# Cornell Guided Notes

Genetics of Disease (Medical Interventions) | 2026-10-27

| Name | Period | Date | Lesson |
|---|---|---|---|
| | | 2026-10-27 | |

**Lesson focus**

Expression data lab

| Key words and questions | Prepared details and student notes |
|---|---|

**Essential question**
**What is today's target?**

Use a gene expression table to calculate fold change and flag upregulated and downregulated genes. Big idea: How do numbers in a spreadsheet reveal which genes a disease turns on or off?

**My notes, examples, and questions**

**Key words**
**What vocabulary unlocks the lesson?**

- gene expression
- mRNA
- upregulated
- downregulated
- correlation
- risk
- diagnosis

**My notes, examples, and questions**

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## Cornell Notes - Continued

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| **Must-know ideas**<br>**What should I understand by the end?** | - Fold change = diseased expression / healthy expression; greater than 1 is upregulated, less than 1 is downregulated.<br>- Microarray data is generated by measuring fluorescence intensity at each probe spot; the numbers in the dataset represent those intensities.<br>- An upregulated gene in diseased tissue may be driving the disease (oncogene) or responding to protect cells (repair gene).<br><br>**My notes, examples, and questions** |
| **Process notes**<br>**What happens during class?** | - 0-8: Hook heat map and fold-change formula introduction; confirm dataset access<br>- 8-25: Open dataset; locate diseased and healthy columns; calculate fold change for genes 1-2<br>- 25-45: Calculate fold change for genes 3-4; label all four as up or downregulated<br>- 45-60: Write one sentence on what an upregulated gene might mean for the disease<br>- 60-72: Partner check: verify each other's calculations for arithmetic errors<br>- 72-80: Save fold-change table to course shell; preview Thursday heat-map work<br><br>**My notes, examples, and questions** |

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| **Steps and evidence**<br>**What do I do and turn in?** | - Open the expression dataset in the shell and find the diseased and healthy sample columns.<br>- For four genes, calculate fold change by dividing diseased expression by healthy expression.<br>- Label each gene upregulated or downregulated based on whether fold change is above or below one.<br>- Write one sentence on what an upregulated gene might mean for the disease.<br>- Save your fold-change table as your lab evidence.<br><br>Evidence: Data table - Fold-change table for four genes with upregulated/downregulated labels and one sentence on the biological meaning of an upregulated gene.<br><br>**My notes, examples, and questions** |
| **Checks for understanding**<br>**How do I know I got it?** | - You'll be able to calculate fold change from expression data.<br>- You'll be able to flag genes as upregulated or downregulated.<br><br>**My notes, examples, and questions** |

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**Lab or safety notes**
**What must I handle carefully?**

Safety:
- No wet lab materials today; all work is computational.
- Dataset is anonymized class-aggregate; do not enter or share personal identifying information.
- Save your work frequently; do not rely on browser auto-save for the dataset.

Supplies:
- Computer or tablet with access to the expression dataset in the course shell (one per student or pair)
- Printed or digital data-table template for recording fold-change calculations
- Colored pencils or digital fill (two colors) for preliminary heat-map shading on Thursday
- Calculator or spreadsheet formula access for division calculations

**My notes, examples, and questions**

## Summary

Today's lesson focused on Expression data lab. The main target was: Use a gene expression table to calculate fold change and flag upregulated and downregulated genes. The evidence of learning is Data table: Fold-change table for four genes with upregulated/downregulated labels and one sentence on the biological meaning of an upregulated gene.. In my own words, the most important idea from today is:

**My summary**

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### My final question or connection