**Lecture #3 – Quiz questions**

**Which RNA type dominates the cellular environment by mass?**

* mRNA
* **rRNA**
* tRNA
* lncRNA

**Which RNA type dominates the cellular environment by number of molecules?**

* rRNA
* **tRNA**
* mRNA
* lncRNA

**Splicing commonly occurs across which donor:acceptor pair?**

* AT:CG
* AU:CG
* **GU:AG**
* GT:AG

**Which of the following statements is TRUE?**

* rRNA-depletion is required for small RNA sequencing (e.g. miRNA-Seq)
* Poly(A) selection yields more reads than rRNA-depletion
* **rRNA-depletion is optimal for degraded RNA or where non-adenylated RNAs are of interest**
* Poly(A) selection can be used to profile lncRNAs

**Which of the following statements is FALSE?**

* **For human rRNA-depletion RNA-Seq, 20-30 million paired reads are sufficient**
* For human poly(A)-selection RNA-Seq, 20-30 million paired reads are sufficient
* Short paired-end reads (2 x 35) are more cost-effective than long paired-end reads (e.g. 2 x 150)
* For human miRNA-Seq, ~10 million paired reads are sufficient

**Which of the following statements is TRUE?**

* Stranded libraries are cheaper to produce than unstranded libraries
* Strand information is not useful for large gene-sparse eukaryotes
* **Strand information encoded in read data is dependent on library preparation method**
* Strand-specificity is perfect so artefacts can never occur

**Which of the following statements is FALSE?**

* Accurate splice-site detection requires long paired-end reads (>= 2 x 50)
* Transcript level changes in expression may not be reflected at gene level
* Good experimental design for RNA-Seq is complicated
* **Read quantification does not require a good annotation**

**What strategies can be used to reconstruct a transcriptome from RNA-Seq data**

* Gene-level alignment (genome alignment)
* Transcript-level alignment (transcriptome alignment)
* *De novo* transcript assembly
* **All of the above**

**The guiding principal of pseudoalignment is for each read…**

* To determine where in a transcript it aligns to
* **To determine with which transcript(s) it is (alignment-)compatible**
* To determine which genome it aligns to
* None of the above

**Which of the following statements regarding pseudoaligners is FALSE?**

* Pseudoaligners are significantly faster than standard aligners
* **Pseudoaligners entirely replace the needed for standard aligners**
* Pseudoaligners have comparable error rates with standard aligners
* Pseudoaligners are much better for the environment than standard aligners