

# Reference Documentation for ODGI

## v0.6.0

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# 1. odgi (1)

## 1.1. NAME

odgi - dynamic succinct variation graph tool

## 1.2. SYNOPSIS

**odgi** **build** -g graph.gfa -o graph.og

**odgi** **stats** -i graph.og -S

**odgi** **depth** -i graph.og

**odgi** **cover** -i graph.og -o graph.paths.og

**odgi** **extract** -i graph.og -p prefix -r path\_name:0-17

**odgi** **explode** -i graph.og -p prefix

**odgi** **squeeze** -f input\_graphs.txt -o graphs.og

**odgi** **position** -i target\_graph.og -g

**odgi** **sort** -i graph.og -o graph.sorted.og -p bSnSnS

**odgi** **view** -i graph.og -g

**odgi** **kmers** -i graph.og -c -k 23 -e 34 -D 50

**odgi** **unitig** -i graph.og -f -t 1324 -l 120

**odgi** **viz** -i graph.og -o graph.og.png -x 1920 -y 1080 -R -t 28

**odgi** **paths** -i graph.og -f

**odgi** **prune** -i graph.og -o graph.pruned.og -c 3 -C 345 -T

**odgi** **unchop** -i graph.og -o graph.unchopped.og

**odgi** **normalize** -i graph.og -o graph.normalized.og -I 100 -d

**odgi** **bin** -i graph.og -j -w 100 -s -g

**odgi** **matrix** -i graph.og -e -d

**odgi** **chop** -i graph.og -o graph.choped.og -c 1000

**odgi** **groom** -i graph.og -o graph.groomed.og

**odgi** **layout** -i graph.og -o graph.svg -R 10 -m 100

**odgi break** -i graph.og -o graph.broken.og -s 100 -d

**odgi pathindex** -i graph.og -o graph.xp

**odgi panpos** -i graph.og -p Chr1 -n 4

**odgi server** -i graph.og -p 4000 -ip 192.168.8.9

**odgi test**

**odgi version**

## 1.3. DESCRIPTION

**odgi**, the **Optimized Dynamic (genome) Graph Interface**, links a thrifty dynamic in-memory variation graph data model to a set of algorithms designed for scalable sorting, pruning, transformation, and visualization of very large **genome graphs**. **odgi** includes **python bindings** that can be used to **directly interface with its data model**. This **odgi** manual provides detailed information about its features and subcommands, including examples.

## 1.4. COMMANDS

Each command has its own man page which can be viewed using e.g. **man odgi\_build.1**. Below we have a brief summary of syntax and subcommand description.

**odgi build** [-g, --gfa=FILE] [-o, --out=FILE] [OPTION]...

The **odgi build(1)** command constructs a succinct variation graph from a GFA. Currently, only GFA1 is supported. For details of the format please see <https://github.com/GFA-spec/GFA-spec/blob/master/GFA1.md>.

**odgi stats** [-i, --idx=FILE] [OPTION]...

The **odgi stats(1)** command produces statistics of a variation graph. Among other metrics, it can calculate the #nodes, #edges, #paths and the total nucleotide length of the graph. Various histogram summary options complement the tool. If [-B, --bed-multicov=BED] is set, the metrics will be produced for the intervals specified in the BED.

**odgi depth** [-i, --input=FILE] [OPTION]... The **odgi depth(1)** command finds the depth of graph as defined by query criteria.

**odgi cover** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The **odgi cover(1)** command finds a path cover of a variation graph, with a specified number of paths per component.

**odgi extract** [-f, --input-graphs=FILE] [-o, --out=FILE] [OPTION]... The **odgi extract(1)** command extracts parts of the graph as defined by query criteria.

**odgi explode** [-i, --idx=FILE] [-p, --prefix=STRING] [OPTION]...

The **odgi explode(1)** command breaks a graph into connected components, writing each component in its own file.

**odgi squeeze** [-f, --input-graphs=FILE] [-o, --out=FILE] [OPTION]... The `odgi squeeze(1)` command squeezes multiple graphs into the same file.

**odgi position** [-i, --target=FILE] [OPTION]... The `odgi position(1)` command position parts of the graph as defined by query criteria.

**odgi sort** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi sort(1)` command sorts a succinct variation graph. `Odgi sort` offers a diverse palette of sorting algorithms to determine the node order:

- A topological sort: A graph can be sorted via [breadth-first search \(BFS\)](#) or [depth-first search \(DFS\)](#). Optionally, a chunk size specifies how much of the graph to grab at once in each topological sorting phase. The sorting algorithm will continue the sort from the next node in the prior graph order that has not been sorted, yet. The cycle breaking algorithm applies a DFS sort until a cycle is found. We break and start a new DFS sort phase from where we stopped.
- A random sort: The graph is randomly sorted. The node order is randomly shuffled from [Mersenne Twister pseudo-random](#) generated numbers.
- A sparse matrix mondriaan sort: We can partition a hypergraph with integer weights and uniform hyperedge costs using the [Mondriaan](#) partitioner.
- A 1D linear SGD sort: `Odgi` implements a 1D linear, variation graph adjusted, multi-threaded version of the [Graph Drawing by Stochastic Gradient Descent](#) algorithm. The force-directed graph drawing algorithm minimizes the graph's energy function or stress level. It applies stochastic gradient descent (SGD) to move a single pair of nodes at a time.
- An eades algorithmic sort: Use [Peter Eades' heuristic for graph drawing](#).

Sorting the paths in a graph may refine the sorting process. For the users' convenience, it is possible to specify a whole pipeline of sorts within one parameter.

**odgi view** [-i, --idx=FILE] [OPTION]...

The `odgi view(1)` command can convert a graph in `odgi` format to `GFAv1`. It can reveal a graph's internal structures for e.g. debugging processes.

**odgi kmers** [-i, --idx=FILE] [-c, --stdout] [OPTION]...

Given a kmer length, the `odgi kmers(1)` command can emit all kmers. The output can be refined by setting the maximum number of furcations at edges or by not considering nodes above a given node degree limit.

**odgi unitig** [-i, --idx=FILE] [OPTION]...

The `odgi unitig(1)` command can print all unitigs of a given `odgi` graph to standard output in `FASTA` format. Unitigs can also be emitted in a fixed sequence quality `FASTQ` format. Various parameters can refine the unitigs to print.

**odgi viz** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi viz(1)` command can produce a linear, static visualization of an `odgi` variation graph. It aggregates the pangenome into bins and directly renders a raster image. The binning level depends on the target width of the PNG to emit. Can be used to produce visualizations for gigabase scale pangenomes. For more information about the binning process, please refer to [odgi bin](#). If reverse coloring was selected, only the bins with a reverse rate of at least 0.5 are colored. Currently, there is

no parameter to color according to the sequence coverage in bins available.

**odgi paths** [-i, --idx=FILE] [OPTION]...

The `odgi paths(1)` command allows the investigation of paths of a given variation graph. It can calculate overlap statistics of groupings of paths.

**odgi prune** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi prune(1)` command can remove complex parts of a graph. One can drop paths, nodes by a certain kind of edge coverage, edges and graph tips. Specifying a kmer length and a maximum number of furcations, the graph can be broken at edges not fitting into these conditions.

**odgi unchop** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi unchop(1)` command merges each unitig into a single node.

**odgi normalize** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi normalize(1)` command [unchops](#) a given variation graph and simplifies redundant furcations.

**odgi matrix** [-i, --idx=FILE] [OPTION]...

The `odgi matrix(1)` command generates a sparse matrix format out of the graph topology of a given variation graph.

**odgi bin** [-i, --idx=FILE] [OPTION]...

The `odgi bin(1)` command bins a given variation graph. The pangenome sequence, the one-time traversal of all nodes from smallest to largest node identifier, can be summed up into bins of a specified size. For each bin, the path metainformation is summarized. This enables a summarized view of gigabase scale graphs. Each step of a path is a bin and connected to its next bin via a link. A link has a start bin identifier and an end bin identifier.

The concept of `odgi bin` is also applied in `odgi viz`. A demonstration of how the `odgi bin` JSON output can be used for an interactive visualization is realized in the [Pantograph](#) project. Per default, `odgi bin` writes the bins to stdout in a tab-delimited format: **path.name**, **path.prefix**, **path.suffix**, **bin** (bin identifier), **mean.cov** (mean coverage of the path in this bin), **mean.inv** (mean inversion rate of this path in this bin), **mean.pos** (mean nucleotide position of this path in this bin), **first.nucl** (first nucleotide position of this path in this bin), **last.nucl** (last nucleotide position of this path in this bin). These nucleotide ranges might span positions that are not present in the bin. Example: A range of 1-100 means that the first nucleotide has position 1 and the last has position 100, but nucleotide 45 could be located in another bin. For an exact positional output, please specify [-j, --json].

**odgi chop** [-i, --idx=FILE] [-o, --out=FILE] [-c, --chop-to=N] [OPTION]...

The `odgi chop(1)` command chops long nodes into short ones while preserving the graph topology.

**odgi layout** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi layout(1)` command draws 2D layouts of the graph using stochastic gradient descent (SGD). The input graph must be sorted and id-compacted. The algorithm itself is described in [Graph Drawing by Stochastic Gradient Descent](#). The force-directed graph drawing algorithm minimizes the graph's energy function or stress level. It applies SGD to move a single pair of nodes at a time. The rendered graph is written in SVG format.

**odgi flatten** [-i, --idx=FILE] [OPTION]...

The `odgi flatten(1)` command projects the graph sequence and paths into FASTA and BED.

**odgi break** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi break(1)` command finds cycles in a graph via [breadth-first search \(BFS\)](#) and breaks them, also dropping the graph's paths.

**odgi pathindex** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

The `odgi pathindex(1)` command generates a path index of a graph. It uses succinct data structures to encode the index. The path index represents a subset of the features of a fully realized [xg index](#). Having a path index, we can use `odgi panpos` to go from **path:position** → **pangenome:position** which is important when navigating large graphs in an interactive manner like in the [Pantograph](#) project.

**odgi panpos** [-i, --idx=FILE] [-p, --path=STRING] [-n, --nuc-pos=N] [OPTION]...

The `odgi panpos(1)` command give a pangenome position for a given path and nucleotide position. It requires a path index, which can be created with `odgi pathindex`. Going from **path:position** → **pangenome:position** is important when navigating large graphs in an interactive manner like in the [Pantograph](#) project. All input and output positions are 1-based.

**odgi server** [-i, --idx=FILE] [-p, --port=N] [OPTION]...

The `odgi server(1)` command starts an HTTP server with a given path index as input. The idea is that we can go from **path:position** → **pangenome:position** via GET requests to the HTTP server. The server headers do not block cross origin requests. Example GET request: [http://localhost:3000/path\\_name/nucleotide\\_position](http://localhost:3000/path_name/nucleotide_position).

The required path index can be created with `odgi pathindex`. Going from **path:position** → **pangenome:position** is important when navigating large graphs in an interactive manner like in the [Pantograph](#) project. All input and output positions are 1-based. If no IP address is specified, the server will run on localhost.

**odgi test** [<TEST NAME | PATTERN | TAGS> ...] [OPTION]...

The `odgi test(1)` command starts all unit tests that are implemented in `odgi`. For targeted testing, a subset of tests can be selected. `odgi test(1)` depends on [Catch2](#). In the default setting, all results are printed to stdout.

**odgi version** [OPTION]...

The `odgi version(1)` command prints the current git version with tags and codename to stdout (like `v-44-g89d022b "back to old ABI"`). Optionally, only the release, version or codename can be printed.

## 1.5. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 1.6. AUTHORS

Erik Garrison from the University of California Santa Cruz wrote the whole **odgi** tool. Simon Heumos from the Quantitative Biology Center Tübingen wrote **odgi pathindex**, **odgi panpos**, **odgi server**, and this documentation. Andrea Guarracino from the University of Rome Tor Vergata wrote **odgi viz**, **odgi extract**, **odgi cover**, **odgi explode**, **odgi squeeze**, **odgi depth**, and this

documentation\*.

## 1.7. RESOURCES

**Project web site:** <https://github.com/pangenome/odgi>

**Git source repository on GitHub:** <https://github.com/pangenome/odgi>

**GitHub organization:** <https://github.com/pangenome>

**Discussion list / forum:** <https://github.com/pangenome/odgi/issues>

## 1.8. COPYING

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## 2. odgi build(1)

### 2.1. NAME

`odgi_build` - construct a dynamic succinct variation graph

### 2.2. SYNOPSIS

**odgi build** [-g, --gfa=FILE] [-o, --out=FILE] [OPTION]...

### 2.3. DESCRIPTION

The `odgi build(1)` command constructs a succinct variation graph from a GFA. Currently, only GFA1



is supported. For details of the format please see <https://github.com/GFA-spec/GFA-spec/blob/master/GFA1.md>.

## 2.4. OPTIONS

### 2.4.1. Graph Files IO

**-g, --gfa=FILE**

GFA1 file containing the nodes, edges and paths to build a dynamic succinct variation graph from.

**-o, --out=FILE**

Write the dynamic succinct variation graph to this file. A file ending with *.og* is recommended.

### 2.4.2. Graph Sorting

**-s, --sort**

Apply a general topological sort to the graph and order the node ids accordingly. A bidirected adaptation of Kahn's topological sort (1962) is used, which can handle components with no heads or tails. Here, both heads and tails are taken into account.

### 2.4.3. Processing Information

**-p, --progress**

Print progress updates to stdout.

**-d, --debug**

Verbosely print graph information to stderr. This includes the maximum node\_id, the minimum node\_id, the handle to node\_id mapping, the deleted nodes and the path metadata.

**--trace**

Include backtrace information when reporting errors.

**-v, --verbose**

Verbosely print processing information to stderr, including debug-level log messages.

**-w, --warnings**

Turn on script warnings (applies to executed code).

**-t, --threads=N**

Number of threads to use for the parallel operations.

### 2.4.4. Program Information

**-h, --help**

Print a help message for **odgi build**.

## 2.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 2.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 2.7. AUTHORS

**odgi build** was written by Erik Garrison.

# 3. odgi stats(1)

## 3.1. NAME

odgi\_stats - metrics describing variation graphs

## 3.2. SYNOPSIS

**odgi stats** [-i, --idx=*FILE*] [*OPTION*]...

## 3.3. DESCRIPTION

The **odgi stats(1)** command produces statistics of a variation graph. Among other metrics, it can calculate the #nodes, #edges, #paths and the total nucleotide length of the graph. Various histogram summary options complement the tool. If [-B, --bed-multicov=*BED*] is set, the metrics will be produced for the intervals specified in the BED.

## 3.4. OPTIONS

### 3.4.1. Graph Files IO

**-i, --idx=***FILE*

File containing the succinct variation graph to create statistics from. The file name usually ends with *.og*.

### 3.4.2. Summary Options

**-S, --summarize**

Summarize the graph properties and dimensions. Print to stdout the #nucleotides, #nodes, #edges and #paths of the graph.

**-W, --weak-connected-components**

Shows the properties of the weakly connected components.

**-b, --base-content**

Describe the base content of the graph. Print to stdout the #A, #C, #G and #T of the graph.

### 3.4.3. Sorting goodness evaluation

**-l, --mean-links-length**

Calculate the mean links length. This metric is path-guided and computable in 1D and 2D.

**-g, --no-gap-links**

Don't penalize gap links in the mean links length. A gap link is a link which connects two nodes that are consecutive in the linear pangenomic order. This option is specifiable only to compute the mean links length in 1D.

**-s, --sum-path-nodes-distances**

Calculate the sum of path nodes distances. This metric is path-guided and computable in 1D and 2D. For each path, it iterates from node to node, summing their distances, and normalizing by the path length. In 1D, if a link goes back in the linearized viewpoint of the graph, this is penalized (adding 3 times its length in the sum).

**-d, --penalize-different-orientation**

If a link connects two nodes which have different orientations, this is penalized (adding 2 times its length in the sum).

**-c, --coords-in**

File containing the layout coordinates of the succinct variation graph specified as input. The file name usually ends with *.lay*. When the layout coordinates are provided, the mean links length and the sum path nodes distances statistics are evaluated in 2D, else in 1D.

**-P, --path-statistics**

Display the statistics (mean links length or sum path nodes distances) for each path.

### 3.4.4. Threading

**-t, --threads=N**

Number of threads to use.

### 3.4.5. Program Information

**-h, --help**

Print a help message for **odgi stats**.

## 3.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 3.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 3.7. AUTHORS

**odgi stats** was written by Erik Garrison and Andrea Guarracino.

# 4. odgi depth(1)

## 4.1. NAME

**odgi\_depth** - find the depth of graph as defined by query criteria

## 4.2. SYNOPSIS

**odgi depth** [-i, --input=*FILE*] [*OPTION*]...

## 4.3. DESCRIPTION

The **odgi depth(1)** command finds the depth of graph as defined by query criteria.

## 4.4. OPTIONS

### 4.4.1. Graph Files IO

**-i, --input=*FILE***

Compute path depths in this graph.

### 4.4.2. Depth Options

**-s, --subset-paths=*FILE***

Compute the depth considering only the paths specified in the *FILE*; the file must contain one path name per line and a subset of all paths can be specified.

**-r, --path=*STRING***

Compute the depth of the given path in the graph

**-R, --paths=FILE**

Compute depth for the paths listed in FILE.

**-g, --graph-pos=[[node\_id]]**

Compute the depth at the given node, e.g. 7 or 3,4 or 42,10,+ or 302,0,-.

**-G, --graph-pos-file=FILE**

A file with graph path position per line.

**-p, --path-pos=[[path\_name]]**

Return depth at the given path position e.g. chrQ or chr3,42 or chr8,1337,+ or chrZ,3929,-.

**-F, --path-pos-file=FILE**

A file with one path position per line.

**-b, --bed-input=FILE**

A BED file of ranges in paths in the graph.

**-d, --graph-depth**

Compute the depth on each node in the graph.

**-d, --search-radius=STRING**

Limit coordinate conversion breadth-first search up to DISTANCE bp from each given position [default: 10000].

### 4.4.3. Threading

**-t, --threads=N**

Number of threads to use.

### 4.4.4. Program Information

**-h, --help**

Print a help message for **odgi depth**.

## 4.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 4.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 4.7. AUTHORS

**odgi depth** was written by Andrea Guarracino.

# 5. odgi sort(1)

## 5.1. NAME

**odgi\_sort** - sort a variation graph

## 5.2. SYNOPSIS

**odgi sort** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

## 5.3. DESCRIPTION

The **odgi sort(1)** command sorts a succinct variation graph. **Odgi sort** offers a diverse palette of sorting algorithms to determine the node order:

- A topological sort: A graph can be sorted via [breadth-first search \(BFS\)](#) or [depth-first search \(DFS\)](#). Optionally, a chunk size specifies how much of the graph to grab at once in each topological sorting phase. The sorting algorithm will continue the sort from the next node in the prior graph order that has not been sorted, yet. The cycle breaking algorithm applies a DFS sort until a cycle is found. We break and start a new DFS sort phase from where we stopped.
- A random sort: The graph is randomly sorted. The node order is randomly shuffled from [Mersenne Twister pseudo-random](#) generated numbers.
- A 1D linear SGD sort: **Odgi** implements a 1D linear, variation graph adjusted, multi-threaded version of the [Graph Drawing by Stochastic Gradient Descent](#) algorithm. The force-directed graph drawing algorithm minimizes the graph's energy function or stress level. It applies stochastic gradient descent (SGD) to move a single pair of nodes at a time.
- A path guided, 1D linear SGD sort: **Odgi** implements a 1D linear, variation graph adjusted, multi-threaded version of the [Graph Drawing by Stochastic Gradient Descent](#) algorithm. The force-directed graph drawing algorithm minimizes the graph's energy function or stress level. It applies stochastic gradient descent (SGD) to move a single pair of nodes at a time. The path index is used to pick the terms to move stochastically. If ran with 1 thread only, the resulting order of the graph is deterministic. The seed is adjustable.

Sorting the paths in a graph may refine the sorting process. For the users' convenience, it is possible to specify a whole pipeline of sorts within one parameter.

## 5.4. OPTIONS

### 5.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to sort. The file name usually ends with *.og*.

**-o, --out=FILE**

Write the sorted dynamic succinct variation graph to this file. A file ending with *.og* is recommended.

**-s, --sort-order=FILE**

File containing the sort order. Each line contains one node identifier.

### 5.4.2. Topological Sorts

**-b, --breadth-first**

Use a (chunked) breadth first topological sort.

**-B, --breadth-first-chunk=N**

Chunk size for breadth first topological sort. Specify how many nucleotides to grap at once in each BFS phase.

**-z, --depth-first**

Use a (chunked) depth first topological sort.

**-Z, --depth-first-chunk=N**

Chunk size for the depth first topological sort. Specify how many nucleotides to grap at once in each DFS phace.

**-w, --two-way**

Use a two-way topological algorithm for sorting. It is a maximum of head-first and tail-first topological sort.

**-n, --no-seeds**

Don't use heads or tails to seed topological sort.

**-c, --cycle-breaking**

Use a cycle breaking sort.

### 5.4.3. Random Sort

**-r, --random**

Randomly sort the graph.

#### 5.4.4. Path Guided 1D Linear SGD Sort

**-Y, --path-sgd**

Apply path guided 1D linear SGD algorithm to organize the graph.

**-X, --path-index=FILE**

Load the path index from this *FILE*.

**-f, --path-sgd-use-paths=FILE**

Specify a line separated list of paths to sample from for the on the fly term generation process in the path guided linear 1D SGD. The default value are *all paths*.

**-G, --path-sgd-min-term-updates-paths=N**

The minimum number of terms to be updated before a new path guided linear 1D SGD iteration with adjusted learning rate eta starts, expressed as a multiple of total path steps. The default value is *1.0*. Can be overwritten by *-U, -path-sgd-min-term-updates-nodes=N*.

**-U, --path-sgd-min-term-updates-nodes=N**

The minimum number of terms to be updated before a new path guided linear 1D SGD iteration with adjusted learning rate eta starts, expressed as a multiple of the number of nodes. Per default, the argument is not set. The default of *-G, path-sgd-min-term-updates-paths=N* is used).

**-j, --path-sgd-delta=N**

The threshold of maximum displacement approximately in bp at which to stop path guided linear 1D SGD. Default values is *0.0*.

**-g, --path-sgd-eps=N**

The final learning rate for path guided linear 1D SGD model. The default value is *0.01*.

**-v, --path-sgd-eta-max=N**

The first and maximum learning rate for path guided linear 1D SGD model. The default value is *squared steps of longest path in graph*.

**-a, --path-sgd-zipf-theta=N**

The theta value for the Zipfian distribution which is used as the sampling method for the second node of one term in the path guided linear 1D SGD model. The default value is *0.99*.

**-x, --path-sgd-iter-max=N**

The maximum number of iterations for path guided linear 1D SGD model. The default value is *30*.

**-F, --iteration-max-learning-rate=N**

The iteration where the learning rate is max for path guided linear 1D SGD model. The default value is *0*.

**-k, --path-sgd-zipf-space=N**

The maximum space size of the Zipfian distribution which is used as the sampling method for the second node of one term in the path guided linear 1D SGD model. The default value is the



*longest path length.*

**-I, --path-sgd-zipf-space-max=*N***

The maximum space size of the Zipfian distribution beyond which quantization occurs. Default value is *100*.

**-l, --path-sgd-zipf-space-quantization-step=*N***

Quantization step size when the maximum space size of the Zipfian distribution is exceeded. Default value is *100*.

**-y, --path-sgd-zipf-max-num-distributions=*N***

Approximate maximum number of Zipfian distributions to calculate. The default value is *100*.

**-q, --path-sgd-seed=*N***

Set the seed for the deterministic 1-threaded path guided linear 1D SGD model. The default value is *pangenomic!*.

**-u, --path-sgd-snapshot=*STRING***

Set the prefix to which each snapshot graph of a path guided 1D SGD iteration should be written to. This is turned off per default. This argument only works when *-Y, --path-sgd* was specified. Not applicable in a pipeline of sorts.

### 5.4.5. Path Sorting Options

**-L, --paths-min**

Sort paths by their lowest contained node identifier.

**-M, --paths-max**

Sort paths by their highest contained node identifier.

**-A, --paths-avg**

Sort paths by their average contained node identifier.

**-R, --paths-avg-rev**

Sort paths in reverse by their average contained node identifier.

**-D, --path-delim=*path-delim***

Sort paths in bins by their prefix up to this delimiter.

### 5.4.6. Pipeline Sorting

**-p, --pipeline=*STRING***

Apply a series of sorts, based on single character command line arguments given to this command. The default sort is *s*. The reverse sort would be specified via *f*.

### 5.4.7. Additional Parameters

**-d, --dagify-sort**

Sort on the basis of a DAGified graph.

**-O, --Optimize**

Use the MutableHandleGraph::optimize method to compact the node identifier space.

### 5.4.8. Threading

**-t, --threads=N**

Number of threads to use for the parallel operations.

### 5.4.9. Processing Information

**-P, --progress**

Print sort progress to stdout.

### 5.4.10. Program Information

**-h, --help**

Print a help message for **odgi sort**.

## 5.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 5.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 5.7. AUTHORS

**odgi sort** was written by Erik Garrison, Simon Heumos, and Andrea Guarracino.

# 6. odgi groom(1)

## 6.1. NAME

odgi\_groom - resolve spurious inverting links

## 6.2. SYNOPSIS

**odgi groom** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 6.3. DESCRIPTION

The `odgi groom(1)` command resolves spurious inverting links.

## 6.4. OPTIONS

### 6.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to groom. The file name usually ends with *.og*.

**-o, --out=*FILE***

Write the groomed succinct variation graph to *FILE*. The file name usually ends with *.og*.

### 6.4.2. Processing Information

**-P, --progress**

Display progress of the grooming to stderr.

### 6.4.3. Program Information

**-h, --help**

Print a help message for **odgi groom**.

## 6.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 6.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 6.7. AUTHORS

**odgi groom** was written by Erik Garrison and Andrea Guarracino.

# 7. odgi cover(1)

## 7.1. NAME

odgi\_cover - find a path cover of the variation graph

## 7.2. SYNOPSIS

**odgi cover** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 7.3. DESCRIPTION

The odgi cover(1) command finds a path cover of a variation graph, with a specified number of paths per component.

## 7.4. OPTIONS

### 7.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph where find a path cover. The file name usually ends with *.og*.

**-o, --out=*FILE***

Write the succinct variation graph with the generated paths to *FILE*. The file name usually ends with *.og*.

### 7.4.2. Cover Options

**-n, --num-paths-per-component=*N***

Number of paths to generate per component.

**-k, --node-windows-size=*N***

Size of the node window to check each time a new path is extended (it has to be greater than or equal to 2).

**-c, --min-node-coverage=*N***

Minimum node coverage to reach (it has to be greater than 0). There will be generated paths until the specified minimum node coverage is reached, or until the maximum number of allowed generated paths is reached (number of nodes in the input variation graph).

**-i, --ignore-paths**

Ignore the paths already embedded in the graph during the nodes coverage initialization.

**-w, --write-node-coverages=*FILE***

Write the node coverages at the end of the paths generation to FILE. The file will contain tab-separated values (header included), and have 3 columns: *component\_id*, *node\_id*, and *coverage*.

### 7.4.3. Threading

**-t, --threads=N**

Number of threads to use for the parallel sorter.

### 7.4.4. Processing Information

**-P, --progress**

Print information about the components and the progress to stderr.

### 7.4.5. Program Information

**-h, --help**

Print a help message for **odgi cover**.

## 7.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 7.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 7.7. AUTHORS

**odgi cover** was written by Andrea Guarracino.

# 8. odgi explode(1)

## 8.1. NAME

**odgi\_explode** - breaks a graph into connected components in their own files

## 8.2. SYNOPSIS

**odgi explode** [-i, --idx=FILE] [-p, --prefix=STRING] [OPTION]...

## 8.3. DESCRIPTION

The `odgi explode(1)` command breaks a graph into connected components, writing each component in its own file.

## 8.4. OPTIONS

### 8.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to break in its components. The file name usually ends with `.og`.

### 8.4.2. Explode Options

**-p, --prefix=STRING**

Write each connected component in a file with the given prefix. The file for the component `i` will be named `STRING.i.og` (default: `component`)

**-O, --optimize**

Compact the node ID space in each connected component.

### 8.4.3. Threading

**-t, --threads=N**

Number of threads to use (to write the components in parallel).

### 8.4.4. Processing Information

**-P, --progress**

Print information about the components and the progress to stderr.

### 8.4.5. Program Information

**-h, --help**

Print a help message for `odgi explode`.

## 8.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 8.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 8.7. AUTHORS

**odgi explode** was written by Andrea Guarracino.

# 9. odgi squeeze(1)

## 9.1. NAME

**odgi\_squeeze** - squeezes multiple graphs into the same file

## 9.2. SYNOPSIS

**odgi squeeze** [-f, --input-graphs=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 9.3. DESCRIPTION

The **odgi squeeze(1)** command merges multiple graphs into the same file.

## 9.4. OPTIONS

### 9.4.1. Graph Files IO

**-f, --input-graphs=*FILE***

Input file containing the list of graphs to squeeze into the same file. The file must contain one path per line.

**-o, --out=*FILE***

Store all the input graphs in this file. The file name usually ends with *.og*.

### 9.4.2. Squeeze Options

**-s, --rank-suffix=*STRING***

Add the separator and the input file rank as suffix to the path names (to avoid path name collisions).

**-O, --optimize**

Compact the node ID space in each input file before imploding.

### 9.4.3. Threading

**-t, --threads=*N***

Number of threads to use.

#### 9.4.4. Processing Information

**-P, --progress**

Print information about the progress to stderr.

#### 9.4.5. Program Information

**-h, --help**

Print a help message for **odgi squeeze**.

### 9.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

### 9.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

### 9.7. AUTHORS

**odgi squeeze** was written by Andrea Guarracino.

## 10. odgi extract(1)

### 10.1. NAME

**odgi\_extract** - extract parts of the graph as defined by query criteria

### 10.2. SYNOPSIS

**odgi extract** [-f, --input-graphs=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

### 10.3. DESCRIPTION

The **odgi extract(1)** command extracts parts of the graph as defined by query criteria.



## 10.4. OPTIONS

### 10.4.1. Graph Files IO

**-f, --input-graphs=FILE**

File containing the succinct variation graph. The file name usually ends with *.og*.

**-o, --out=FILE**

Store all subgraph in this file. The file name usually ends with *.og*.

### 10.4.2. Extract Options

**-s, --split-subgraphs=STRING**

Instead of writing the target subgraphs into a single graph, write one subgraph per given target to a separate file named *path:start-end.og* (0-based coordinates).

**-I, --inverse**

Extract parts of the graph that do not meet the query criteria.

**-l, --node-list::\_FILE\_**

A file with one node id per line. The node specified will be extracted from the input graph.

**-n, --node::\_STRING\_**

A single node from which to begin our traversal.

**-c, --context::\_NUMBER\_**

The number of steps away from our initial subgraph that we should collect.

**-L, --use-length**

Treat the context size as a length in bases (and not as a number of steps).

**-r, --path-range**

Find the node(s) in the specified path range TARGET=path[:pos1[-pos2]] (0-based coordinates)

**-r, --bed-file::\_FILE\_**

Find the node(s) in the path range(s) specified in the given BED FILE

**-E, --full-range**

Collects all nodes in the sorted order of the graph in the min and max position touched by the given path ranges. Be careful to use it with very complex graphs.

### 10.4.3. Threading

**-t, --threads=N**

Number of threads to use (to embed the subpaths in parallel).

#### 10.4.4. Processing Information

**-P, --progress**

Print information to stderr.

#### 10.4.5. Program Information

**-h, --help**

Print a help message for **odgi extract**.

### 10.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

### 10.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

### 10.7. AUTHORS

**odgi extract** was written by Andrea Guarracino.

## 11. odgi view(1)

### 11.1. NAME

odgi\_view - projection of graphs into other formats

### 11.2. SYNOPSIS

**odgi view** [-i, --idx=*FILE*] [*OPTION*]...

### 11.3. DESCRIPTION

The **odgi view(1)** command can convert a graph in **odgi** format to GFAv1. It can reveal a graph's internal structures for e.g. debugging processes.

### 11.4. OPTIONS

### 11.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to convert from. The file name usually ends with *.og*.

**-g, --to-gfa**

Write the graph in GFAv1 format to standard output.

### 11.4.2. Summary Options

**-d, --display**

Show the internal structures of a graph. Print to stdout the maximum node identifier, the minimum node identifier, the nodes vector, the delete nodes bit vector and the path metadata, each in a separate line.

### 11.4.3. Program Information

**-h, --help**

Print a help message for **odgi view**.

## 11.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 11.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 11.7. AUTHORS

**odgi view** was written by Erik Garrison.

# 12. odgi kmers(1)

## 12.1. NAME

**odgi\_kmers** - show and characterize the kmer space of the graph

## 12.2. SYNOPSIS

**odgi kmers** [-i, --idx=FILE] [-c, --stdout] [OPTION]...

## 12.3. DESCRIPTION

Given a kmer length, the `odgi kmers(1)` command can emit all kmers. The output can be refined by setting the maximum number of furcations at edges or by not considering nodes above a given node degree limit.

## 12.4. OPTIONS

### 12.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to convert from. The file name usually ends with `.og`.

**-c, --stdout=**

Write the kmers to standard output. Kmers are line-separated.

### 12.4.2. Kmer Options

**-k, --kmer-length=N**

The kmer length to generate kmers from.

**-e, --max-furcations=N**

Break at edges that would induce this many furcations when generating a kmer.

**-D, --max-degree=N**

Don't take nodes into account that have a degree greater than *N*.

### 12.4.3. Threading

**-t, --threads=N**

Number of threads to use.

### 12.4.4. Program Information

**-h, --help**

Print a help message for **odgi kmers**.

## 12.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 12.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 12.7. AUTHORS

**odgi kmers** was written by Erik Garrison.

# 13. odgi unitig(1)

## 13.1. NAME

`odgi_unitig` - output unitigs of the graph

## 13.2. SYNOPSIS

**odgi unitig** [-i, --idx=*FILE*] [*OPTION*]...

## 13.3. DESCRIPTION

The `odgi unitig(1)` command can print all [unitigs](#) of a given `odgi` graph to standard output in FASTA format. Unitigs can also be emitted in a fixed sequence quality FASTQ format. Various parameters can refine the unitigs to print.

## 13.4. OPTIONS

### 13.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to convert from. The file name usually ends with `.og`.

### 13.4.2. FASTQ Options

**-f, --fake-fastq**

Write the unitigs in FASTQ format to stdout with a fixed quality value of *I*.

### 13.4.3. Unitig Options

**-t, --sample-to=*N***

Continue unitigs with a random walk in the graph so that they have at least the given *N* length.

**-p, --sample-plus=*N***

Continue unitigs with a random walk in the graph by *N* past their natural end.

**-l, --min-begin-node-length=*N***

Only begin unitigs collection from nodes which have at least length *N*.

#### 13.4.4. Program Information

**-h, --help**

Print a help message for **odgi unitig**.

### 13.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

### 13.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

### 13.7. AUTHORS

**odgi unitig** was written by Erik Garrison.

## 14. odgi viz(1)

### 14.1. NAME

odgi\_viz - variation graph visualizations

### 14.2. SYNOPSIS

**odgi viz** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

### 14.3. DESCRIPTION

The **odgi viz(1)** command can produce a linear, static visualization of an **odgi** variation graph. It can aggregate the pangenome into bins and directly renders a raster image. The binning level can be specified in input or it is calculated from the target width of the PNG to emit. Can be used to produce visualizations for gigabase scale pangenomes. For more information about the binning process, please refer to [odgi bin](#).

## 14.4. OPTIONS

### 14.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to convert from. The file name usually ends with *.og*.

**-o, --out=FILE**

Write the visualization in PNG format to this file.

### 14.4.2. Visualization Options

**-x, --width=N**

Set the width in pixels of the output image.

**-y, --height=N**

Set the height in pixels of the output image.

**-P, --path-height=N**

The height in pixels for a path.

**-X, --path-x-padding=N**

The padding in pixels on the x-axis for a path.

**-R, --pack-paths**

Pack all paths rather than displaying a single path per row.

**-L, --link-path-pieces=FLOAT**

Show thin links of this relative width to connect path pieces.

**-A, --alignment-prefix=STRING**

Apply alignment related visual motifs to paths which have this name prefix. It affects the **[-S, --show-strand]** and **[-d, --change-darkness]** options.

**-S, --show-strand**

Use red and blue coloring to display forward and reverse alignments. This parameter can be set in combination with **[-A, --alignment-prefix=STRING]**.

**-z, --color-by-mean-inversion-rate**

Change the color respect to the node strandness (black for forward, red for reverse); in binned mode (**-b, --binned-mode**), change the color respect to the mean inversion rate of the path for each bin, from black (no inversions) to red (bin mean inversion rate equals to 1).

**-s, --color-by-prefix**

Colors paths by their names looking at the prefix before the given character C.

### 14.4.3. Intervals selection

#### -r, --path-range

Nucleotide range to visualize: `STRING=[PATH:]start-end`. `*-end` for `[0,end]`; `start-*` for `[start,pangenome_length]`. If no PATH is specified, the nucleotide positions refer to the pangenome's sequence (i.e., the sequence obtained arranging all the graph's node from left to right).

### 14.4.4. Paths selection

#### -p, --paths-to-display

List of paths to display in the specified order; the file must contain one path name per line and a subset of all paths can be specified.

### 14.4.5. Path names visualization Options

#### -H, --hide-path-names

Hide the path names on the left of the generated image.

#### -C, --color-path-names-background

Color path names background with the same color as paths

#### -c, --max-num-of-characters

Maximum number of characters to display for each path name (max 128 characters). The default value is *the length of the longest path name* (up to 32 characters).

### 14.4.6. Binned Mode Options

#### -b, --binned-mode

The variation graph is binned before its visualization. Each pixel in the output image will correspond to a bin. For more information about the binning process, please refer to [odgi bin](#).

#### -w, --bin-width=N

The bin width specifies the size of each bin in the binned mode. If it is not specified, the bin width is calculated from the width in pixels of the output image.

#### -g, --no-gap-links

We divide links into 2 classes:

1. the links which help to follow complex variations. They need to be drawn, else one could not follow the sequence of a path.
2. the links helping to follow simple variations. These links are called **gap-links**. Such links solely connecting a path from left to right may not be relevant to understand a path's traversal through the bins. Therefore, when this option is set, the gap-links are not drawn in binned mode.

#### -m, --color-by-mean-coverage



Change the color respect to the mean coverage of the path for each bin, from black (no coverage) to blue (max bin mean coverage in the entire graph).

### 14.4.7. Gradient Mode (also known as Position Mode) Options

#### **-d, --change-darkness**

Change the color darkness based on nucleotide position in the path. When it is used in binned mode, the mean inversion rate of the bin node is considered to set the color gradient starting position: when this rate is greater than 0.5, the bin is considered inverted, and the color gradient starts from the right-end of the bin. This parameter can be set in combination with [-A, --alignment-prefix=STRING].

#### **-l, --longest-path**

Use the longest path length to change the color darkness.

#### **-u, --white-to-black**

Change the color darkness from white (for the first nucleotide position) to black (for the last nucleotide position).

### 14.4.8. Program Information

#### **-h, --help**

Print a help message for **odgi viz**.

## 14.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 14.6. BUGS

Refer to the *odgi* issue tracker at <https://github.com/pangenome/odgi/issues>.

## 14.7. AUTHORS

**odgi viz** was written by Erik Garrison and Andrea Guarracino.

## 15. odgi paths(1)

## 15.1. NAME

odgi\_paths - embedded path interrogation

## 15.2. SYNOPSIS

**odgi\_paths** [-i, --idx=*FILE*] [*OPTION*]...

## 15.3. DESCRIPTION

The `odgi_paths(1)` command allows the investigation of paths of a given variation graph. It can calculate overlap statistics of groupings of paths.

## 15.4. OPTIONS

### 15.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to investigate the paths from. The file name usually ends with *.og*.

**-O, --overlaps=*FILE***

Read in the path grouping file to generate the overlap statistics from. The file must be tab-delimited. The first column lists a grouping and the second the path itself. Each line has one path entry. For each group the pairwise overlap statistics for each pairing will be calculated and printed to stdout.

### 15.4.2. Investigation Options

**-L, --list-paths**

Print the paths in the graph to stdout. Each path is printed in its own line.

**-H, --haplotypes**

Print to stdout the paths in an approximate binary haplotype matrix based on the graph's sort order. The output is tab-delimited: **path.name**, **path.length**, **node.count**, **node.1**, **node.2**, **node.n**. Each path entry is printed in its own line.

**-D, --delim=*CHAR***

The part of each path name before this delimiter is a group identifier. This parameter should only be set in combination with **[-H, --haplotypes]**. Prints an additional, first column **group.name** to stdout.

**-d, --distance**

Provides a sparse distance matrix for paths. If **[-D, --delim]** is set, it will be path groups distances.

**-f, --fasta**

Print paths in FASTA format to stdout.

### 15.4.3. Threading

**-t, --threads=N**

Number of threads to use.

### 15.4.4. Program Information

**-h, --help**

Print a help message for **odgi paths**.

## 15.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 15.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 15.7. AUTHORS

**odgi paths** was written by Erik Garrison.

# 16. odgi prune(1)

## 16.1. NAME

**odgi\_prune** - remove complex parts of the graph

## 16.2. SYNOPSIS

**odgi prune** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

## 16.3. DESCRIPTION

The **odgi prune(1)** command can remove complex parts of a graph. One can drop paths, nodes by a certain kind of edge coverage, edges and graph tips. Specifying a kmer length and a maximum number of furcations, the graph can be broken at edges not fitting into these conditions.

## 16.4. OPTIONS

### 16.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to load in. The file name usually ends with *.og*.

**-o, --out=FILE**

Write the pruned graph to *FILE*. The file name should end with *.og*.

### 16.4.2. Kmer Options

**-k, --kmer-length=N**

The length of the kmers to consider.

**-e, --max-furcations=N**

Break at edges that would induce *N* many furcations in a kmer.

### 16.4.3. Node Options

**-d, --max-degree=N**

Remove nodes that have a higher node degree than *N*.

**-c, --min-coverage=N**

Remove nodes covered by fewer than *N* number of path steps.

**-C, --max-coverage=N**

Remove nodes covered by more than *N* number of path steps.

**-T, --cut-tips=N**

Remove nodes which are graph tips.

### 16.4.4. Edge Options

**-E, --edge-coverage**

Remove edges outside of the minimum and maximum coverage rather than nodes. Only set this argument in combination with **[-c, --min-coverage=N]** and **[-C, --max-coverage=N]**.

**-b, --best-edges=N**

Only keep the *N* most covered inbound and output edges of each node.

### 16.4.5. Path Options

**-D, --drop-paths**

Remove the paths from the graph.

### 16.4.6. Threading

**-t, --threads=N**

Number of threads to use.

### 16.4.7. Program Information

**-h, --help**

Print a help message for **odgi prune**.

## 16.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 16.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 16.7. AUTHORS

**odgi prune** was written by Erik Garrison.

# 17. odgi unchop(1)

## 17.1. NAME

**odgi\_unchop** - merge unitigs into single nodes

## 17.2. SYNOPSIS

**odgi unchop** [-i, --idx=FILE] [-o, --out=FILE] [OPTION]...

## 17.3. DESCRIPTION

The **odgi unchop(1)** command merges each unitig into a single node preserving the node order.

## 17.4. OPTIONS

### 17.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to unchop. The file name usually ends with *.og*.

**-o, --out=FILE**

Write the unchopped dynamic succinct variation graph to this file. A file ending with *.og* is recommended.

### 17.4.2. Processing Information

**-d, --debug**

Print information about the process to stderr.

### 17.4.3. Threading

**-t, --threads=N**

Number of threads to use for the parallel operations.

### 17.4.4. Program Information

**-h, --help**

Print a help message for **odgi unchop**.

## 17.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 17.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 17.7. AUTHORS

**odgi unchop** was written by Erik Garrison and Andrea Guarracino.

# 18. odgi normalize(1)

## 18.1. NAME

**odgi\_normalize** - compact unitigs and simplify redundant furcations

## 18.2. SYNOPSIS

**odgi normalize** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 18.3. DESCRIPTION

The `odgi normalize(1)` command [unchops](#) a given variation graph and simplifies redundant furcations.

## 18.4. OPTIONS

### 18.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to normalize. The file name usually ends with *.og*.

**-o, --out=*FILE***

Write the normalized dynamic succinct variation graph to this file. A file ending with *.og* is recommended.

**-I, --max-iterations=*N***

Iterate the normalization up to *N* many times. The default is 10.

### 18.4.2. Program Debugging

**-d, --debug**

Print information about the normalization process to stdout.

### 18.4.3. Program Information

**-h, --help**

Print a help message for **odgi normalize**.

## 18.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 18.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 18.7. AUTHORS

**odgi normalize** was written by Erik Garrison.

## 19. odgi bin(1)

### 19.1. NAME

**odgi\_bin** - binning of pangenome sequence and path information in the graph

### 19.2. SYNOPSIS

**odgi bin** [-i, --idx=FILE] [OPTION]...

### 19.3. DESCRIPTION

The **odgi bin(1)** command bins a given variation graph. The pangenome sequence, the one-time traversal of all nodes from smallest to largest node identifier, can be summed up into bins of a specified size. For each bin, the path metainformation is summarized. This enables a summarized view of gigabase scale graphs. Each step of a path is a bin and connected to its next bin via a link. A link has a start bin identifier and an end bin identifier.

The concept of **odgi bin** is also applied in **odgi viz**. A demonstration of how the **odgi bin** JSON output can be used for an interactive visualization is realized in the [Pantograph](#) project. Per default, **odgi bin** writes the bins to stdout in a tab-delimited format: **path.name**, **path.prefix**, **path.suffix**, **bin** (bin identifier), **mean.cov** (mean coverage of the path in this bin), **mean.inv** (mean inversion rate of this path in this bin), **mean.pos** (mean nucleotide position of this path in this bin), **first.nucl** (first nucleotide position of this path in this bin), **last.nucl** (last nucleotide position of this path in this bin). These nucleotide ranges might span positions that are not present in the bin. Example: A range of 1-100 means that the first nucleotide has position 1 and the last has position 100, but nucleotide 45 could be located in another bin. For an exact positional output, please specify [-j, --json].

Running **odgi bin** in [HaploBlocker](#) mode, only arguments [-b, --haplo-blocker], [-p[N], --haplo-blocker-min-paths[N]], and [-c[N], --haplo-blocker-min-coverage[N]] are required. A TSV is printed to stdout: Each row corresponds to a node. Each column corresponds to a path. Each value is the coverage of a specific node of a specific path.

### 19.4. OPTIONS

#### 19.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to investigate the bin from. The file name usually ends with *.og*.



## 19.4.2. FASTA Options

**-f, --fasta=FILE**

Write the pangenome sequence to *FILE* in FASTA format.

## 19.4.3. Bin Options

**-n, --number-bins=N**

The number of bins the pangenome sequence should be chopped up to.

**-w, --bin-width=N**

The bin width specifies the size of each bin.

**-D, --path-delim=STRING**

Annotate rows by prefix and suffix of this delimiter.

**-a, --aggregate-delim**

Aggregate on path prefix delimiter. Argument depends on **[-D, --path-delim=STRING]**.

**-j, --json**

Print bins and links to stdout in pseudo JSON format. Each line is a valid JSON object, but the whole file is not a valid JSON! First, each bin including its pangenome sequence is printed to stdout per line. Second, for each path in the graph, its traversed bins including meta-information: **bin** (bin identifier), **mean.cov** (mean coverage of the path in this bin), **mean.inv** (mean inversion rate of this path in this bin), **mean.pos** (mean nucleotide position of this path in this bin), and an array of ranges determining the nucleotide position of the path in this bin. Switching first and last nucleotide in a range represents a complement reverse orientation of that particular sequence.

**-s, --no-seqs**

If **[-j, --json]** is set, no nucleotide sequences will be printed to stdout in order to save disk space.

**-g, --no-gap-links**

We divide links into 2 classes:

1. the links which help to follow complex variations. They need to be drawn, else one could not follow the sequence of a path.
2. the links helping to follow simple variations. These links are called **gap-links**. Such links solely connecting a path from left to right may not be relevant to understand a path's traversal through the bins. Therefore, when this option is set, the gap-links are left out saving disk space

## 19.4.4. HaploBlocker Options

**-b, --haplo-blocker**

Write a TSV to stdout formatted in a way ready for HaploBlocker: Each row corresponds to a node. Each column corresponds to a path. Each value is the coverage of a specific node of a specific path.

**-p[N], --haplo-blocker-min-paths[N]**

Specify the minimum number of paths that need to be present in the bin to actually report that bin. The default value is 1.

**-c[N], --haplo-blocker-min-coverage[N]**

Specify the minimum coverage a path needs to have in a bin to actually report that bin. The default value is 1.

### 19.4.5. Program Information

**-h, --help**

Print a help message for **odgi bin**.

**-P, --progress**

Write the current progress to stderr.

## 19.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 19.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 19.7. AUTHORS

**odgi bin** was written by Erik Garrison and Simon Heumos

# 20. odgi matrix(1)

## 20.1. NAME

odgi\_matrix - write the graph topology in sparse matrix formats

## 20.2. SYNOPSIS

**odgi matrix** [-i, --idx=FILE] [OPTION]...

## 20.3. DESCRIPTION

The `odgi matrix(1)` command generates a sparse matrix format out of the graph topology of a given variation graph.

## 20.4. OPTIONS

### 20.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to create the sparse matrix from. The file name usually ends with `.og`.

### 20.4.2. Matrix Options

**-e, --edge-depth-weight**

Weigh edges by their path depth.

**-d, --delta-weight**

Weigh edges by their inverse id delta.

### 20.4.3. Program Information

**-h, --help**

Print a help message for **odgi matrix**.

## 20.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 20.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 20.7. AUTHORS

**odgi matrix** was written by Erik Garrison.

## 21. odgi chop(1)

## 21.1. NAME

odgi\_chop - divide nodes into smaller pieces

## 21.2. SYNOPSIS

**odgi chop** [-i, --idx=*FILE*] [-o, --out=*FILE*] [-c, --chop-to=*N*] [*OPTION*]...

## 21.3. DESCRIPTION

The odgi chop(1) command chops long nodes into short ones while preserving the graph topology and node order.

## 21.4. OPTIONS

### 21.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to chop. The file name usually ends with *.og*.

**-o, --out=*FILE***

Write the chopped succinct variation graph to *FILE*. The file name usually ends with *.og*.

### 21.4.2. Chop Options

**-c, --chop-to=*N***

Divide nodes that longer than *N* into nodes no longer than *N* while maintaining graph topology.

### 21.4.3. Threading

**-t, --threads=*N***

Number of threads to use for the parallel operations.

### 21.4.4. Processing Information

**-d, --debug**

Print information about the process to stderr.

### 21.4.5. Program Information

**-h, --help**

Print a help message for **odgi chop**.

## 21.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 21.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 21.7. AUTHORS

**odgi chop** was written by Erik Garrison and Andrea Guarracino.

# 22. odgi layout(1)

## 22.1. NAME

`odgi_layout` - use SGD to make 2D layouts of the graph

## 22.2. SYNOPSIS

**odgi layout** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 22.3. DESCRIPTION

The `odgi layout(1)` command draws 2D layouts of the graph using stochastic gradient descent (SGD). The input graph must be sorted and id-compacted. The algorithm itself is described in [Graph Drawing by Stochastic Gradient Descent](#). The force-directed graph drawing algorithm minimizes the graph's energy function or stress level. It applies SGD to move a single pair of nodes at a time. The rendered graph is written in SVG format.

## 22.4. OPTIONS

### 22.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to layout. The file name usually ends with `.og`.

**-o, --out=*FILE***

Write the rendered layout in SVG format to *FILE*.

## 22.4.2. SGD Options

**-m, --iter-max=*N***

The maximum number of iterations to run the layout. Default is 30.

**-p, --n-pivots=*N***

The number of pivots for sparse layout. Default is 0 leading to a non-sparse layout.

**-e, --eps=*N***

The learning rate for SGD layout. Default is 0.01.

## 22.4.3. SVG Options

**-x, --x-padding=*N***

The padding between the connected component layouts. Default is 10.0.

**-R, --render-scale=*N***

SVG scaling Default is 5.0.

## 22.4.4. Processing Information

**-d, --debug**

Print information about the components to stdout.

## 22.4.5. Program Information

**-h, --help**

Print a help message for **odgi layout**.

## 22.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 22.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 22.7. AUTHORS

**odgi layout** was written by Erik Garrison, Andrea Guarracino, and Simon Heumos.

# 23. odgi flatten(1)

## 23.1. NAME

odgi\_flatten - generate linearization of the graph

## 23.2. SYNOPSIS

**odgi flatten** [-i, --idx=*FILE*] [*OPTION*]...

## 23.3. DESCRIPTION

The odgi flatten(1) command projects the graph sequence and paths into FASTA and BED.

## 23.4. OPTIONS

### 23.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to flatten. The file name usually ends with *.og*.

### 23.4.2. Output Options

**-f, --fasta=*FILE***

Write the concatenated node sequences in FASTA format to *FILE*.

**-n, --name-seq=*STRING***

The name to use for the concatenated graph sequence. Default is the name of the input file which was specified via [-i, --idx=*FILE*].

**-b, --bed=*FILE***

Write the mapping between graph paths and the linearized FASTA sequence in BED format to *FILE*.

### 23.4.3. Program Information

**-h, --help**

Print a help message for **odgi flatten**.

## 23.5. EXIT STATUS

0

Success.

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 23.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 23.7. AUTHORS

**odgi flatten** was written by Erik Garrison.

# 24. odgi break(1)

## 24.1. NAME

**odgi\_break** - break cycles in the graph and drop its paths

## 24.2. SYNOPSIS

**odgi break** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 24.3. DESCRIPTION

The **odgi break(1)** command finds cycles in a graph via [breadth-first search \(BFS\)](#) and breaks them, also dropping the graph's paths.

## 24.4. OPTIONS

### 24.4.1. Graph Files IO

**-i, --idx=*FILE***

File containing the succinct variation graph to break. The file name usually ends with *.og*.

**-o, --out=*FILE***

Write the broken graph to *FILE*.

### 24.4.2. Cycle Options

**-c, --cycle-max-bp=*N***

The maximum cycle length at which to break.

**-s, --max-search-bp=*N***

The maximum search space of each BFS given in number of base pairs.



**-u, --repeat-up-to=*N***

Iterate cycle breaking up to *N* times or stop if no new edges are removed.

**-d, --show**

Print the edges we would remove to stdout.

### 24.4.3. Program Information

**-h, --help**

Print a help message for **odgi break**.

## 24.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 24.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 24.7. AUTHORS

**odgi break** was written by Erik Garrison.

# 25. odgi pathindex(1)

## 25.1. NAME

**odgi\_pathindex** - create a path index for a given path

## 25.2. SYNOPSIS

**odgi pathindex** [-i, --idx=*FILE*] [-o, --out=*FILE*] [*OPTION*]...

## 25.3. DESCRIPTION

The **odgi pathindex(1)** command generates a path index of a graph. It uses succinct data structures to encode the index. The path index represents a subset of the features of a fully realized [xg index](#). Having a path index, we can use **odgi panpos** to go from **path:position** → **pangenome:position** which is important when navigating large graphs in an interactive manner like in the [Pantograph](#) project.

## 25.4. OPTIONS

### 25.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph to generate a path index from. The file name usually ends with *.og*.

**-o, --out=FILE**

Write the path index to *FILE*.

### 25.4.2. Program Information

**-h, --help**

Print a help message for **odgi pathindex**.

## 25.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 25.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 25.7. AUTHORS

**odgi pathindex** was written by Simon Heumos.

# 26. odgi panpos(1)

## 26.1. NAME

**odgi\_panpos** - get the pangenome position of a given path and nucleotide position (1-based)

## 26.2. SYNOPSIS

**odgi panpos** [-i, --idx=FILE] [-p, --path=STRING] [-n, --nuc-pos=N] [OPTION]...

## 26.3. DESCRIPTION

The `odgi panpos(1)` command give a pangenome position for a given path and nucleotide position. It requires a path index, which can be created with `odgi pathindex`. Going from **path:position** → **pangenome:position** is important when navigating large graphs in an interactive manner like in the [Pantograph](#) project. All input and output positions are 1-based.

## 26.4. OPTIONS

### 26.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph index to find the pangenome position in. The file name usually ends with `.xp`.

### 26.4.2. Position Options

**-p, --path=STRING**

The path name of the query.

**-n, --nuc-pos=STRING**

The nucleotide sequence of the query.

### 26.4.3. Program Information

**-h, --help**

Print a help message for **odgi panpos**.

## 26.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 26.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 26.7. AUTHORS

**odgi panpos** was written by Simon Heumos.

# 27. odgi position(1)

## 27.1. NAME

odgi\_position - position parts of the graph as defined by query criteria

## 27.2. SYNOPSIS

**odgi position** [-i, --target=FILE] [OPTION]...

## 27.3. DESCRIPTION

The `odgi position(1)` command translates positions and coordinate ranges between nodes and embedded paths. It provides liftover functionality, allowing us to translate a position between any reference paths embedded in the `-i`, `--target` graph. We can additionally project coordinates and annotations from a source graph `-x`, `--source` into the `target`. When completing this "graph lift", the intersecting set of paths in the two graphs are used to complete the coordinate projection.

## 27.4. OPTIONS

### 27.4.1. Graph Files IO

**-i, --target=FILE**

Describe positions in this graph.

**-x, --source=FILE**

Translate positions from this graph into the target graph using common `--lift-paths` shared between both graphs [default: use the same source/target graph]

### 27.4.2. Position Options

**-r, --ref-paths=STRING**

Translate the given positions into positions relative to this reference path.

**-R, --ref-paths=FILE**

Use the ref-paths in FILE.

**-l, --lift-path=STRING**

Lift positions from `--source` to `--target` via coordinates in this path common to both graphs [default: all common paths between `--source` and `--target`].

**-g, --graph-pos=[[node\_id]]**

A graph position, e.g. 42,10,+ or 302,0,-.

**-F, --path-pos-file=FILE**

A file with one path position per line.

**-b, --bed-input=FILE**

A BED file of ranges in paths in the graph to lift into the target graph **-v, --give-graph-pos** emit graph positions.

**-v, --give-graph-pos**

Emit graph positions (node,offset,strand) rather than path positions.

**-d, --search-radius=STRING**

Limit coordinate conversion breadth-first search up to DISTANCE bp from each given position [default: 10000].

### 27.4.3. Threading

**-t, --threads=N**

Number of threads to use.

### 27.4.4. Program Information

**-h, --help**

Print a help message for **odgi position**.

## 27.5. EXIT STATUS

0

Success.

1

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 27.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 27.7. AUTHORS

**odgi position** was written by Erik Garrison.

# 28. odgi server(1)

## 28.1. NAME

**odgi\_server** - start a HTTP server with a given index file to query a pangenome position

## 28.2. SYNOPSIS

**odgi server** [-i, --idx=*FILE*] [-p, --port=*N*] [*OPTION*]...

## 28.3. DESCRIPTION

The `odgi server`(1) command starts an HTTP server with a given path index as input. The idea is that we can go from **path:position** → **pangenome:position** via GET requests to the HTTP server. The server headers do not block cross origin requests. Example GET request: [http://localhost:3000/path\\_name/nucleotide\\_position](http://localhost:3000/path_name/nucleotide_position).

The required path index can be created with `odgi pathindex`. Going from **path:position** → **pangenome:position** is important when navigating large graphs in an interactive manner like in the [Pantograph](#) project. All input and output positions are 1-based. If no IP address is specified, the server will run on localhost.

## 28.4. OPTIONS

### 28.4.1. Graph Files IO

**-i, --idx=FILE**

File containing the succinct variation graph index to host in a HTTP server. The file name usually ends with *.xp*.

### 28.4.2. HTTP Options

**-p, --port=N**

Run the server under this port.

**-a, --ip=IP**

Run the server under this IP address. If not specified, *IP* will be *localhost*.

### 28.4.3. Program Information

**-h, --help**

Print a help message for **odgi server**.

## 28.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 28.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 28.7. AUTHORS

**odgi server** was written by Simon Heumos.

# 29. odgi test(1)

## 29.1. NAME

`odgi_test` - run odgi unit tests

## 29.2. SYNOPSIS

**odgi test** [<TEST NAME|PATTERN|TAGS> ...] [*OPTION*]...

## 29.3. DESCRIPTION

The `odgi test(1)` command starts all unit tests that are implemented in `odgi`. For targeted testing, a subset of tests can be selected. `odgi test(1)` depends on [Catch2](#). In the default setting, all results are printed to stdout.

## 29.4. OPTIONS

### 29.4.1. Testing Options

**-l, --list-tests**

List all test cases. If a pattern was specified, all matching test cases are listed.

**-t, --list-tags**

List all tags. If a pattern was specified, all matching tags are listed.

**-s, --success**

Include successful tests in output.

**-b, --break**

Break into debugger mode upon failed test.

**-e, --nothrow**

Skip exception tests.

**-i, --invisibles**

Show invisibles like tabs or newlines.

**-o, --out=FILE**

Write all output to *FILE*.

**-r, --reporter=STRING**

Reporter to use. Default is console.

**-n, --name=STRING**

Suite name.

**-a, --abort**

Abort at first failure.

**-x, --abortx=N**

Abort after *N* failures.

**-w, --warn=STRING**

Enable warnings.

**-d, --durations=yes|no**

Show test durations. Default is *no*.

**-f, --input-file=FILE**

Load test names from a file.

**-#, --filenames-as-tags**

Adds a tag for the file name.

**-c, --section=STRING**

Specify the section to run the tests on.

**-v, --verbosity=quiet|normal|high**

Set output verbosity. Default is *normal*.

**--list-test-names-only**

List all test cases names only. If a pattern was specified, all matching test cases are listed.

**--list-reporters**

List all reporters.

**--order=decl|lex|rand**

Test case order. Default is *decl*.

**--rng-seed=time|number**

Set a specific seed for random numbers.

**--use-color=yes|no**

Should the output be colorized? Default is *yes*.



### **--libidentify**

Report name and version according to libidentify.

### **--wait-for-keypress=*start* | *exit* | *both***

Waits for a keypress before *start* | *exit* | *both*.

### **--benchmark-resolution-multiple**

Multiple of clock resolution to run benchmarks.

## **29.4.2. Program Information**

### **-, -h, --help**

Print a help message for **odgi test**.

## **29.5. EXIT STATUS**

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## **29.6. BUGS**

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## **29.7. AUTHORS**

**odgi test** was written by Erik Garrison, Simon Heumos, and Andrea Guarracino.

# **30. odgi version(1)**

## **30.1. NAME**

**odgi\_version** - display the version of odgi

## **30.2. SYNOPSIS**

**odgi version** [*OPTION*]...

## **30.3. DESCRIPTION**

The **odgi version(1)** command prints the current git version with tags and codename to stdout (like *v-44-g89d022b "back to old ABI"*). Optionally, only the release, version or codename can be printed.

## 30.4. OPTIONS

### 30.4.1. Version Options

**-v, --version=**

Print only the version (like *v-44-g89d022b*).

**-c, --codename**

Print only the codename (like *back to old ABI*).

**-r, --release**

Print only the release (like *v*).

### 30.4.2. Program Information

**-h, --help**

Print a help message for **odgi version**.

## 30.5. EXIT STATUS

**0**

Success.

**1**

Failure (syntax or usage error; parameter error; file processing failure; unexpected error).

## 30.6. BUGS

Refer to the **odgi** issue tracker at <https://github.com/pangenome/odgi/issues>.

## 30.7. AUTHORS

**odgi version** was written by Simon Heumos.