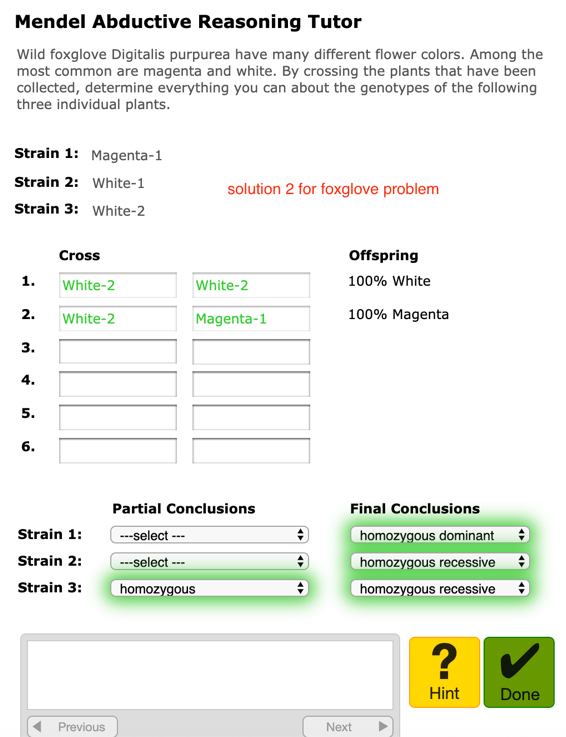
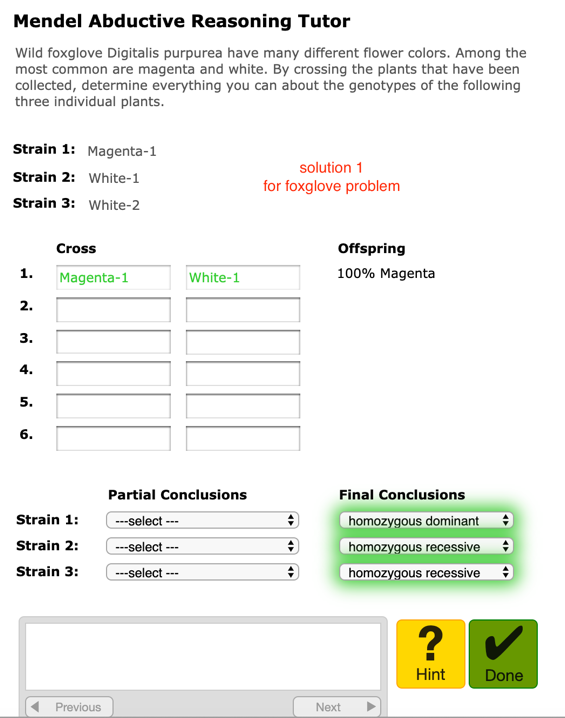
**Assignment 6 Deliverables ------ Henry & Jiachen**

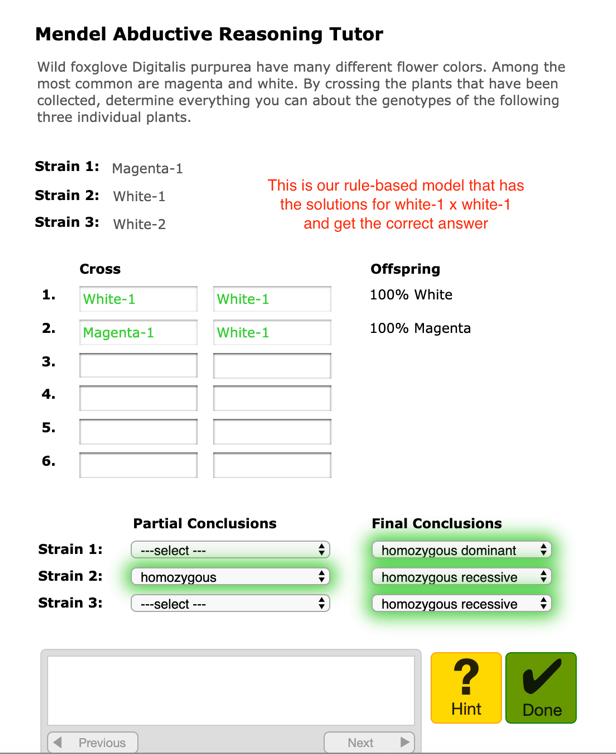
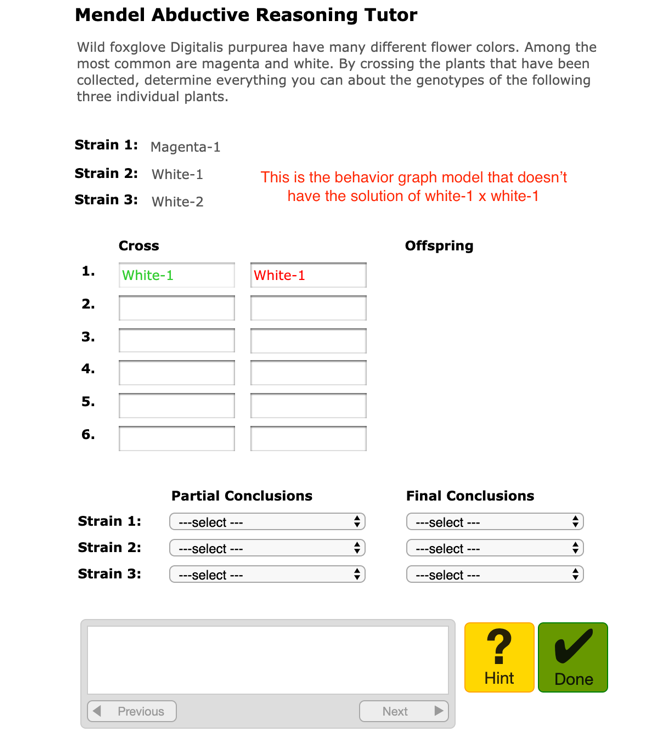
* A short report with:
  + Evidence that your tutor can handle *all* solutions to the two problems provided (foxglove and lupine).

**For the foxglove problem:**

Solutions:

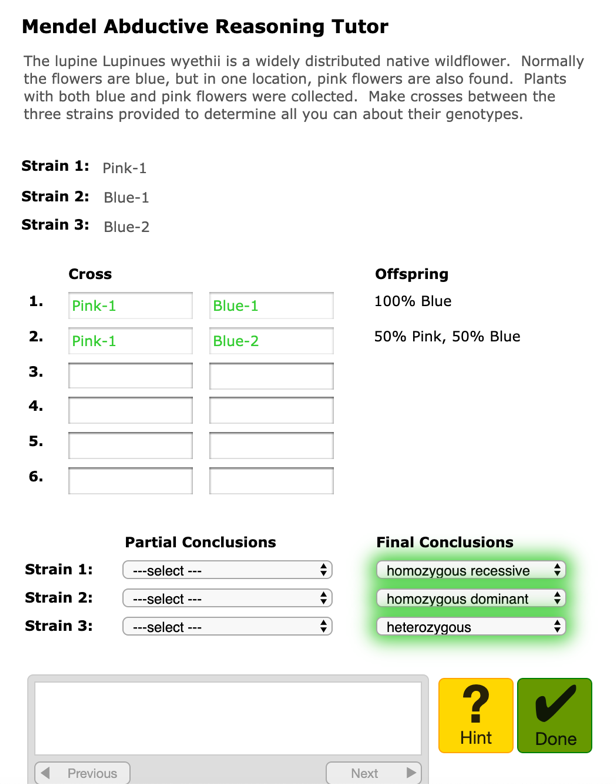
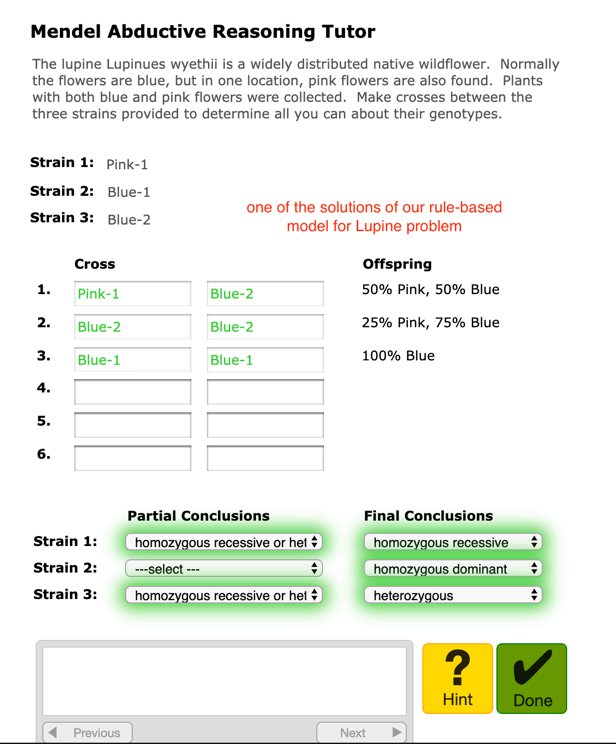
****

Comparing with behavior graph model:

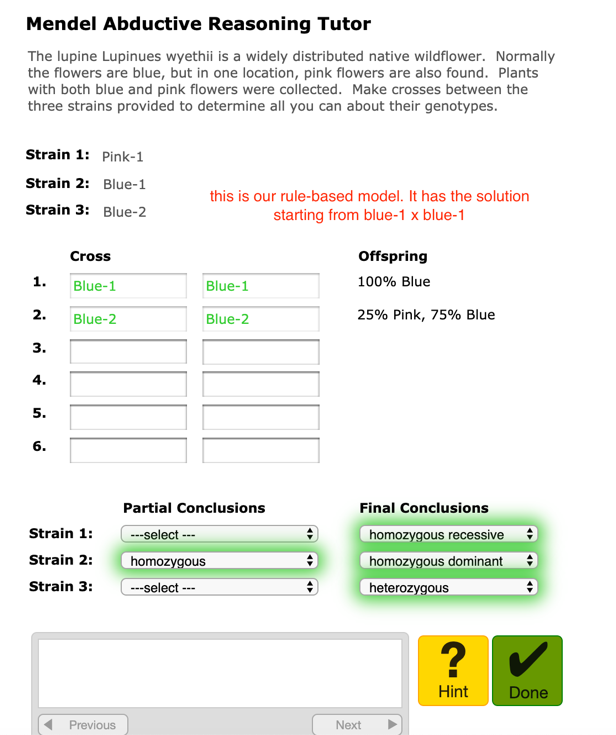
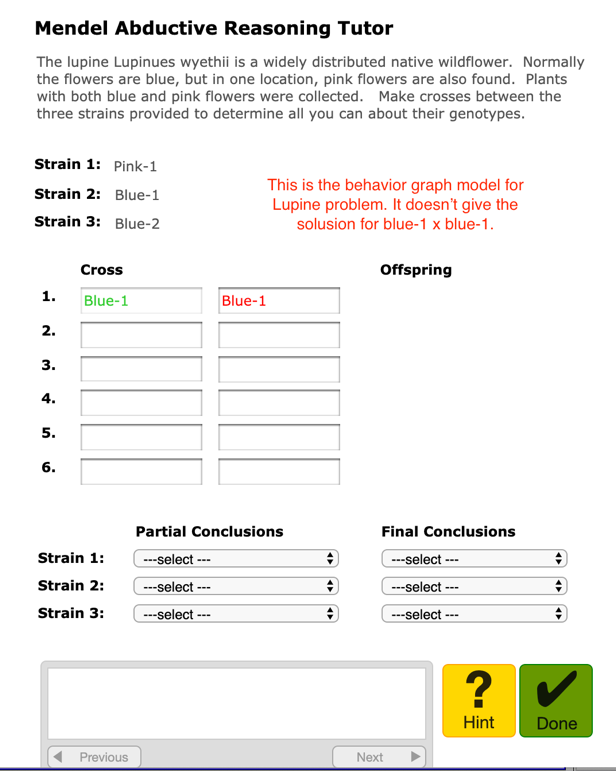


**For the lupine problem:**

Solutions:

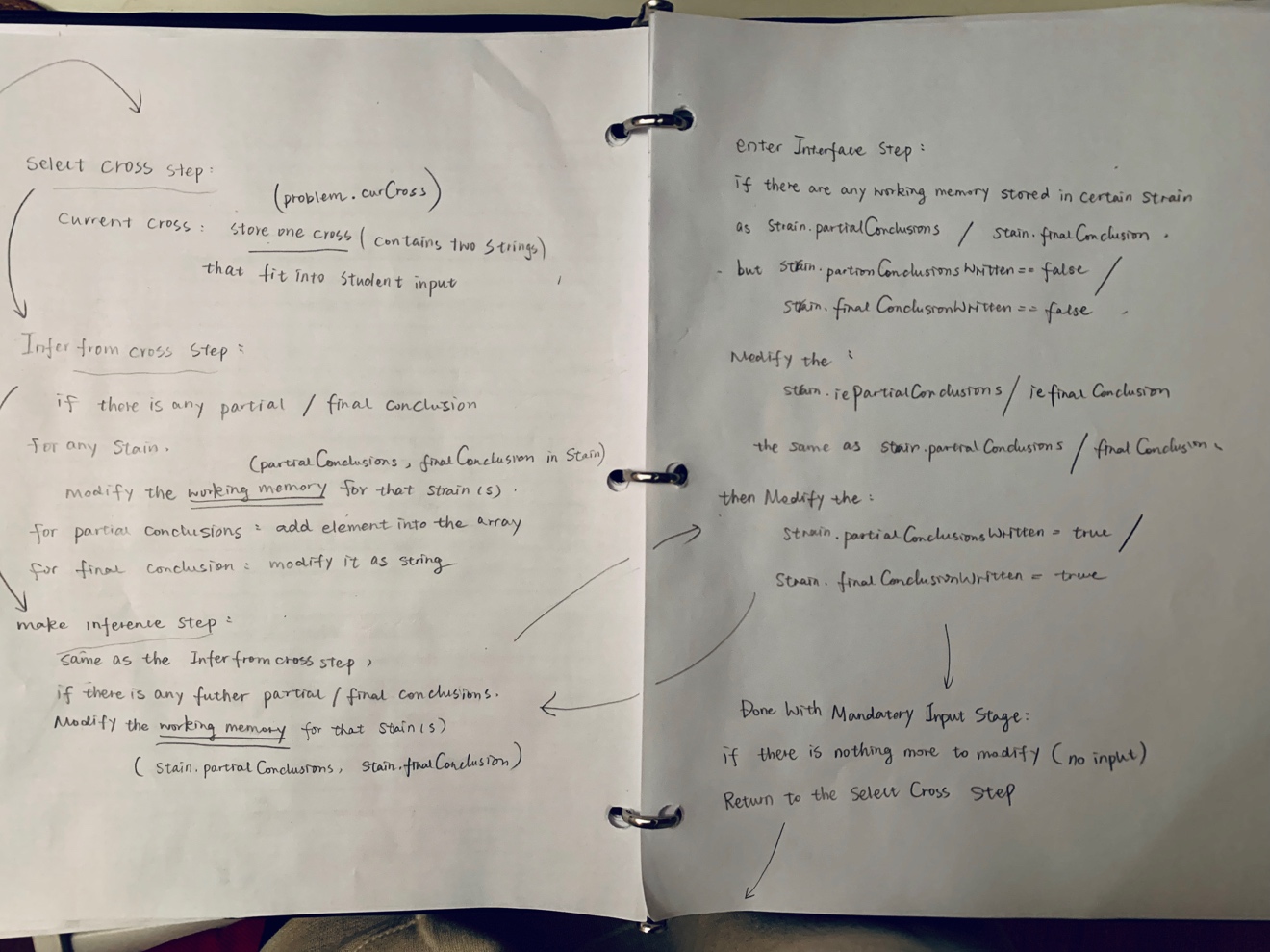
 

Comparing with behavior graph model:

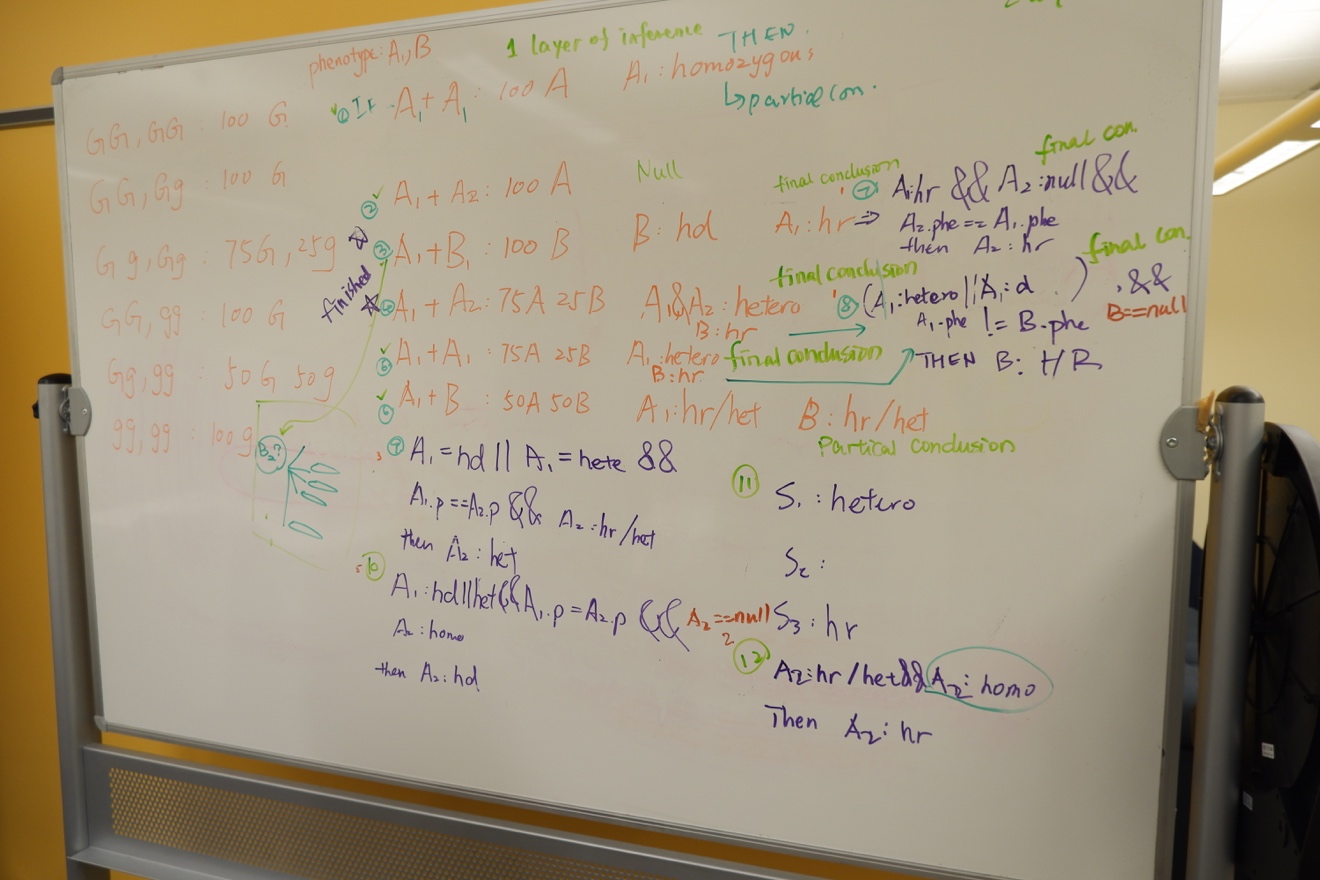


* + Documentation for the model
* Lo-fi diagram that shows working memory structure

**Lo-fi diagram for working memory structure:**



**Lo-fi diagram for rules:**



* English versions of all rules, included with the rules themselves in the rules file

**Nools Code in English**

NOTE: RULE 1-6 ARE infer\_from\_cross RULES

RULE 7-13 ARE make\_further\_inference RULES

**RULE 1**

**inferFromS1xS1\_100A**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is not defined

And S1’s final conclusion is not defined

And the two strains are the identical plant

And the cross for S1xS1 result is equal to 100 percent of phenotype A

**THEN**

Write S1’s partial conclusion as Homozygous

**RULE 2 – No Conclusion**

**inferFromS1xS2\_100A**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is not defined

And S1’s final conclusion is not defined

And S2’s partial conclusion is not defined

And S2’s final conclusion is not defined

And the cross for S1xS2 result is equal to 100 percent of phenotype A

**THEN**

We cannot draw any conclusion

Do not change anything to the working memory

**RULE 3**

**inferFromS1xS3\_100B**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is not defined

And S1’s final conclusion is not defined

And S3’s partial conclusion is not defined

And S3’s final conclusion is not defined

And the phenotype of S1 is different from the phenotype of S3

And the cross for S1xS3 result is equal to 100 percent of phenotype B

**THEN**

Write S1’s final conclusion as Homozygous Recessive

Write S3’s final conclusion as Homozygous Dominant

**RULE 4**

**inferFromS1xS2\_75A**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is not defined

And S1’s final conclusion is not defined

And S2’s partial conclusion is not defined

And S2’s final conclusion is not defined

And the phenotype of S1 is the same as the phenotype of S2

And the cross for S1xS2 result is equal to 75 percent of phenotype A, and 25 percent of phenotype B

**THEN**

Write S1’s final conclusion as Heterozygous

Write S2’s final conclusion as Heterozygous

**RULE 5 – the same as RULE 4**

**inferFromS1xS1\_75A**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is not defined

And S1’s final conclusion is not defined

And the two strains are the identical plant

And the cross for S1xS1 result is equal to 75 percent of phenotype A, and 25 percent of phenotype B

**THEN**

Write S1’s final conclusion as Heterozygous

**RULE 6**

**inferFromS1xS3\_50B**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is not defined

And S1’s final conclusion is not defined

And S3’s partial conclusion is not defined

And S3’s final conclusion is not defined

And the phenotype of S1 is different from the phenotype of S3

And the cross for S1xS3 result is equal to 50 percent of phenotype A, and 50 percent of phenotype B

**THEN**

Write S1’s partial conclusion as “Heterozygous or Homozygous recessive”

Write S3’s partial conclusion as “Heterozygous or Homozygous recessive”

**RULE 7**

**makeInferenceFromS1xS2\_HR**

**IF** there is a goal to determine the gene type of S

And S1’s final conclusion is Homozygous Recessive

And the phenotype of S1 is the same as the phenotype of S2

**THEN**

Write S2’s final conclusion as Homozygous Recessive

**RULE 8**

**makeInferenceFromS1xS3\_HR**

**IF** there is a goal to determine the gene type of S

And S1’s final conclusion is Heterozygous or Homozygous Dominant

And the phenotype of S1 is the different from the phenotype of S3

**THEN**

Write S3’s final conclusion as Homozygous Recessive

**RULE 9**

**makeInferenceFromS1xS2\_HET**

**IF** there is a goal to determine the gene type of S

And S1’s final conclusion is Heterozygous or Homozygous Dominant

And the phenotype of S1 is the same as the phenotype of S2

And S2’s partial conclusion is “Heterozygous or Homozygous recessive”

**THEN**

Write S2’s final conclusion as Heterozygous

**RULE 10**

**makeInferenceFromS1xS2\_same\_HD**

**IF** there is a goal to determine the gene type of S

And S1’s final conclusion is Heterozygous or Homozygous Dominant

And the phenotype of S1 is the same as the phenotype of S2

And S2’s partial conclusion is “Homozygous”

**THEN**

Write S2’s final conclusion as Homozygous Dominant

**RULE 11**

**makeInferenceFromS1xS2\_HD**

**IF** there is a goal to determine the gene type of S

And S1’s final conclusion is Heterozygous

And S3’s final conclusion is Homozygous Recessive

And the phenotype of S1 is the same as the phenotype of S2

And the cross for S1xS2 result is equal to 100 percent of phenotype A

**THEN**

Write S2’s final conclusion as Homozygous Dominant

**RULE 12**

**makeInferenceFromS1xS1\_HR**

**IF** there is a goal to determine the gene type of S

And S1’s partial conclusion is “Heterozygous or Homozygous recessive”

And the two strains are the identical plant

And the cross for S1xS1 result is equal to 100 percent of phenotype A

**THEN**

Write S1’s final conclusion as Homozygous Recessive

**RULE 13**

**makeInferenceFromTwoPartial**

**IF** there is a goal to determine the gene type of S

And S1 has two partial conclusions

And S1 has no final conclusion

**THEN**

Write S1’s final conclusion as Homozygous recessive

* + Reflection on the strengths and limitations (in a pedagogical sense) of the tutor you built.

For Strengths:

* The tutor allows student to explore different possibilities of crossing genes by accepting all sequence of crosses.
* Students are not restricted to follow a specific pattern of drawing inferences when there are multiple inference options, reflecting the natural of abductive reasoning.
* Students are structured to think of inferences before making another cross. This forces students to draw the complete picture of all inferences regarding the information the problem reveals.

For limitations:

* The inference process is a little oblique for students in terms of how many total inferences can be drawn for a cross selected or conclusion made.
* There are no hint right now to aid students who are stuck.
  + A few sentences on how you worked together as a team

1. Regarding the suggested E/T roles, we firstly had a 4-hour meeting discussing the diagrams of rules and working memory.
2. Then, I (Jiachen) wrote down 13 rules in English, and Henry built up the code frame of productionrules.nools.
3. After building up the framework of rules, Henry set up the first several rules, and then I joined in the coding part, we co-coded these rules through git hub.
4. Throughout the coding process, we debugged all the rules together, and completed the coding part of productionrules.nools.
5. As for the deliverables, Henry reflected on our strengths and weaknesses, and I wrote down other parts.
   * What was hard about this assignment?

We didn’t notice the rules given in the slides, so we spent 4 hours figuring out all possible rules by ourselves. This part is very difficult as it requires strong logic and thorough understanding about this knowledge component. But it is indeed a worthy procedure as it helped us have a clear understanding of all the rules. Another hard part is the debugging part. We spent a lot of time debugging the rules, as well as testing again and again in the html interface.

* + What was good and bad about CTAT including the tools for Nools modeling

The good part is that we can define/code every rule we want in nools, as the nools framework is very flexible. The bad part is that it is extremely hard to debug. We had to put halt() in different places to testify our code. It would be better if we could do the debugging/halt() process in a debugger program just as python has.