**Key files or work summary**

* Excel files:
  + Software.Packages.July16.2019: Summary of the software packages languages, input formats, installation status, ect.
  + Software.Compare.June3.2019: Summarizes Haplotype assembly algorithms & software packages includes multiple sheets with comparison of evaluation parameters, model & methods, parameters used for formulation, ect.
  + Comparisons.May13.2019: Contains the number of software packages used to compare a software package and how often a specific package is used for comparison.
  + Review.Paper.Check.List.May7.2019: Excel file of the sections within the word writing paper
* PPT files:
  + Aug13.2019.work.report: Contains meeting to-do lists
  + Problem Formulation.Apr30.2019: Contains problem and formulation sections
  + Literature.Reviews.Dec19.2018: Overview of what type of sequencing technologies, samples, size of read length, tools and reconstruction method was used for haplotype assembly in HA papers.
* WORD Files:
  + Intro&KeyFeatures.May7.2019: Paper containing summaries of most common algorithmic and evaluation features and which software packages utilize certain features.
  + HA\_s.package\_input.outputs.July16.2019: word doc of input and output format for software packages.
* Text files (scripts):
  + Dataset Alignment Scripts:
    - Datasets.june9.2019: Alignment script for pair end datasets: 826T, 827T, 832T, 847T & 850T: tail -4000000 (1 million reads)
    - 826T\_1\_sequence.chr10.Alignment.July1.2019: Single end dataset 826T\_1, aligned and extracted chromosome 10 into .bam and .vcf files. Additionally, .bam & .vcf files were created for chromosome position ranges centered around position “125737910” correlated to position “480” from extractHAIRS(HapCUT2) fragment file.
    - Alignment.whole\_pair\_end\_826T.July9.2019: Whole pair-end. 826T dataset, alignment script
    - sbatch.NA12878.alignment.July31.2019: sbatch script of Alignment ran on NA12878 obtained via fastq-dump on July 22nd 2019
    - Alignment\_1mil\_reads\_NA12878,Aug6.2019: Sbatch script for the alignment of the last 1 million reads of NA12878 fastq-dump dataset downloaded on Aug. 6 2019.
    - Alignment\_NA12892\_fastq\_dump.Aug7.2019: Alignment of NA12892 fastq files (entire dataset) obtained via fastq-dump procedure on Aug. 7 2019
    - Alignment\_NA12891\_fastq\_dump.Aug7.2019: Alignment of NA12891 fastq files (entire dataset) obtained via fastq-dump procedure on Aug. 7 2019
    - Alignment\_NA12878\_fastq\_dump.Aug7.2019: Alignment of NA12878 fastq files (entire dataset) obtained via fastq-dump procedure on Aug. 7 2019
    - Alignment\_NA12878\_wget.Aug7.2019: Alignment of NA12878 fastq files (entire dataset) obtained via wget procedure on Aug. 7 2019
    - Alignment.sbatch\_NA12892\_fastdump\_Aug8.2019: Alignment of NA12892 data set last 10 million reads, extracting only chr10 from the fastq-dump data downloaded on Aug 8th 2019.
    - Alignment.sbatch\_NA12892\_wget\_Aug8.2019: : Alignment of NA12892 data set last 10 million reads, extracting only chr10 from the weget data downloaded on Aug. 8 2019.
    - Alignment.sbatch\_NA12891\_10mil\_reads\_wget\_Aug13.2019: Alignment of NA12891 (father) data set last 10 million reads, extracting only chr10 from the weget data.
    - Alignment.sbatch\_NA12891\_10mil\_reads\_fastq\_dump\_Aug13.2019: Alignment of NA12891 (father) data set last 10 million reads, extracting only chr10 from the fastq-dump data.
  + HapCompass Scripts:
    - HapCompass.Real.Data.Jun9.2019: Script of HapCompass being run on the aligned datasets 826T, 827T, 832T, 847T & 850T pair-end (tail -4000000, last million reads).
    - HapCompass.826T\_1\_chr10.July1.2019: Script of HapCompass being run on the aligned dataset for only chr10 of 826T\_1\_sequence single-end.
    - HapCompass.whole\_pairend\_826T.July9.2019: Script of HapCompass being run on the aligned whole pair-end 826T dataset.
    - HapCompass\_NA12891\_fastqdump\_10mil\_reads.Aug13.2019: Script of HapCompass being run on the fastq-dump obtained data of NA12891 (last 10 million reads, extracting chr10 only).
    - HapCompass\_NA12891\_wget\_10mil\_reads.Aug13.2019: Script of HapCompass being run on the wget obtained data of NA12891 (last 10 million reads, extracting chr10 only).
    - HapCompass\_NA12892\_fastqdump\_10mil\_reads.Aug13.2019: Script of HapCompass being run on the fastq-dump obtained data of NA12892 (last 10 million reads, extracting chr10 only).
    - HapCompass\_NA12892\_wget\_10mil\_reads.Aug13.2019: Script of HapCompass being run on the wget obtained data of NA12892 (last 10 million reads, extracting chr10 only).
  + HapCUT Scripts:
    - HapCUT.Example.Run.June3.2019: Script of HapCUT being installed and ran on its example data and script.
    - HapCUT.Real.Data.Jun9.2019: Script of HapCUT being run on the aligned pair-end datasets 826T, 827T, 832T, 847T & 850T (tail -4000000, last million reads).
    - HapCUT.826T\_1\_chr10.July1.2019: Script of HapCUT being run on the aligned single-end dataset 826T\_1\_sequence, only chromosome 10.
  + HapCUT2 Scripts:
    - HapCUT2.Real.Data.Jun9.2019: Script of HapCUT2 being run on the aligned pair-end datasets 826T, 827T, 832T, 847T & 850T (tail -4000000, last million reads).
    - HapCUT2.826T\_1\_chr10.July1.2019: Script of HapCUT2 being run on the aligned single-end dataset 826T\_1\_sequence, only chromosome 10.
    - HapCUT2.whole\_pairend\_826T.July9.2019: Script HapCUT2 being run on the aligned whole pair-end 826T dataset
    - HapCUT2\_NA12891\_fastqdump\_10mil\_reads.Aug13.2019: Script HapCUT2 being run on the fastq-dump obtained data of NA12891 (last 10 million reads, extracting chr10 only).
    - HapCUT2\_NA12891\_wget\_10mil\_reads.Aug13.2019: Script HapCUT2 being run on the wget obtained data of NA12891 (last 10 million reads, extracting chr10 only).
    - HapCUT2\_NA12892\_fastqdump\_10mil\_reads.Aug13.2019: Script HapCUT2 being run on the fastq-dump obtained data of NA12892 (last 10 million reads, extracting chr10 only).
    - HapCUT2\_NA12892\_wget\_10mil\_reads.Aug13.2019: Script HapCUT2 being run on the wget obtained data of NA12892 (last 10 million reads, extracting chr10 only).
  + AltHap Scripts:
    - AltHap.Example.Run.and.1mil.826T.June15.2019: Script of AltHap being run on its example data and script. Incorrectly formatted real data was ran on AltHap at the bottom of this script.
    - AltHap.June27.2019: Corrected script of AltHap (including read and colum numbers) being run on the aligned last 1 million reads of pair-end 826T dataset.
    - AltHap.Input.826T\_1\_chr10.July1.2019: Script of AltHap being run on the aligned single-end dataset 826T\_1\_sequence, only chromosome 10.
    - AltHap.whole\_pairend\_826T.July9.2019: Script of AltHap being run on the aligned whole pair-end 826T dataset
  + MixSIH Scripts:
    - MixSIH.Example.Run.June19.2019: Script of MixSIH run on its example data using the manual’s example script.
    - MixSIH.826TRealData.June16.2019: Script of MixSIH being run on the aligned last 1 million reads of pair-end 826T dataset.
    - MixSIH.826T\_1\_chr10.July1.2019: Script of MixSIH being run on the aligned single-end dataset 826T\_1\_sequence, only chromosome 10.
    - MixSIH.whole\_pairend\_826T.July9.2019: Script of MixSIH being run on the aligned whole pair-end 826T dataset
    - MixSIH\_corrections\_826T.PE\_and\_1mil.826T.PE.July16.2019: Corrected formatting errors and reran MixSIH on 826T PE dataset & 1mil 826T Pe corrected fragment files.
  + PEATH: Script:
    - PEATH\_Example.Run.July8.2019: Compiled PEATH.cpp and ran PEATH on example data using example script
    - PEATH\_826T\_chr10\_PE.July16.2019: Script of PEATH being run on pair-end 826T chr10 dataset.
    - PEATH\_826T.PE\_and\_826T\_chr10.SE.July16.2019: Script of PEATH being run on whole PE 826T and SE 826T chr10 datasets.
  + CSP Scripts:
    - CSP.Example.Run.May21.2019: Script of CSP being installed and ran on its example data and script.
  + GenHap Scripts:
    - GenHap.Example.Run.June5.2019: Script of GenHap run on its example data using the manual’s example script.
  + DBM Scripts:
    - DBM.Example.Run.May21.2019: Script of DBM being installed and ran on its example data and script.
  + HapCol Scripts:
    - HapCol.Example.Run.May22.2019: Script of HapCol being installed and ran on its example data and script.
  + IMPUTE2 Scripts:
    - IMPUTE2.Example.Run.May28.2019: Script of IMPUTE2 run on its example data using the manual’s example script.
  + ParticleHap Scripts:
    - ParticleHap.Example.Run.May20.2019: Script of ParticleHap run on its example data using the manual’s example script.
  + HapSeq2:
    - HapSeq2.Example.Run.June.3.2019: Script of HapSeq2 being installed and ran on its example data and script.
  + SDhaP Scripts:
    - SDhaP.Example.Run.July9.2019: Installed, compiled and ran SDhaP on provided example data and example script.