Practical Bioinformatics

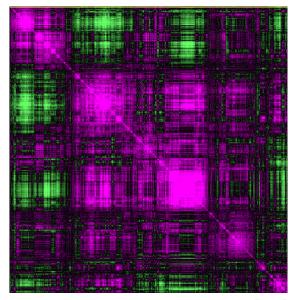
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Dictionaries

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\begin{array}{ll} \mbox{dictionary} &= \{ \mbox{"A"} : \mbox{"T"} , \mbox{"T"} : \mbox{"A"} , \mbox{"G"} : \mbox{"C"} , \mbox{"C"} : \mbox{"G"} \} \\ \mbox{dictionary} \left[ \mbox{"N"} \right] &= \mbox{"N"} \\ \mbox{dictionary} : \mbox{has} \mbox{key} \left( \mbox{"C"} \right) \end{array}
```

Clustering exercises – Visualizing the distance matrix



Homework

- Download the mouse transcriptome GTF file linked on the website. This is a gzipped, tab-delimited text file.
- Filter the file for lines with "transcript" in the third column.
- The first column gives the chromosome. transcript_id in the nineth column gives the transcript_id, as used in the count matrices that we've been working with. Create a dictionary mapping transcript_ids to chromosomes.
- Filter est_counts.cdt from the course website to remove transcripts on the X and Y chromosomes.
- Sonus: columns 4, 5, and 7 of the GTF give 1-based start, stop, and strand coordinates for the transcripts. Try writing a simple matplotlib-based genome browser for the mouse genome. Try including exon rows to plot detailed gene structures.

