Chapter 12: Guidelines and important considerations for 'omics-level studies

1. Intro on RNA-seq (500)
   1. what it is, what can we learn from this data, advantage over microarrays, different types of RNA-seq
   2. Focus on Poly-A RNA-seq
2. Box on other types of RNA-seq
   1. What they are good for, what's different in terms of protocol/samples prep, what's different analytically, reference to actual protocol
   2. Total RNA-seq
   3. miRNA-seq
   4. MPRA/Targeted RNA-seq
3. Protocol (500)
   1. Example protocol?
   2. Step-by-step explanation but no specific protocol?

Protocol Workflow figure - where can you stop?

* Similar for other types of RNA-seq
* Size selection considerations
* How to starting with small amounts

1. Study design considerations - definitions (1000)
   1. RNA quality
   2. Confounders
      1. Batch effects - sample, sequencing, RNA-extraction, library prep
      2. Sample collection
      3. Variation between groups or samples
   3. Replicates - technical vs biological
   4. Sequencing depth -> question
   5. Read length & single/paired end
   6. [multiplexing]
2. Questions and study design (4000-5000)
   1. mRNA quantifications (1000)
      1. Study design
      2. Analysis metrics/methods - basic principles (then examples of software)
   2. Comparing groups (1000)
   3. eQTL mapping (1000)
   4. Splicing/RNA processing (1000)

Workflow figure - questions

* mRNA quantification? → only: reference free

→ + other steps: mapping, TPMs

Figures:

Box/Table: software - all types of analysis they can be used for, references, etc