The MC model from Research Group 2 had an RMSEA of 0.029, and values of 0.99 for the CFI and TLI. All of these indices exceed accepted criteria for good model fit (Hu & Bentler, 1995).

Comparison between Research Group 1's two instructional conditions

We first compared the path analyses of Research Group 1's two respective instructional sequences molecular-then-classical (MC) and classical-then-molecular (CM). In this comparison the students are from the same research context and the intervention activities are identical except for the sequencing of the classical and molecular modules (see Table 1). The path models in the form of progression maps are shown in Figure 1. The nodes represent levels of the progression for each construct, i.e. B1, B2, and B3 nodes are three successive levels of the B construct (gene code for proteins). The constructs are color coded with darker shades indicating more sophisticated levels understanding. Constructs E and F are in shaded in green and blue. The molecular constructs B and C (proteins do the work of the cell) are shaded in orange and yellow. The arrows indicate connections between levels within and between constructs. The red arrows denote connections between constructs and the strength of the connection is reflected in the arrow width. Note that arrows are directional. A connection between F2 and E2 (classical constructs: inheritance patterns and meiosis, with an arrow from F to E) means that students

who achieved a level 2 understanding on construct E usually had already attained a level 2 understanding on the F construct. Knowing F at a level 2 affords learning of E at a level 2.

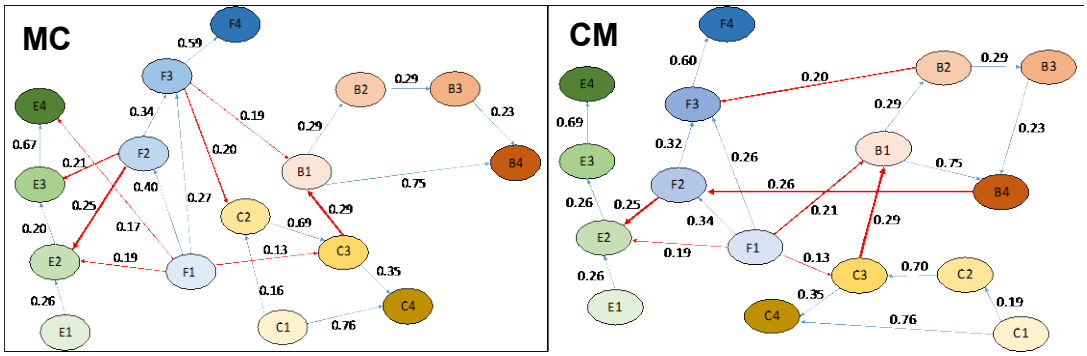

Figure 1. Path models (progression maps) for MC (Left) and CM (Right) conditions.

Figure 1 illustrates these connections, both across constructs in the same genetic model (between E and F or B and C) and between the classical and molecular constructs (between F and C, F and B). The F1 nodes in both maps have the greatest number of connections. This means that F1 functions as a central idea in both conditions. Interestingly, construct E is connected only to construct F in both conditions. Students' understandings of construct E (meiotic model) do not bootstrap the learning of other constructs; however, understanding the ideas embodied in construct E is afforded by understanding construct F (patterns of inheritance). This is not surprising, as students often know more about inheritance patterns compared to meiosis, as these concepts are often part of the middle school curriculum. The understanding that each individual has two alleles (one from each parent) can bootstrap understandings that sex cells have half the genetic content and that alleles are randomly distributed in sex cells.

In comparing the two progression maps we can see that the (red) arrows in the MC condition are mostly originating from construct F towards other constructs (B, C and E); thus construct F seems to be a bootstrapping construct in this condition. Progressing along construct F affords learning ideas in other constructs. This was a bit surprising to us since in the MC condition students learned molecular ideas first and yet it seems that students may not have fully understood ideas in other constructs before they had a strong grasp of construct F. The opposite seems to be true in the CM condition. In that progression map for construct B levels B2 and B4 seems to point to construct F. This suggests that understanding construct B (genes are instructions for proteins) affords learning ideas about patterns of inheritance. This makes sense given the nature of the higher levels of construct F (levels 2-4), which involve understanding the molecular basis of inheritance patterns (e.g. mutations in genes can result in recessive alleles). However, we find it odd that these connections are present in the CM condition, in which students learned about classical genetics first and only then about molecular genetics. Moreover, there are no connections originating from construct B to construct F in the MC (molecular first) condition. One potential explanation that may account for these seemingly unexpected patterns has to do with the bridging module. It may be that when students in the MC condition, who had just completed the classical module, learned about the connection between the molecular and inheritance models (bridge) they developed deeper understanding of the molecular constructs. That is the bridge helped make the more recently learned construct a scaffold for deepening understandings of the molecular constructs, which were revisited in the bridge module. The opposite is true for the CM condition. These students had just completed the molecular module before starting the bridge module. In the bridge module their understandings of the molecular construct B scaffolded the deeper understanding of the revisited classical constructs.

Comparison between Research Group 1 and Research Group 2 interventions

Below we show a comparison of the progression maps from the MC condition from Research Group 1 and the instructional intervention of Research Group 2. Both of these interventions were of the molecular-first ilk but involved different phenomena. Further, whereas Group 1's unit was model-based, Group 2's unit was project-based. In both cases students were guided by driving questions and strived to explain a variety of genetic phenomena. The best-fitting path models are shown in Figure 2. There are several points to note here. First, we wish to point out that the two progressions have different numbers of levels. This is because Group 2's progression is a revision of the progression used by Group 1 and it has more levels for all constructs. To help in comparing these we color-coded the levels using similar shades. Thus for construct F, Group 2 has an extra level not included

construct F from Group 1. However, in construct C, the terminal levels are the same; C5 (Grp 2) is equivalent to C4 (Grp 1), and levels C1-3 in Group 2 are all part of level C1 for Group 1. While this is somewhat confusing, the extra levels in Group 2 do not change the overall pattern of findings.

Second, there are more connections in Group 1's map, in particular from construct F to the other constructs. This suggests that F is a central construct and progressing in understanding of this construct afforded the learning of ideas in other constructs. We suspect that the bridge module may have contributed to this phenomenon as it afforded students with additional opportunities to revisit constructs B and C in the context of discussing inheritance patterns (F) right after they learned about classical genetics. It may be that learning about the molecular mechanisms underlying inheritance patterns allowed students to develop more sophisticated understandings of the molecular constructs in and of themselves (resulting in a bootstrapping effect between F and the molecular constructs).

Third, in both progression maps the constructs grow in sophistication meaning the arrows within a construct all originate from prior levels to subsequent levels and the values are all positive. Moreover, the initial and terminal nodes are very similar. Initial nodes are those that only have arrows originating with them, in both maps the initial nodes E1 and F1belong to the classical genetics constructs; whereas C1 is initial only in the Group 1 map, and B1 is initial only in the Group 2 map. The terminal nodes, those that have only have arrows pointing to them, are also similar with F4/F5, B4/B6, and E4/E5 respectively, whereas C4 is terminal only in Group 1 map.

We discuss our interpretation of the similarities and differences between these maps and their implications next.

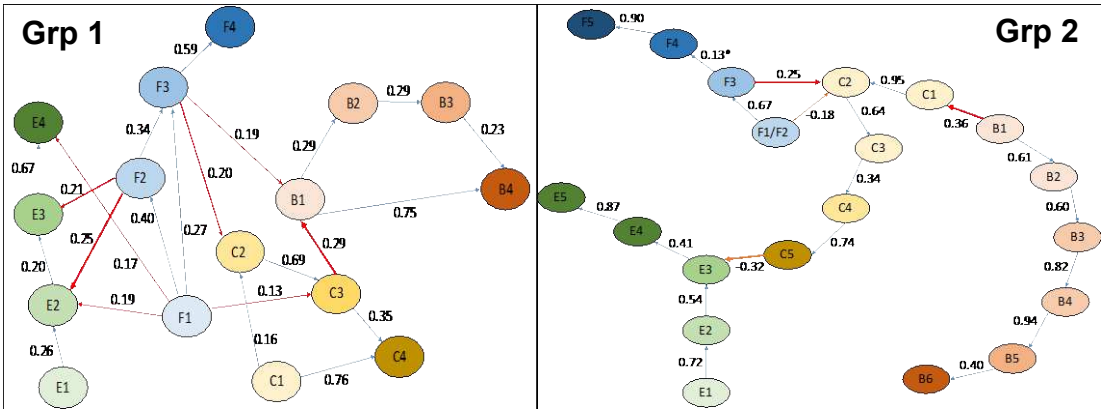

Figure 2. Path models (progression maps) of MC conditions for Research Group 1 (left) and Research Group 2 (right).

Discussion and instructional implications

As noted above, all three the progression maps (the MC, CM maps for Group 1 and the MC Group 2 map) show noticeable similarities and differences. In terms of commonalities, the similar initial and terminal nodes suggest that students ground their understanding of genetics in ideas from the classical genetics constructs E and F since these serve as initial nodes in both maps. Students begin with classical genetics ideas and then use these to develop understandings of molecular genetics. The order of introduction of classical versus molecular genetics does not seem to matter much in terms of initial and terminal ideas (Figure 1). Students seem to have similar start and end points. However, the order of instruction does seem to matter in terms of which constructs bootstrap the learning, and here our findings are somewhat counterintuitive. Beginning with the molecular module does not mean that the molecular constructs will facilitate learning of the classical constructs, and the reverse is also true—classical constructs do not bootstrap learning in the classical first condition. We believe that the odd patterns we identified in the Group 1 progression maps may be due to the role of the bridging module in revisiting constructs that were introduced first and deepening them at this later stage.

Differences mostly comprised the connections between constructs. There were more connections in the Group 1 maps in comparison to the Group 2 map. This plurality of connections suggests that the instructional intervention of Group 1 may have afforded multiple paths (while resulting in similar end points). Again, it may be that the bridging module, by focusing on connections between ideas, allowed students to deepen their understandings of different ideas and to forge new paths through the terrain of these constructs.

To conclude, we wish to return to our question: What do the progression maps suggest about the nature of the constraints on learning? Our findings do not provide the clear and conclusive answer we had hoped for. Overall, we see both strong similarities and important differences between the maps across the three conditions.

Certain instructional opportunities and foci may impact some learning paths more than others. Overall, our findings do not support the existence of strong constraints on learning; however, they do imply some weaker constraints given the similarities in initial and terminal nodes and the progression within constructs. We also point out that the differing study contexts (e.g. schools, students) and measures may have exaggerated some of the differences between the two MC instructional contexts. We hope that in future collaboration between our groups we can develop more elegant and streamlined designs that can provide stronger evidence and help us better understand students' learning trajectories and the impacts of instruction on these trajectories.

References

Alonzo, A. & Gotwals, A. (Eds.). (2012). Learning progressions in science: Current challenges and future directions. Rotterdam, Netherlands: Sense Publishers

Corcoran, T., Mosher, F. A., & Rogat, A. (2009). Learning Progressions in Science: An Evidence-Based Approach to Reform. CPRE Research Report# RR-63. Consortium for Policy Research in Education.

Duncan, R. G., Choi, J., Castro-Faix, M., & Cavera, V. L. (2017). A Study of Two Instructional Sequences Informed by Alternative Learning Progressions in Genetics. *Science & Education*, 1-27.

Duncan, R. G.,&Hmelo-Silver,C.E. (2009). Learning progressions: Aligning curriculum, instruction, and assessment. Journal of Research in ScienceTeaching, 46(6), 606–609.

Duncan, R. G.,&Rivet, A. E. (2013). Science learning progressions. Science, 339, 396–397.

Duncan, R. G., Rogat, A., & Yarden, A. (2009). A learning progression for deepening students' understandings of modern genetics across the 5th-10th grades. Journal of Research in Science Teaching, 46, 655–674.

Freidenreich, H. B., Chinn, C. A., & Bausch, A. (2011). Promoting middle school students' understandings of molecular genetics. Research in Science Education, 41(2), 147–167.

Glymour, C., Scheines, Spirtes, P. Ramsey, J. TETRAD [Computer software] (2016). Center for Causal Discovery. Retrieved from http://www.phil.cmu.edu/tetrad/current.html

Guttman, L. (1950). The principal components of scale analysis. In S. A. Stouffer, L. Guttman, E. A. Suchman, P.F. Lazarsfeld, S. A. Star, & J. A. Clausen (Eds.), Measurement and prediction (pp. 312–361). New York: Wiley.

Hu, L.T. & Bentler, P. M. (1999). Cutoff criteria for fit indexes in covariance structure analysis: Conventional criteria versus new alternatives. Structural equation modeling: a multidisciplinary journal, 6(1), 1-55.

Hu, L.T. & Bentler, PM. (1995). Evaluating Model Fit. In RH Hoyle (Ed.), Structural Equation Modeling: Concepts, Issues, and Applications. Thousand Oaks: Sage

Lave, J. (1987). Cognition in practice. New York: Cambridge University Press.

Link,W.A. &Barker, R. J. (2006). Model weights and the foundations of multimodel inference. Ecology, 87(10), 2626-2635.

Madigan, D., & Raftery, A. E. (1994). Model selection and accounting for model uncertainty in graphical models using Occam's window. Journal of the American Statistical Association, 89(428), 1535-1546.

Raftery, A. E. (1995). Bayesian model selection in social research. *Sociological methodology*, 111-163.

Sevian, H., & Talanquer, V. (2014). Rethinking chemistry: A learning progression on chemical thinking. Chemistry Education Research and Practice, 15(1), 10-23

Shea, N. A., & Duncan, R. G. (2013). From theory to data: The process of refining learning progressions. *Journal of the Learning Sciences*, *22*(1), 7-32

Todd, A. N. (2013). The molecular genetics learning progressions: Revisions and refinements based on empirical testing in three 10th grade classrooms. (Doctoral dissertation, Wright State University).

Todd, A., & Kenyon, L. (2016). Empirical refinements of a molecular genetics learning progression: The molecular constructs. Journal of Research in Science Teaching, 53(9), 1385–1418.

Todd, A., Romine, W. L., & Cook Whitt, K. (2017). Development and Validation of the Learning Progression–Based Assessment of Modern Genetics in a High School Context. Science Education, 101(1), 32-65.

Todd, A., Romine, W. L., & Correa-Menendez, J. (2017). Modeling the Transition from a Phenotypic to Genotypic Conceptualization of Genetics in a University-Level Introductory Biology Context. Research in Science Education, 1-21.

Todd, A., & Romine, W. L. (2017). Empirical validation of a modern genetics progression web for college biology students. *International Journal of Science Education*, *39*(4), 488-505.

Acknowledgments

We thank the Center for Causal Discovery, supported by grant U54HG008540, for use of the TETRAD software package. The research presented herein was also supported by a National Science Foundation Award # REESE-1053953.