This is to calculate pairwise distance and should generate all pairwise exonic regions and fragments

For gene G with Transcripts T1 and T2

Input: pair of transcripts, each converted into a BED file of exons (1 line per exon)

Generate exon regions (ERs) and determine how many overlap and how many do not: Bedtools intersect transcripts T1 and T2 -v and the reciprocal (bedtools intersect -v T2 to T1)

* If the resulting concatenation of the reciprocal bedtools intersect -v is empty then the two transcripts have all of the same ERs overlapping
  + Go to ER module with complete input BED files to compare
  + Count how many ER are overlapping, 0 are unique to T1, 0 are unique to T2
* Else there is at least one region not overlapping these should now be annotated accordingly
  + “subtract” non overlapping regions for T1 and T2 from the original input bed files, go to ER module with the subset original BED files with the non-overlapping removed
    - Count how many exonic regions overlap and how many are unique to either T1 or T2
    - Count how many nucleotides are in the unique ER for each transcript

ER module - here input is two bed files of the ER that overlap in T1 and T2

1. Identify all shared fragments between T1 and T2: bedtools intersect T1 to T2 (no reciprocal needed, either direction works)
   * Count how many fragments are shared
   * Count how many nucleotides in shared fragments
2. Identify unique fragments in T1: bedtools subtract T1 from the intersection (A)
   * Count how many fragments are unique to T2
   * Count how many nucleotides in T1 only fragments in shared ER
3. Identify unique fragments in T2: bedtools subtract T2 from the intersection (A)
   * Count how many fragments are unique to T2
   * Count how many nucleotides in T2 only fragments in shared ER