The DRAGEN command line works by allowing users to configure various options for processing genomic data. The command line is built by combining different components that can be reused, depending on the specific workflow being executed (e.g., germline or somatic tumor workflows). Here’s a detailed breakdown of how it works and the various groupings of options:

1. **Input Options**: These are configured based on the input files you have, such as FASTQ files for sequencing data. You can do a single fastq, two fastq files or a list of fastq file. It also takes existing mapped and aligned data in BAM and CRAM format. You generally either need to input FASTQ or BAM or CRAM but not all of them. The input section will usually include --ref-dir with the reference genome hash table. Also --RGSM and --RGID are required/recommended with fastq inputs but not with --bam-input or --cram-input.
2. **Output Options**: You need to specify where the output will be saved using --output-directory and --output-file-prefix
3. **Map/Align Options**: This is used for all FASTQ sample, but also used if importing BAM or CRAM where realignment is desired. You turn it on with --enable-map-align true to enable mapping and alignment features.
4. **Variant Callers**: Depending on your application, you can configure different variant callers:
   * For example, enabling PGx callers like CYP2D6 and HLA requires setting specific flags in the command line.
5. **Additional Options**: Any other necessary configurations can be added based on your specific use case.

**Constructing Final Command Line**: You can either create a command line directly or you can create a bash/shell file which groups the various options in a readable way, stores these into variables and then these are combined / concatenated into a final command line that executes the desired analysis.

**This is important to remember: the order of the command line options doesn’t matter, but by convention related options are grouped for readability. DRAGEN will process the pipeline intelligently regardless of the order of the options. The order of operations (order of pipeline steps) in DRAGEN is as follows:** decompressing the data (automatic), mapping & aligning (optional for BAM and CRAM inputs), sorting (turned on by default but can be disabled with --enable-sort false), duplicate marking with optional removal (using enable-duplicate-marking and optionally remove-duplicates), and variant calling (enable-variant-caller, enable-cnv, and enable-sv). At the end, everything that is produced is dumped into an output directory with a defined prefix. Separate runs can be kept separate by either having different output directories or by having different prefixes within a single output directory.

By following this structured approach and ensuring that related options are grouped correctly, users can effectively utilize the DRAGEN platform for their genomic analyses.

**A typical multi-caller (multi-step) pipeline call in shell file format is as follows:**

#!/bin/bash

set -euo pipefail

DRAGEN\_HASH\_TABLE=<REF\_DIR>

FASTQ1=<fastq1>

FASTQ2=<fastq2>

RGSM=<RGSM>

RGID=<RGID>

OUTPUT=<OUT\_DIR>

PREFIX=<OUT\_PREFIX>

INPUT\_OPTIONS="

--ref-dir $DRAGEN\_HASH\_TABLE \

--fastq-file1 $FASTQ1 \

--fastq-file2 $FASTQ2 \

--RGSM $RGSM \

--RGID $RGID \

"

OUTPUT\_OPTIONS="

--output-directory $OUTPUT \

--output-file-prefix $PREFIX \

"

MA\_OPTIONS="

--enable-map-align true \

... <any other optional settings> \

"

CNV\_OPTIONS="

--enable-cnv true \

... <any other optional settings> \

"

SNV\_OPTIONS="

--enable-variant-caller true \

... <any other optional settings> \

"

SV\_OPTIONS="

--enable-sv true \

... <any other optional settings> \

"

CMD="

dragen \

$INPUT\_OPTIONS \

$OUTPUT\_OPTIONS \

$MA\_OPTIONS \

$CNV\_OPTIONS \

$SNV\_OPTIONS \

$SV\_OPTIONS \

"

echo $CMD

bash -c $CMD

**Equivalently, the above could be put directly as one long command line call like the following abbreviated version:**

dragen \

--ref-dir $DRAGEN\_HASH\_TABLE \

--fastq-file1 $FASTQ1 \

--fastq-file2 $FASTQ2 \

--RGSM $RGSM \

--RGID $RGID \

--output-directory $OUTPUT \

--output-file-prefix $PREFIX \

--enable-map-align true \

--enable-cnv true \

--enable-variant-caller true \

--enable-sv true \

Please note that the shorthand for --fastq-file1 is -1 and for --fastq-file2 is -2.

If using BAM input, it would look more like this:

dragen \

--ref-dir $DRAGEN\_HASH\_TABLE \

--bam-input $BAM\_FILE

--output-directory $OUTPUT \

--output-file-prefix $PREFIX \

--enable-map-align true \

--enable-cnv true \

--enable-variant-caller true \

--enable-sv true \

With CRAM input it would substitute bam-input for cram-input.

**An important distinction is between WGS and WES.** In general the default in DRAGEN is WGS as all the variant calling scenarios will scan the entire genome by default. In situations where a more limited WES analysis is desired, the analysis is restricted by using options like cnv-target-bed, cnv-combined-counts, vc-target-bed, sv-exome, and sv-call-regions-bed.

**This is also very important.** Each input command line option comes with multiple versions of the command line: a normal version and a tumor version. Below is the correspondence between these with the normal version first and the tumor version second:

fastq-file1, tumor-fastq1

fastq-file2, tumor-fastq2

bam-input, tumor-bam-input

bam-list, tumor-bam-list

cram-list, tumor-cram-list

cram-input, tumor-cram-input

fastq-list, tumor-fastq-list

Any time you are doing germline sequencing and analysis, you will only use the normal versions of these input options. Anytime you are doing tumor-only analysis, you will only use the tumor versions of these input options. When you are doing tumor-normal analysis, you include BOTH because you are comparing tumor sequences and normal sequences.

The way to say “I’m doing germline analysis” is simply to only provide input options that do not include the word “tumor.” The way to say “I’m doing tumor-only analysis” is simply to only provide input options that include the word “tumor.” And the way to do tumor-normal analysis is to include input options of both normal and tumor (including and non including “tumor” in the option name).

**This is also important!** Each time there are input files (e.g. input-bam option or –fastq1 etc.) you should definitely have an --output-directory option and possibly also an –output-file-prefix option.

**Please note:** any time you output a command line or a bash shell file you should do it as a code block like this:

```dragen \

--ref-dir <REF\_DIR> \

--tumor-bam-input <TUMOR\_BAM> \

--output-directory <OUT\_DIR> \

--output-file-prefix <OUT\_PREFIX> \

--enable-map-align true \

--enable-variant-caller true

```