Antibiotic Sequencing Basics

1.	True or False: The human genome is the longest genome of any organism on Earth.
	True
	False
2.	What is a cycle that visits every node in a graph called?
	de Bruijnian
	Nashlike
	Erdosian
	Eulerian
	Hamiltonian
3.	What is a cycle that visits every edge in a graph called?
	de Bruijnian
	Nashlike
	Erdosian
	Eulerian
	Hamiltonian

4. Below is the adjacency list of a graph. Which of the following is a Hamiltonian cycle in this graph? (Select all that apply.)

$$3 -> 1,2,5$$

5. Which of the following are 3-universal linear binary strings? (Select all that apply.)

1111000111

0101010100

0100011101

0011101000

0111010001

1100011011

6. What is the indegree of AGA in the de Bruijn graph constructed for the following collection of 4-mers? (Hint: how can you answer this question without having to construct the de Bruijn graph?)

GCGA CAAG A<mark>AGA</mark> GCCG ACAA AGTA TAGG AGTA ACGT AGCC TTCG AGTT AGTA CGTA GCGC GCGA GGTC GCAT AAGC T<mark>AGA</mark> ACAG T<mark>AGA</mark> TCCT CCCC GCGC ATCC AGTA A<mark>AGA</mark> GCGA CGTA

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Antibiotic Sequencing Noisy Spectra

1. Give a linear string having the following 4-mer composition.

AAAT AATG ACCC ACGC ATAC ATCA ATGC CAAA CACC CATA CATC CCAG CCCA CGCT CTCA GCAT GCTC TACG TCAC TCAT TGCA

CAAATGCATACGCTCATCACCCAG

2. Below is the adjacency list of a graph. What is the minimum number of edges we must add to this graph in order to make each node balanced? (You may add duplicate edges connecting the same two nodes, but do not add new nodes.)

1 -> 2,3,5

 $2 \rightarrow 1,4$ $3 \rightarrow 2,5$ $4 \rightarrow 1,2,5$ $5 \rightarrow 3,4$

2

3. There is a single (linear) string with the following (3,1)-mer composition. Find it.

(ACCIATA) (ACTIATT) (ATAITGA) (ATTITGA) (CACIGAT) (CCGITAC) (CGAIACT) (CTGIAGC) (CTG|TTC) (GAA|CTT) (GAT|CTG) (GAT|CTG) (TAC|GAT) (TCT|AAG) (TGA|GCT) (TGA|TCT) (TTC|GAA)

CACCGATACTGATTCTGAAGCTT

4. True or False: every Eulerian path in the paired de Bruijn graph constructed from a (k, d)mer composition must spell out a solution to the String Reconstruction from Read-Pairs Problem.

True

False

5. True or False: read breaking can transform reads with imperfect coverage into reads with perfect coverage.

True

False

Genome Assembly Basics

1.	True or False: Tyrocidine B1 is synthesized by the ribosome.
	True
	False (it is an NRP)
2.	Which of the following RNA strings could translate into the amino acid string PRTEIN? (Select all that apply.)
	CCAAGUACAGAGAUUAAC
	CCAAGAACAGAUAUCAAU
	CCACGUACUGAAAUUAAC
	CCGAGGACCGAAAUCAAC
3.	How many DNA strings transcribe and translate into the amino acid string CYCLIC?
	288
4.	What is the integer mass of tryptophan?
	186
5.	Which of the following cyclic peptides could have generated the theoretical spectrum 0 71 101 113 131 184 202 214 232 285 303 315 345 416? (Select all that apply.)
	TMIA TAIM IAMT MTAL MAIT MLAT
6.	Which of the following linear peptides is consistent with Spectrum = {0 71 99 101 103 128 129 199 200 204 227 230 231 298 303 328 330 332 333}? (Select all that apply.)
	ETC QCV TCQ TVQ TCE AVQ

Genome Assembly via Euler's Theorem

1.	True or False: In practice, the charge of a fragment ion is irrelevant when dealing with real spectra.
	True
	False
2.	True or False: Increasing the size of the leaderboard can increase the likelihood of LeaderboardCyclopeptideSequencing identifying a highest-scoring peptide.
	True
	False
3.	If Peptide = MAMA and Spectrum = {0 71 98 99 131 202 202 202 202 202 299 333 333 333 503}, then what is Score(Peptide, Spectrum)?
	9
4.	If Peptide = PEEP and Spectrum = {0 97 97 129 194 196 226 226 244 258 323 323 452} then what is LinearScore(Peptide, Spectrum)?
	8
5.	What element has largest multiplicity in the spectral convolution of Spectrum = $\{0.57.118.179.236.240.301\}$?
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