Question 1. (2 pts.) True or False. BLAST performs Smith-Waterman local alignments between the query and all sequences in the database.

**ANSWER:** False.

Question 2. (2 pts.) Suppose the scoring scheme for a BLAST DNA search is +1 for match and −1 for mismatch or indel. True or False, a significant alignment can have entirely mismatches.

**ANSWER:** False.

Question 3. (2 pts.) fastQ files have how many rows per read-pair?

(A) Two
(B) Four
(C) Six
(D) Eight ← THIS ONE

**Question 4.** (2 pts.) True or False. SNP calling is primarily done with microarrays.

**ANSWER:** True.

**Question 5.** (2 pts.) What does blastx do?

**ANSWER:** It translates the query sequence into protein in all six ways and aligns each to a protein database.