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# CNVisualizer Documentation

*Release 0.1a1*

**UConn**

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CNVisualizer is an extension of the HTML-5 version of the [Integrated Genome Viewer](#), forked off of [igv.js](#).

It extends the project by improving the implementation of segmented CNV tracks as well as adding an implementation for raw CNV read values. It also packages the product in an electron app as an example of using the library that was created.



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**Note:** This is subject to change, mostly minor aesthetic changes.

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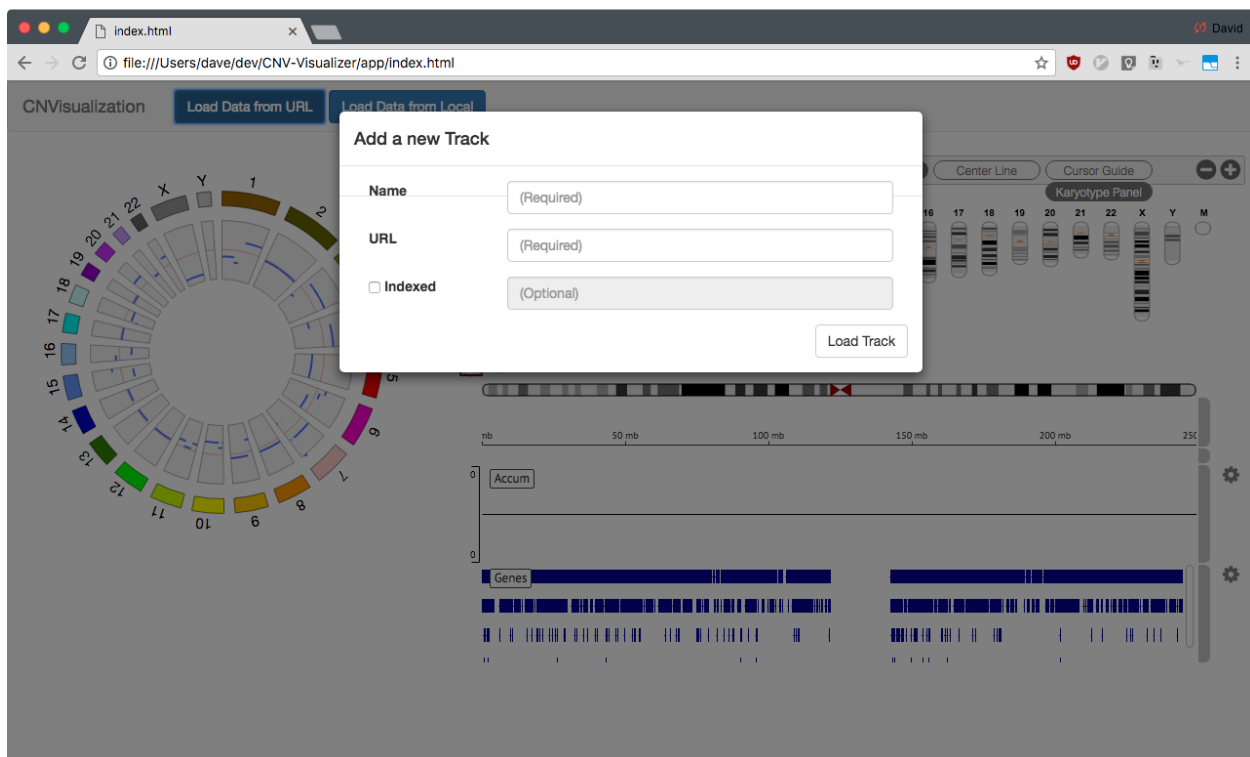
### Loading Tracks

In order to view the data, files must be loaded from one of the top two menu buttons. Choose which button based on where the file is being loaded from:

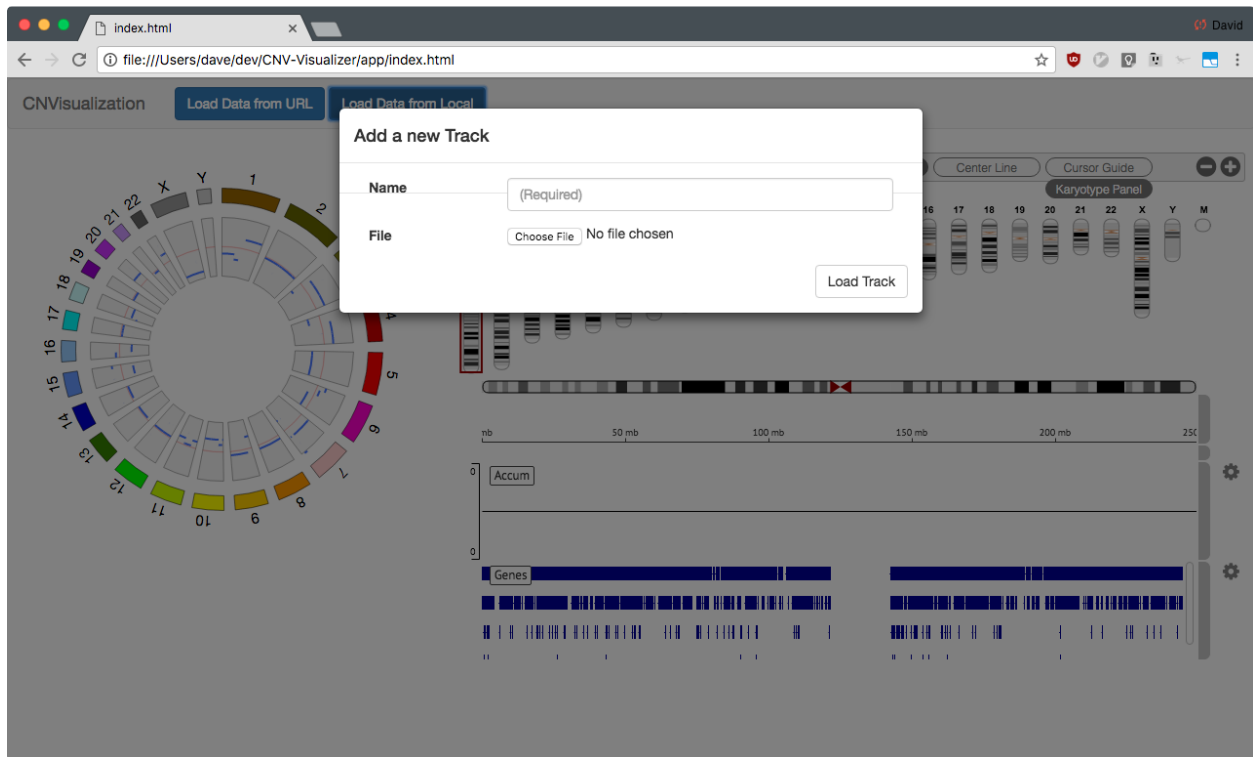


1. File from a web server, must support [Range Requests](#).
2. File found locally on the computer.

And then you can input the relevant information, including







- *URL* or *File*, which is the data to be loaded. Track type is inferred off of the extension itself.
- *Name*, which can be changed later (todo: ref)
- *Indexed*, can **NOT** be used for local files. When used for URL files, it expects the indexed file to have the same *URL*, with the extra indexed extension (i.e. <http://files.com/a.bam> would be <http://files.com/a.bam.bai>).

Track configuration can be partially controlled with the gear icon, found to the right of each track. All of the following have an ability to set the threshold, which determines values that should not be shown. Color controls may be added in the future.

## Using Local Files

In order to use local files, you have to select the file from the regular menu. However, this does have its limitations. The two main ones being:

1. The file cannot be indexed, and therefore must be uploaded entirely.
2. The track cannot be opened in a new window.

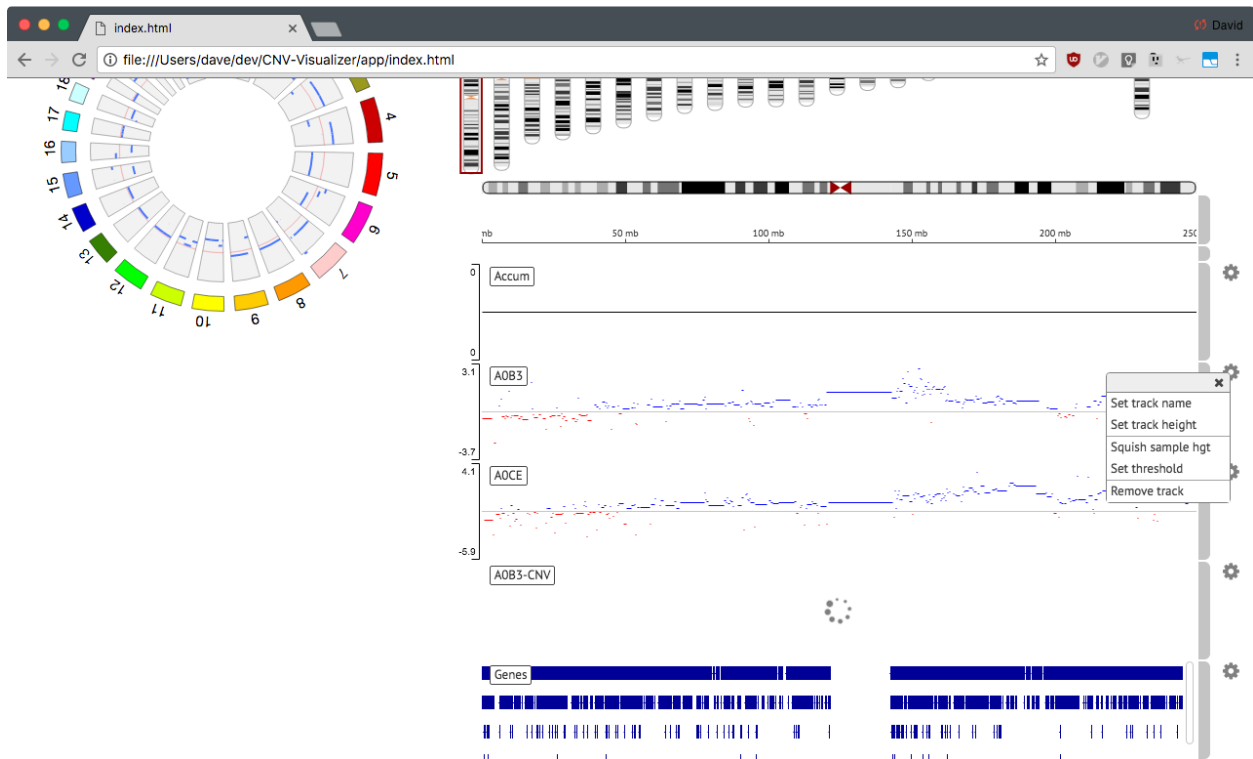
There are two solutions to this. First, you may upload the file directly to a server which can support range requests. This is possibly the easiest, if you have one available to you.

The other is to start a server from the folder with holds your files. This can just be a local server that you launch with a script.

If you have Python installed, first download this [cors\\_server.py](#) script. Then try running:

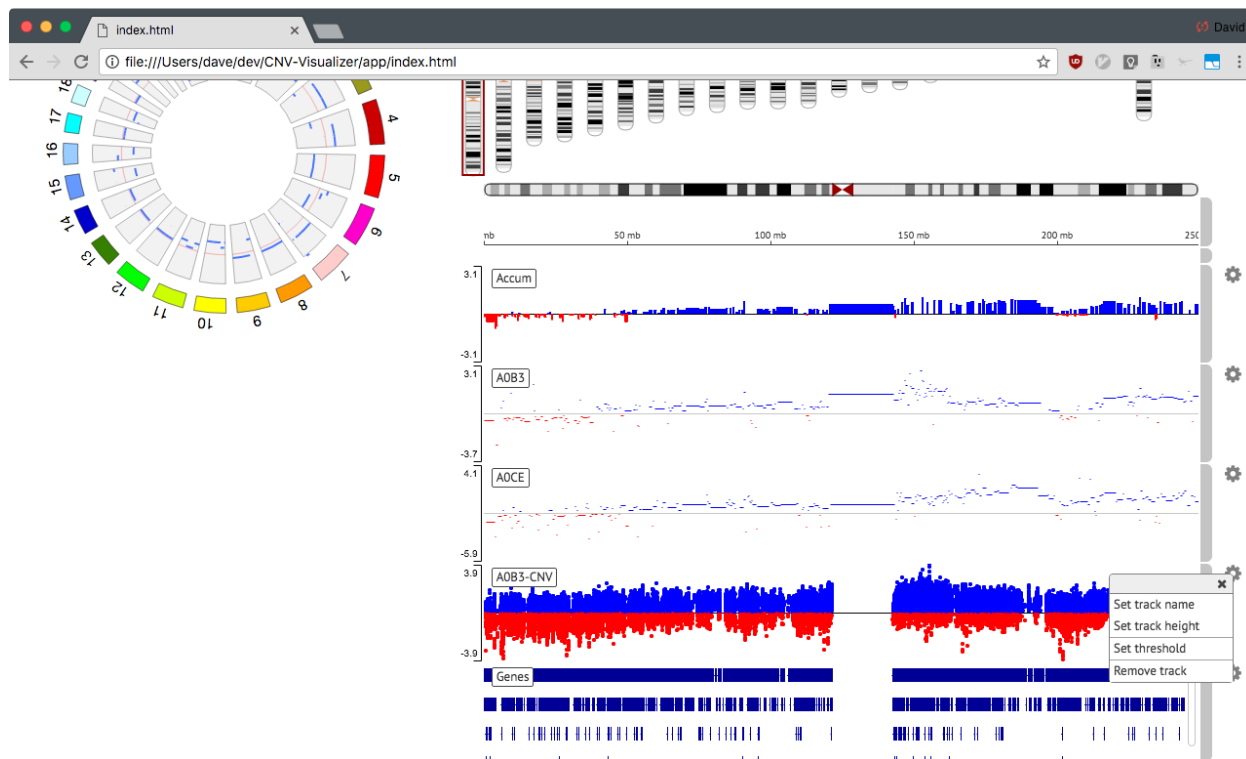
```
$ cd directory/with/your/data
$ python directory/with/cors_server.py
```

## Segment Track



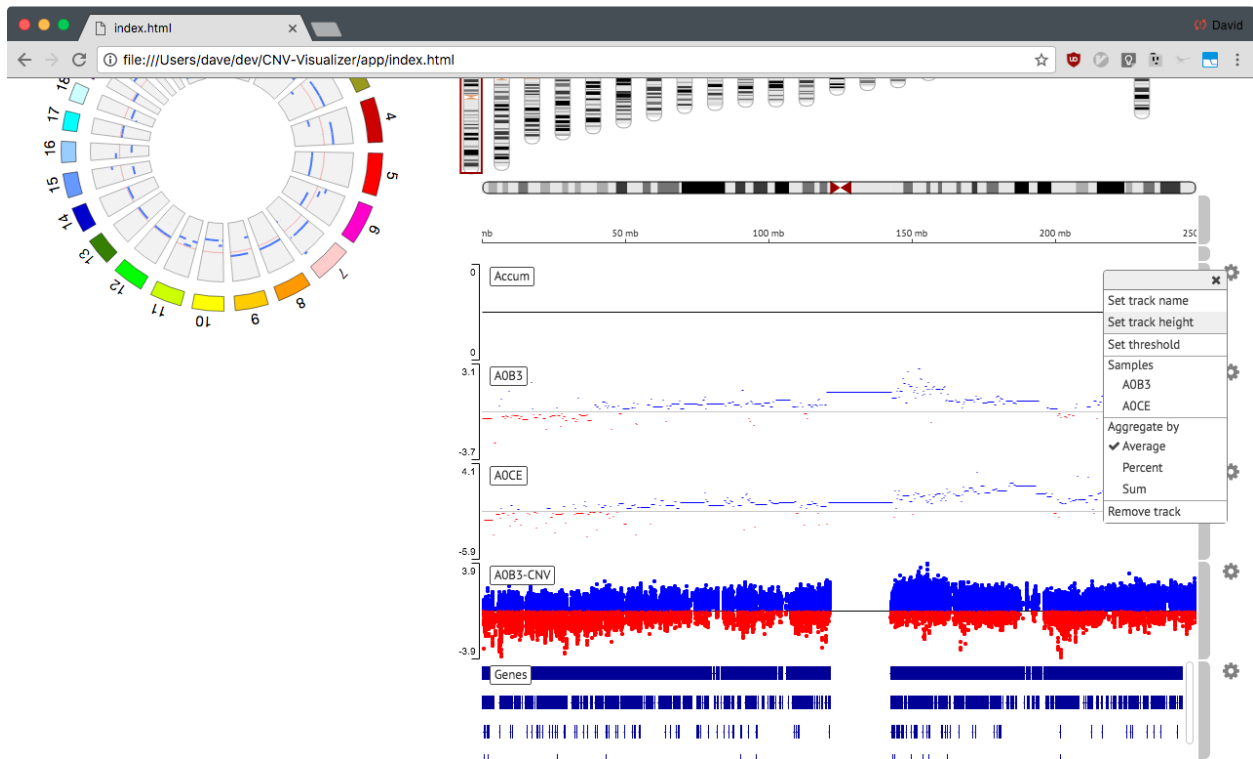
Segment tracks have no truly unique options to select from, as the sample height is a remnant from having multiple segments per track.

## CNV Called Track



CNV called tracks allow controlling the threshold, but that's it.

## CNV Accumulated Track



Accumulation tracks allow choosing the segment tracks to include in the aggregation of data, as well as selecting an aggregation method. These can be seen as above.

1. Selected samples are marked with a checkmark.
2. Enabled aggregation method is marked with a checkmark.

While the main use of CNVisualizer is to be a web application, the browser does have functions available to be interfaced with or to extend the functionality of different tracks or views.

**The web application is less suitable for**

- Forcing other elements to react to the genomic locations.
- Customizing the loading of various files.

The internals are exposed via practically all of the functions, however some are not implemented on specific tracks.

## API Quickstart

### igv

#### IGV Classes

```
class Browser (options, trackContainerDiv)  
  browser.js  
  
  Browser.prototype.disableZoomWidget ()  
    browser.js  
  
  Browser.prototype.enableZoomWidget (zoomHandlers)  
    browser.js  
  
  Browser.prototype.toggleCursorGuide (genomicStateList)  
    browser.js  
  
  Browser.prototype.toggleCenterGuide (genomicStateList)  
    browser.js  
  
  Browser.prototype.getFormat (name)  
    browser.js
```

```
Browser.prototype.loadTracksWithConfigList (configList)
    browser.js

Browser.prototype.loadTrack (config)
    browser.js

Browser.prototype.addTrack (track)
    browser.js

Browser.prototype.reorderTracks ()
    browser.js

Browser.prototype.removeTrack (track)
    browser.js

Browser.prototype.findTracks (property, value)
    browser.js

Browser.prototype.reduceTrackOrder (trackView)
    browser.js

Browser.prototype.increaseTrackOrder (trackView)
    browser.js

Browser.prototype.setTrackHeight (newHeight)
    browser.js

Browser.prototype.resize ()
    browser.js

Browser.prototype.repaint ()
    browser.js

Browser.prototype.repaintWithLocusIndex (locusIndex)
    browser.js

Browser.prototype.update ()
    browser.js

Browser.prototype.updateWithLocusIndex (locusIndex)
    browser.js

Browser.prototype.loadInProgress ()
    browser.js

Browser.prototype.updateLocusSearchWithGenomicState (genomicState)
    browser.js

Browser.prototype.syntheticViewportContainerBBox ()
    browser.js

Browser.prototype.syntheticViewportContainerWidth ()
    browser.js

Browser.prototype.viewportContainerWidth ()
    browser.js

Browser.prototype.minimumBasesExtent ()
    browser.js

Browser.prototype.goto (chrName, start, end)
    browser.js
```

```
Browser.prototype.zoomIn()
    browser.js

Browser.prototype.zoomOut()
    browser.js

Browser.prototype.selectMultiLocusPanelWithGenomicState(genomicState)
    browser.js

Browser.prototype.closeMultiLocusPanelWithGenomicState(genomicState)
    browser.js

Browser.prototype.multiLocusPanelLayoutWithTruthFunction(filterFunction)
    browser.js

Browser.prototype.emptyViewportContainers($trackContainer)
    browser.js

Browser.prototype.buildViewportsWithGenomicStateList(genomicStateList)
    browser.js

Browser.prototype.parseSearchInput(string)
    browser.js

Browser.prototype.getGenomicStateList(loci, viewportContainerWidth, continuation)
    browser.js

Browser.prototype.on(eventName, fn)
    browser.js

Browser.prototype.un(eventName, fn)
    browser.js

Browser.prototype.fireEvent(eventName, args, thisObj)
    browser.js

Browser.prototype.search(feature, callback, force)
    browser.js

class EncodeTable(parentModalBodyObject, continuation)
    encode/encode.js

    EncodeTable.prototype.loadWithDataSource(dataSource)
        encode/encode.js

    EncodeTable.prototype.encodeTrackLabel(record)
        encode/encode.js

class EncodeDataSource(config)
    encode/encode.js

    EncodeDataSource.prototype.loadJSON(continuation)
        encode/encode.js

    EncodeDataSource.prototype.ingestJSON(json, continuation)
        encode/encode.js

    EncodeDataSource.prototype.ingestFile(file, continuation)
        encode/encode.js

    EncodeDataSource.prototype.dataTablesData()
        encode/encode.js
```

```
EncodeDataSource.prototype.columnHeadings ()  
    encode/encode.js
```

```
class FastaSequence (reference)
```

```
    fasta.js
```

```
FastaSequence.prototype.init ()  
    fasta.js
```

```
FastaSequence.prototype.getSequence (chr, start, end)  
    fasta.js
```

```
FastaSequence.prototype.getIndex ()  
    fasta.js
```

```
FastaSequence.prototype.loadAll ()  
    fasta.js
```

```
FastaSequence.prototype.readSequence (chr, qstart, qend)  
    fasta.js
```

```
class TribbleIndex (chrIndexTable)
```

```
    feature/tribble.js
```

```
TribbleIndex.prototype.blocksForRange (queryChr, min, max)  
    feature/tribble.js
```

```
class IdeoPanel ($content_header)
```

```
    ideogram.js
```

```
IdeoPanel.prototype.buildPanels ($content_header)  
    ideogram.js
```

```
IdeoPanel.prototype.panelWithLocusIndex (locusIndex)  
    ideogram.js
```

```
IdeoPanel.prototype.resize ()  
    ideogram.js
```

```
IdeoPanel.prototype.repaint ()  
    ideogram.js
```

```
class AbortLoad ()
```

```
    igvxhr.js
```

```
class IntervalTree ()
```

```
    intervalTree.js
```

```
IntervalTree.prototype.insert (start, end, value)  
    intervalTree.js
```

```
IntervalTree.prototype.findOverlapping (start, end)  
    intervalTree.js
```

```
IntervalTree.prototype.logIntervals ()  
    intervalTree.js
```

```
IntervalTree.prototype.mapIntervals (func)  
    intervalTree.js
```

```
IntervalTree.prototype.treeInsert (x)  
    intervalTree.js
```



```
class KaryoPanel ($parent, config)
  karyo/karyo.js

  KaryoPanel.prototype.resize ()
    karyo/karyo.js

  KaryoPanel.prototype.repaint ()
    karyo/karyo.js

class ReferenceFrame (chrName, start, bpPerPixel)
  referenceFrame.js

  ReferenceFrame.prototype.toPixels (bp)
    referenceFrame.js

  ReferenceFrame.prototype.toBP (pixels)
    referenceFrame.js

  ReferenceFrame.prototype.shiftPixels (pixels)
    referenceFrame.js

  ReferenceFrame.prototype.description ()
    referenceFrame.js

class SVG ()
  svg.js

  SVG.prototype.setProperties (properties)
    svg.js

  SVG.prototype.setTransforms (transforms, x, y)
    svg.js

  SVG.prototype.clearRect (x, y, w, h)
    svg.js

  SVG.prototype.strokeLine (x1, y1, x2, y2, properties, transforms)
    svg.js

  SVG.prototype.fillRect (x, y, w, h, properties, transforms)
    svg.js

  SVG.prototype.fillRectWithCenter (centerX, centerY, width, height, properties, transforms)
    svg.js

  SVG.prototype.fillPolygon (x, y, properties, transforms)
    svg.js

  SVG.prototype.fillText (text, x, y, properties, transforms)
    svg.js

  SVG.prototype.strokeText (text, x, y, properties, transforms)
    svg.js

  SVG.prototype.strokeCircle (x, y, radius, properties, transforms)
    svg.js

  SVG.prototype.string ()
    svg.js

  SVG.prototype.innerString ()
    svg.js
```

```
class Viewport (trackView, locusIndex)
  viewport.js

  Viewport.prototype.setWidth (width)
    viewport.js

  Viewport.prototype.initializationHelper (trackView, locusIndex)
    viewport.js

  Viewport.prototype.addMouseHandlers ()
    viewport.js

  Viewport.prototype.addRulerMouseHandlers ()
    viewport.js

  Viewport.prototype.removeRulerMouseHandlers ()
    viewport.js

  Viewport.prototype.goto (chr, start, end)
    viewport.js

  Viewport.prototype.startSpinner ()
    viewport.js

  Viewport.prototype.stopSpinner ()
    viewport.js

  Viewport.prototype.resize ()
    viewport.js

  Viewport.prototype.update ()
    viewport.js

  Viewport.prototype.repaint ()
    viewport.js

  Viewport.prototype.setContentHeight (newHeight)
    viewport.js

  Viewport.prototype.paintImageWithReferenceFrame (referenceFrame)
    viewport.js

  Viewport.prototype.isLoading ()
    viewport.js

  Viewport.prototype.redrawTile (features)
    viewport.js

class WindowSizePanel ($parent)
  windowSizePanel.js

  WindowSizePanel.prototype.show ()
    windowSizePanel.js

  WindowSizePanel.prototype.hide ()
    windowSizePanel.js

  WindowSizePanel.prototype.updateWithGenomicState (genomicState)
    windowSizePanel.js
```

## Genome Helper Classes

```

class Genome (sequence, ideograms, aliases)
    genome.js

    Genome.prototype.getChromosomeName (str)
        genome.js

    Genome.prototype.getChromosome (chr)
        genome.js

    Genome.prototype.getCytobands (chr)
        genome.js

    Genome.prototype.getLongestChromosome ()
        genome.js

    Genome.prototype.getChromosomes ()
        genome.js

    Genome.prototype.getGenomeCoordinate (chr, bp)
        genome.js

    Genome.prototype.getChromosomeCoordinate (genomeCoordinate)
        genome.js

    Genome.prototype.getCumulativeOffset (chr)
        genome.js

class Chromosome (name, order, bpLength)
    genome.js

class Cytoband (start, end, name, typestain)
    genome.js

class GenomicInterval (chr, start, end, features)
    genome.js

    GenomicInterval.prototype.contains (chr, start, end)
        genome.js

    GenomicInterval.prototype.containsRange (range)
        genome.js

```

## Feature Sourcing Classes

```

class FeatureCache (featureList, range)
    feature/featureCache.js

    FeatureCache.prototype.queryFeatures (chr, start, end)
        feature/featureCache.js

    FeatureCache.prototype.allFeatures ()
        feature/featureCache.js

class FeatureSource (config)
    feature/featureSource.js

    FeatureSource.prototype.getFileHeader ()
        feature/featureSource.js

```

```
FeatureSource.prototype.getFeatures (chr, bpStart, bpEnd, bpPerPixel)
feature/featureSource.js
```

```
class AneuFeatureSource (config, thefilename)
feature/aneuSource.js
```

```
AneuFeatureSource.prototype.getFeatures (chr, bpStart, bpEnd, success)
feature/aneuSource.js
```

```
AneuFeatureSource.prototype.getFeatureCache (success)
feature/aneuSource.js
```

```
AneuFeatureSource.prototype.loadFeatures (continuation, range)
feature/aneuSource.js
```

```
class T2DVariantSource (config)
gwas/t2dVariantSource.js
```

```
T2DVariantSource.prototype.getFeatures (chr, bpStart, bpEnd)
gwas/t2dVariantSource.js
```

```
class TDFSource (config)
tdf/tdfSource.js
```

```
TDFSource.prototype.getFeatures (chr, bpStart, bpEnd, bpPerPixel)
tdf/tdfSource.js
```

```
class BamSource (config)
bam/bamSource.js
```

```
BamSource.prototype.setViewAsPairs (bool)
bam/bamSource.js
```

```
BamSource.prototype.getAlignments (chr, bpStart, bpEnd)
bam/bamSource.js
```

## Track Classes

Tracks are meant to be created with a few specifics demands in mind. Every track needs to implement the following functions:

```
Track.prototype.getFeatures (chr, bpStart, bpEnd)
Track.prototype.draw (options)
```

Where *getFeatures()* must return a *Promise* for an array of the data. And *draw()* doesn't return anything.

The other functions that are optional include (but not limited to):

```
TrackName.prototype.menuItemList (popover)
TrackName.prototype.popupData (genomicLocation, x, y, referenceFrame)
TrackName.prototype.altClick (genomicLocation, referenceFrame, event)
TrackName.prototype.popupMenuItemList (config)
TrackName.prototype.paintAxis (ctx, pixelWidth, pixelHeight)
TrackName.prototype.computePixelHeight (features)
```

You can find examples of these functions below.

## Configuration

When creating a track, the *config*, it follows the structure (where everthing left without a value has no default):

```
config = {
  name:           , /* **REQUIRED** Display name (label). */
  url:            , /* **REQUIRED** URL to the track data resource,
                    such as a file or webservice. */
  indexURL:       , /* URL to a file index, such as a BAM .bai,
                    Tabix .tbi, or Tribble .idx file. */
  sourceType: "file" , /* Type of data source. Valid values are "file",
                    "gcs" for Google Cloud Storage, and "ga4gh" for
                    the Global Alliance API */
  type:           , /* Track type, infered from file extension if none */
  format:         , /* File format, infered from file extension if none */
  indexed:        , /* Flag used to indicate if a file is indexed or not.
                    If indexURL is provided this flag is redundant,
                    its main purpose is to indicate that a file is not
                    indexed. */
  order:          , /* Integer value specifying relative order of track
                    position on the screen. To pin a track to the
                    bottom use Number.MAX_VALUE. If no order is
                    specified, tracks appear in order of their addition.
→ */
  color:          , /* CSS color value for track features, e.g. "#ff0000"
                    or "rgb(100,0,100)" */
  height: 50      , /* Initial height of track viewport in pixels */
  autoHeight: true , /* If true, then track height is adjusted dynamically,
                    within the bounds set by minHeight and maxHeight,
                    to accomodate features in view */
  minHeight: 50   , /* Minimum height of track in pixels */
  maxHeight: 500  , /* Maximum height of track in pixels */
  visibilityWindow: 30000 , /* Maximum window size in base pairs for which indexed
                    annotations or variants are displayed */

  /** ANNOTATIONS ONLY */
  displayMode: "COLLAPSED" , /* Annotation display mode, one of "COLLAPSED",
                    "EXPANDED", "SQUISHED" */
  expandedRowHeight: 30 , /* Height of each row of features in "EXPANDED" mode */
  squishedRowHeight: 15 , /* Height of each row of features in "SQUISHED" mode */
  nameField: "Name" , /* For GFF/GTF file formats. Name of column 9 property
                    to be used for feature label */
  maxRows: 500 , /* Maximum number of rows of features to display */
  searchable: false , /* If true, feature names for this track can be
                    searched for. Use this option with caution, it
                    is memory intensive. This option should
                    **will not work** with indexed tracks. */

  /** WIG ONLY */
  min: 0 , /* Sets the minimum value for the data (y-axis)
                    scale. Usually zero. */
  max:   , /* Sets the maximum value for the data (y-axis)
                    scale. */
  color: "rgb(150,150,150)" , /* Track color. */
  /** ALIGNMENT ONLY (BAM, etc) */
  viewAsPairs: false , /* If true, paired reads are drawn as a single
                    alignment. */
  pairsSupported: true , /* If false, mate information in paired reads is
                    ignored during downsampling and the
                    'View as Pairs' option is removed from the
```

```

                                alignment track menu. */
deletionColor: "black"; , /* Color of line representing a deletion */
skippedColor: "rgb(150, 170, 170)" , /* Color of line representing a
                                skipped region (e.g. splice
                                junction) */
insertionColor: "rgb(138, 94, 161)" , /* Color of marker for insertions */
negStrandColor: "rgba(150, 150, 230, 0.75)" , /* Color of alignment on negative
                                strand.
                                Applicable if colorBy = "strand"
→ */
posStrandColor: "rgba(230, 150, 150, 0.75)" , /* Color of alignment or position
                                strand.
                                Applicable if colorBy = "strand"
→ */
colorBy: "none" , /* Alignment color option:
                  one of "none", "strand",
                  "firstInPairStrand", or "tag".
                  Specify tag with colorByTag */
colorByTag: , /* Specific tag to color alignment by. */
bamColorTag: "YC" , /* Specifies a special tag that
                  explicitly encodes an r,g,b color
                  value. If "YC" does not encode
                  an r,g,b color value set bamColorTag
                  to null. Must also set "colorBy"
                  to "tag" to enable this option. */
samplingWindowSize: 100 , /* Window (bucket) size for
                  alignment downsampling in base pairs */
samplingDepth: 50. , /* Number of alignments to keep per
                  bucket.
                  WARNING: Setting this sampling
                  depth to a high value will likely
                  freeze the browser when viewing
                  areas of deep coverage. */
maxRows: 1000 , /* Maximum number of rows of alignments
                  to display.
                  Note: due to a limit on canvas
                  height the maximum value for this
                  parameter is ~2300 at the default
                  row height of 14. */
alignmentRowHeight: 14 , /* Height in pixels of an alignment
                  row when in expanded mode */
filter: , /* Alignment filter object. */
/** GA4GH ALIGNMENT (sourceType: "ga4gh") **/
url: , /* **REQUIRED** URL to the ga4gh endpoint
                  (e.g. https://www.googleapis.com/genomics/v1beta2). */
readGroupSetIds: , /* **REQUIRED** ID of the read group set represented
                  by this track. (e.g. 'CMvnhpKTFhCjz9_25e_lCw'). */
/** ALIGNMENT FILTER **/
vendorFailed: true , /* filter alignments marked as failing vendor
                  quality checks (bit 0x200) */
duplicates: true , /* filter alignments marked as a duplicate
                  (bit 0x400) */
secondary: false , /* filter alignments marked secondary
                  (bit 0x100) */
supplementary: false , /* filter alignments marked as supplementary
                  (bit 0x800) */
mqThreshold: 0 , /* filter alignments with mapping quality < supplied
                  value (a number) */

```

```

/** VARIANT ONLY */
displayMode: EXPANDED , /* Display option.
                        COLLAPSED => show variants only,
                        SQUISHED and EXPANDED => show calls. */
homvarColor: "rgb(17,248,254)" , /* CSS color used to represent homozygous
                                non-reference calls. */
hetvarColor: "rgb(34,12,253)" , /* CSS color used to represent
                                heterozygous calls. */
homrefColor: "rgb(200, 200, 200)" , /* CSS color used to represent homozygous
                                reference calls. */
/** GA4GH VARIANT (sourceType: "ga4gh") */
url: , /* **REQUIRED** URL to the ga4gh endpoint
        (e.g. https://www.googleapis.com/genomics/v1beta2). */
variantSetId: , /* **REQUIRED** ID of the variant set represented by
                this track. (e.g. '10473108253681171589'). */
callSetIds: , /* Array of GACallSet IDs to include with track.
                Optional. If omitted, all call sets are included */
}

```

```

class AneuTrack (config)
  feature/aneuTrack.js

  AneuTrack.prototype.getSummary (chr, bpStart, bpEnd, continuation)
    feature/aneuTrack.js

  AneuTrack.prototype.loadSummary (chr, bpStart, bpEnd, continuation)
    feature/aneuTrack.js

  AneuTrack.prototype.getFeatures (chr, bpStart, bpEnd)
    feature/aneuTrack.js

  AneuTrack.prototype.getColor (value)
    feature/aneuTrack.js

  AneuTrack.prototype.paintAxis (ctx, pixelWidth, pixelHeight)
    feature/aneuTrack.js

  AneuTrack.prototype.draw (options)
    feature/aneuTrack.js

  AneuTrack.prototype.computePixelHeight (features)
    feature/aneuTrack.js

  AneuTrack.prototype.sortSamples (chr, bpStart, bpEnd, direction, callback)
    feature/aneuTrack.js

  AneuTrack.prototype.altClick (genomicLocation, referenceFrame, event)
    feature/aneuTrack.js

  AneuTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
    feature/aneuTrack.js

class CNVAccumTrack (config)
  feature/cnvAccumTrack.js

  CNVAccumTrack.prototype.addToSelectFrom (thisObj)
    feature/cnvAccumTrack.js

  CNVAccumTrack.prototype.removeFromSelectFrom (thisObj)
    feature/cnvAccumTrack.js

```

```
CNVAccumTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
    feature/cnvAccumTrack.js

CNVAccumTrack.prototype.menuItemList (popover)
    feature/cnvAccumTrack.js

CNVAccumTrack.prototype.toggleTrack (sampleName)
    feature/cnvAccumTrack.js

CNVAccumTrack.prototype.getFeatures (chr, bpStart, bpEnd)
    feature/cnvAccumTrack.js

CNVAccumTrack.prototype.draw (options)
    feature/cnvAccumTrack.js

class CNVTrack (config)
    feature/cnvTrack.js

    CNVTrack.prototype.menuItemList (popover)
        feature/cnvTrack.js

    CNVTrack.prototype.getFeatures (chr, bpStart, bpEnd)
        feature/cnvTrack.js

    CNVTrack.prototype.draw (options)
        feature/cnvTrack.js

class Eqt1Track (config)
    gtex/eqtlTrack.js

    Eqt1Track.prototype.paintAxis (ctx, pixelWidth, pixelHeight)
        gtex/eqtlTrack.js

    Eqt1Track.prototype.getFeatures (chr, bpStart, bpEnd)
        gtex/eqtlTrack.js

    Eqt1Track.prototype.draw (options)
        gtex/eqtlTrack.js

    Eqt1Track.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
        gtex/eqtlTrack.js

class FeatureTrack (config)
    feature/featureTrack.js

    FeatureTrack.prototype.getFileHeader ()
        feature/featureTrack.js

    FeatureTrack.prototype.getFeatures (chr, bpStart, bpEnd, bpPerPixel)
        feature/featureTrack.js

    FeatureTrack.prototype.computePixelHeight (features)
        feature/featureTrack.js

    FeatureTrack.prototype.draw (options)
        feature/featureTrack.js

    FeatureTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
        feature/featureTrack.js

    FeatureTrack.prototype.menuItemList (popover)
        feature/featureTrack.js
```



```
class GWASTrack (config)
  gwas/gwasTrack.js

  GWASTrack.prototype.getFeatures (chr, bpStart, bpEnd)
    gwas/gwasTrack.js

  GWASTrack.prototype.draw (options)
    gwas/gwasTrack.js

  GWASTrack.prototype.paintAxis (ctx, pixelWidth, pixelHeight)
    gwas/gwasTrack.js

  GWASTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
    gwas/gwasTrack.js

class RulerTrack ()
  rulerTrack.js

  RulerTrack.prototype.locusLabelWithViewport (viewport)
    rulerTrack.js

  RulerTrack.prototype.getFeatures (chr, bpStart, bpEnd)
    rulerTrack.js

  RulerTrack.prototype.draw (options)
    rulerTrack.js

class SegTrack (config)
  feature/segTrack.js

  SegTrack.prototype.menuItemList (popover)
    feature/segTrack.js

  SegTrack.prototype.toggleSampleHeight ()
    feature/segTrack.js

  SegTrack.prototype.getFeatures (chr, bpStart, bpEnd)
    feature/segTrack.js

  SegTrack.prototype.draw (options)
    feature/segTrack.js

  SegTrack.prototype.computePixelHeight (features)
    feature/segTrack.js

  SegTrack.prototype.sortSamples (chr, bpStart, bpEnd, direction)
    feature/segTrack.js

  SegTrack.prototype.altClick (genomicLocation, referenceFrame, event)
    feature/segTrack.js

  SegTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
    feature/segTrack.js

  SegTrack.prototype.popupMenuItemList (config)
    feature/segTrack.js

class SequenceTrack (config)
  sequenceTrack.js

  SequenceTrack.prototype.getFeatures (chr, bpStart, bpEnd, bpPerPixel)
```

```
SequenceTrack.prototype.draw (options)  
    sequenceTrack.js
```

```
class VariantTrack (config)  
    variant/variantTrack.js
```

```
VariantTrack.prototype.getFileHeader ()  
    variant/variantTrack.js
```

```
VariantTrack.prototype.getFeatures (chr, bpStart, bpEnd)  
    variant/variantTrack.js
```

```
VariantTrack.prototype.computePixelHeight (features)  
    variant/variantTrack.js
```

```
VariantTrack.prototype.draw (options)  
    variant/variantTrack.js
```

```
VariantTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)  
    variant/variantTrack.js
```

```
VariantTrack.prototype.menuItemList (popover)  
    variant/variantTrack.js
```

```
class WIGTrack (config)  
    feature/wigTrack.js
```

```
WIGTrack.prototype.getFeatures (chr, bpStart, bpEnd, bpPerPixel)  
    feature/wigTrack.js
```

```
WIGTrack.prototype.menuItemList (popover)  
    feature/wigTrack.js
```

```
WIGTrack.prototype.draw (options)  
    feature/wigTrack.js
```

## File Reader Classes

```
class CustomServiceReader (config)  
    feature/customServiceReader.js
```

```
CustomServiceReader.prototype.readFeatures (chr, start, end)  
    feature/customServiceReader.js
```

```
class FeatureFileReader (config)  
    feature/featureFileReader.js
```

```
FeatureFileReader.prototype.readHeader ()  
    feature/featureFileReader.js
```

```
FeatureFileReader.prototype.readFeatures (chr, start, end)  
    feature/featureFileReader.js
```

```
class Ga4ghVariantReader (config)  
    ga4gh/ga4ghVariantReader.js
```

```
Ga4ghVariantReader.prototype.readHeader ()  
    ga4gh/ga4ghVariantReader.js
```

```
Ga4ghVariantReader.prototype.readFeatures (chr, bpStart, bpEnd)  
    ga4gh/ga4ghVariantReader.js
```

```
Ga4ghVariantReader.prototype.readMetadata ()
    ga4gh/ga4ghVariantReader.js

class Ga4ghAlignmentReader (config)
    ga4gh/ga4ghAlignmentReader.js

    Ga4ghAlignmentReader.prototype.readAlignments (chr, bpStart, bpEnd)
        ga4gh/ga4ghAlignmentReader.js

    Ga4ghAlignmentReader.prototype.readMetadata ()
        ga4gh/ga4ghAlignmentReader.js

class ImmVarReader (config)
    gtex/immvarReader.js

    ImmVarReader.prototype.readFeatures (queryChr, queryStart, queryEnd)
        gtex/immvarReader.js

class GtexFileReader (config)
    gtex/gtexFileReader.js

    GtexFileReader.prototype.readFeatures (chr, bpStart, bpEnd)
        gtex/gtexFileReader.js

class GtexReader (config)
    gtex/gtexReader.js

    GtexReader.prototype.readFeatures (chr, bpStart, bpEnd)
        gtex/gtexReader.js

class HiCReader (config)
    hic/hicReader.js

    HiCReader.prototype.readHeader ()
        hic/hicReader.js

    HiCReader.prototype.readFooter (key)
        hic/hicReader.js

    HiCReader.prototype.readMatrix (key)
        hic/hicReader.js

    HiCReader.prototype.readBlock (blockNumber, zd)
        hic/hicReader.js

class TDFReader (config)
    tdf/tdfReader.js

    TDFReader.prototype.readHeader ()
        tdf/tdfReader.js

    TDFReader.prototype.readDataset (chr, windowFunction, zoom)
        tdf/tdfReader.js

    TDFReader.prototype.readRootGroup ()
        tdf/tdfReader.js

    TDFReader.prototype.readGroup (name)
        tdf/tdfReader.js

    TDFReader.prototype.readTile (indexEntry, nTracks)
        tdf/tdfReader.js
```

```
class BamReader (config)
    bam/bamReader.js

    BamReader.prototype.readAlignments (chr, bpStart, bpEnd)
        bam/bamReader.js

    BamReader.prototype.readHeader ()
        bam/bamReader.js

class BWReader (config)
    bigwig/bwReader.js

    BWReader.prototype.getZoomHeaders ()
        bigwig/bwReader.js

    BWReader.prototype.loadHeader ()
        bigwig/bwReader.js

    BWReader.prototype.loadRPTree (offset)
        bigwig/bwReader.js

class BufferedReader (config, contentLength, bufferSize)
    bigwig/bufferedReader.js

    BufferedReader.prototype.dataViewForRange (requestedRange, asUInt8)
        bigwig/bufferedReader.js
```

## Parser Classes

```
class FeatureParser (format, decode, config)
    feature/featureParsers.js

    FeatureParser.prototype.parseHeader (data)
        feature/featureParsers.js

    FeatureParser.prototype.parseFeatures (data)
        feature/featureParsers.js

class SegParser ()
    feature/segParser.js

    SegParser.prototype.parseHeader (data)
        feature/segParser.js

    SegParser.prototype.parseFeatures (data)
        feature/segParser.js

class CNVParser ()
    feature/cnvParser.js

    CNVParser.prototype.parseHeader (data)
        feature/cnvParser.js

    CNVParser.prototype.parseFeatures (data)
        feature/cnvParser.js

class VcfParser ()
    variant/vcfParser.js

    VcfParser.prototype.parseHeader (data)
        variant/vcfParser.js
```

```
VcfParser.prototype.parseFeatures (data)  
    variant/vcfParser.js  
class BinaryParser (dataView, littleEndian)  
    binary.js  
  
BinaryParser.prototype.remLength ()  
    binary.js  
  
BinaryParser.prototype.hasNext ()  
    binary.js  
  
BinaryParser.prototype.getBytes ()  
    binary.js  
  
BinaryParser.prototype.getShort ()  
    binary.js  
  
BinaryParser.prototype.getInt ()  
    binary.js  
  
BinaryParser.prototype.getUInt ()  
    binary.js  
  
BinaryParser.prototype.getLong ()  
    binary.js  
  
BinaryParser.prototype.getString (len)  
    binary.js  
  
BinaryParser.prototype.getFixedLengthString (len)  
    binary.js  
  
BinaryParser.prototype.getFloat ()  
    binary.js  
  
BinaryParser.prototype.getDouble ()  
    binary.js  
  
BinaryParser.prototype.skip (n)  
    binary.js  
  
BinaryParser.prototype.getVPointer ()  
    binary.js
```

## BAM Helper Classes

```
class BamAlignment ()  
    bam/bamAlignment.js  
  
BamAlignment.prototype.isMapped ()  
    bam/bamAlignment.js  
  
BamAlignment.prototype.isPaired ()  
    bam/bamAlignment.js  
  
BamAlignment.prototype.isProperPair ()  
    bam/bamAlignment.js  
  
BamAlignment.prototype.isFirstOfPair ()  
    bam/bamAlignment.js
```

```
BamAlignment.prototype.isSecondOfPair()
    bam/bamAlignment.js

BamAlignment.prototype.isSecondary()
    bam/bamAlignment.js

BamAlignment.prototype.isSupplementary()
    bam/bamAlignment.js

BamAlignment.prototype.isFailsVendorQualityCheck()
    bam/bamAlignment.js

BamAlignment.prototype.isDuplicate()
    bam/bamAlignment.js

BamAlignment.prototype.isMateMapped()
    bam/bamAlignment.js

BamAlignment.prototype.isNegativeStrand()
    bam/bamAlignment.js

BamAlignment.prototype.isMateNegativeStrand()
    bam/bamAlignment.js

BamAlignment.prototype.tags()
    bam/bamAlignment.js

BamAlignment.prototype.popupData (genomicLocation)
    bam/bamAlignment.js

class BamFilter (options)
    bam/bamAlignment.js

    BamFilter.prototype.pass (alignment)
        bam/bamAlignment.js

class BAMTrack (config)
    bam/bamTrack.js

    BAMTrack.prototype.getFeatures (chr, bpStart, bpEnd)
        bam/bamTrack.js

    BAMTrack.prototype.altClick (genomicLocation, referenceFrame, event)
        bam/bamTrack.js

    BAMTrack.prototype.computePixelHeight (alignmentContainer)
        bam/bamTrack.js

    BAMTrack.prototype.draw (options)
        bam/bamTrack.js

    BAMTrack.prototype.paintAxis (ctx, pixelWidth, pixelHeight)
        bam/bamTrack.js

    BAMTrack.prototype.popupMenuItemList (config)
        bam/bamTrack.js

    BAMTrack.prototype.popupData (genomicLocation, xOffset, yOffset, referenceFrame)
        bam/bamTrack.js

    BAMTrack.prototype.popupDataWithConfiguration (config)
        bam/bamTrack.js
```

```
BAMTrack.prototype.menuItemList (popover)
    bam/bamTrack.js

class AlignmentContainer (chr, start, end, samplingWindowSize, samplingDepth, pairsSupported)
    bam/alignmentContainer.js

    AlignmentContainer.prototype.push (alignment)
        bam/alignmentContainer.js

    AlignmentContainer.prototype.forEach (callback)
        bam/alignmentContainer.js

    AlignmentContainer.prototype.finish ()
        bam/alignmentContainer.js

    AlignmentContainer.prototype.contains (chr, start, end)
        bam/alignmentContainer.js

    AlignmentContainer.prototype.hasDownsampledIntervals ()
        bam/alignmentContainer.js

    CoverageMap.prototype.incCounts (alignment)
        bam/alignmentContainer.js

class CoverageMap (chr, start, end, alignments, refSeq)
    bam/coverageMap.js

class BamAlignmentRow ()
    bam/bamAlignmentRow.js

    BamAlignmentRow.prototype.findCenterAlignment (bpStart, bpEnd)
        bam/bamAlignmentRow.js

    BamAlignmentRow.prototype.updateScore (genomicLocation, genomicInterval, sortOption)
        bam/bamAlignmentRow.js

    BamAlignmentRow.prototype.calculateScore (bpStart, bpEnd, interval, sortOption)
        bam/bamAlignmentRow.js

class PairedAlignment (firstAlignment)
    bam/pairedAlignment.js

    PairedAlignment.prototype.setSecondAlignment (alignment)
        bam/pairedAlignment.js

    PairedAlignment.prototype.popupData (genomicLocation)
        bam/pairedAlignment.js

    PairedAlignment.prototype.isPaired ()
        bam/pairedAlignment.js

    PairedAlignment.prototype.firstOfPairStrand ()
        bam/pairedAlignment.js

class BamIndex (indices, blockMin, blockMax, sequenceIndexMap, tabix)
    bam/bamIndex.js

    BamIndex.prototype.blocksForRange (refId, min, max)
        bam/bamIndex.js

class BGZFile (config)
    bam/bgzf.js
```

```
BGZFile.prototype.nextBlock()  
bam/bgzf.js
```

## BigWig Helper Classes

```
class BWTotalsSummary (byteBuffer)  
    bigwig/bwTotalSummary.js  
  
    BWTotalsSummary.prototype.updateStats (stats)  
        bigwig/bwTotalSummary.js  
  
class BPTree (binaryParser, treeOffset)  
    bigwig/bwBPTree.js  
  
class BWSource (config)  
    bigwig/bwSource.js  
  
    BWSource.prototype.getFeatures (chr, bpStart, bpEnd, bpPerPixel)  
        bigwig/bwSource.js  
  
class RPTree (fileOffset, contentLength, config, littleEndian)  
    bigwig/bwRPTree.js  
  
    RPTree.prototype.load ()  
        bigwig/bwRPTree.js  
  
    RPTree.prototype.readNode (filePosition, bufferedReader)  
        bigwig/bwRPTree.js  
  
    RPTree.prototype.findLeafItemsOverlapping (chrIdx, startBase, endBase)  
        bigwig/bwRPTree.js
```

## Misc Classes

```
class Ga4ghAlignment (json, genome)  
    ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isMapped ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isPaired ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isProperPair ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isFirstOfPair ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isSecondOfPair ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isSecondary ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isSupplementary ()  
        ga4gh/ga4gAlignment.js  
  
    Ga4ghAlignment.prototype.isFailsVendorQualityCheck ()  
        ga4gh/ga4gAlignment.js
```



```
Ga4ghAlignment.prototype.isDuplicate()
    ga4gh/ga4gAlignment.js

Ga4ghAlignment.prototype.isMateMapped()
    ga4gh/ga4gAlignment.js

Ga4ghAlignment.prototype.mateStrand()
    ga4gh/ga4gAlignment.js

Ga4ghAlignment.prototype.tags()
    ga4gh/ga4gAlignment.js

Ga4ghAlignment.prototype.popupData (genomicLocation)
    ga4gh/ga4gAlignment.js

class GFFHelper (format)
    feature/gffHelper.js

    GFFHelper.prototype.combineFeatures (features)
        feature/gffHelper.js

class GtexSelection (selection)
    gtex/gtex.js

    GtexSelection.prototype.addGene (geneName)
        gtex/gtex.js

    GtexSelection.prototype.colorForGene (geneName)
        gtex/gtex.js

class Set ()

    set.js

    Set.prototype.add ()
        set.js

    Set.prototype.addAll (arrayOrSet)
        set.js

    Set.prototype.__add (key, val)
        set.js

    Set.prototype.__getKey (arg)
        set.js

    Set.prototype.__makeKey (arg)
        set.js

    Set.prototype.__removeItem (key)
        set.js

    Set.prototype.__isPseudoArray (item)
        set.js

    Set.prototype.delete (key)
        set.js

    Set.prototype.has (key)
        set.js

    Set.prototype.hasAll (args)
        set.js
```

```
Set.prototype.makeSet (args)  
    set.js  
  
Set.prototype.equals (otherSet)  
    set.js  
  
Set.prototype.isEmpty ()  
    set.js  
  
Set.prototype.size ()  
    set.js  
  
Set.prototype.keys ()  
    set.js  
  
Set.prototype.clear ()  
    set.js  
  
Set.prototype.makeNew ()  
    set.js  
  
Set.prototype.union (otherSet)  
    set.js  
  
Set.prototype.intersection (otherSet)  
    set.js  
  
Set.prototype.difference (otherSet)  
    set.js  
  
Set.prototype.notInBoth (otherSet)  
    set.js  
  
Set.prototype.isSubset (otherSet)  
    set.js  
  
Set.prototype.isSuperset (otherSet)  
    set.js  
  
Set.prototype.each (fn)  
    set.js  
  
Set.prototype.eachReturn (fn)  
    set.js  
  
Set.prototype.filter (fn)  
    set.js  
  
Set.prototype.map (fn)  
    set.js  
  
Set.prototype.some (fn)  
    set.js  
  
Set.prototype.every (fn)  
    set.js  
  
Set.prototype.isEmpty ()  
    set.js  
  
Set.prototype.addAll (arrayOrSet)  
    set.js
```

```
class Variant ()
  variant/variant.js

  Variant.prototype.popupData (genomicLocation)
    variant/variant.js
```

## UI Helper Classes

```
class TrackView (track, browser)
  trackView.js

  TrackView.prototype.configureViewportContainer ($viewportContainer, viewports)
    trackView.js

  TrackView.prototype.attachDragWidget ()
    trackView.js

  TrackView.prototype.appendLeftHandGutterDivToTrackDiv ($track)
    trackView.js

  TrackView.prototype.createRightHandGutter ()
    trackView.js

  TrackView.prototype.setContentHeightForViewport (viewport, height)
    trackView.js

  TrackView.prototype.setTrackHeight (newHeight, update)
    trackView.js

  TrackView.prototype.isLoading ()
    trackView.js

  TrackView.prototype.resize ()
    trackView.js

  TrackView.prototype.update ()
    trackView.js

  TrackView.prototype.repaint ()
    trackView.js

class TrackScrollbar ($viewportContainer, viewports)
  trackView.js

  TrackScrollbar.prototype.update ()
    trackView.js

class ColorPicker ($parent, userPalette)
  ui/colorpicker.js

  ColorPicker.prototype.configure (trackView)
    ui/colorpicker.js

  ColorPicker.prototype.hide ()
    ui/colorpicker.js

  ColorPicker.prototype.show ()
    ui/colorpicker.js

class DataRangeDialog ($parent)
  ui/dataRangeDialog.js
```

```
DataRangeDialog.prototype.configureWithTrackView (trackView)
    ui/dataRangeDialog.js

DataRangeDialog.prototype.hide ()
    ui/dataRangeDialog.js

DataRangeDialog.prototype.show ()
    ui/dataRangeDialog.js

class CenterGuide ($parent, config)
    ui/centerGuide.js

CenterGuide.prototype.repaint ()
    ui/centerGuide.js

CenterGuide.prototype.resize ()
    ui/centerGuide.js

class AlertDialog ($parent, id)
    ui/alertDialog.js

AlertDialog.prototype.alertTextContainer ()
    ui/alertDialog.js

AlertDialog.prototype.rowOfOk ()
    ui/alertDialog.js

AlertDialog.prototype.hide ()
    ui/alertDialog.js

AlertDialog.prototype.show ($host)
    ui/alertDialog.js

class Popover ($parent)
    ui/popover.js

Popover.prototype.initializationHelper ($parent)
    ui/popover.js

Popover.prototype.hide ()
    ui/popover.js

Popover.prototype.presentTrackGearMenu (pageX, pageY, trackView)
    ui/popover.js

Popover.prototype.presentTrackPopupMenu (e, viewport)
    ui/popover.js

Popover.prototype.presentTrackPopup (e, viewport)
    ui/popover.js

Popover.prototype.presentContent (pageX, pageY, content)
    ui/popover.js

class TrackMenuPopupDialog (trackMenu, dialogLabel, inputValue, ok, width, height)
    ui/trackMenuPopupDialog.js

TrackMenuPopupDialog.prototype.updateTips (t)
    ui/trackMenuPopupDialog.js

class Dialog ($parent, constructorHelper)
    ui/dialog.js
```

```
Dialog.prototype.rowOfOk()  
    ui/dialog.js  
  
Dialog.prototype.rowOfOkCancel()  
    ui/dialog.js  
  
Dialog.prototype.rowOfLabel()  
    ui/dialog.js  
  
Dialog.prototype.rowOfInput()  
    ui/dialog.js  
  
Dialog.prototype.configure(labelHTMLFunction, inputValue, clickFunction)  
    ui/dialog.js  
  
Dialog.prototype.hide()  
    ui/dialog.js  
  
Dialog.prototype.show($host)  
    ui/dialog.js
```

```
class UserFeedback($parent)  
    ui/userFeedback.js  
  
UserFeedback.prototype.show()  
    ui/userFeedback.js  
  
UserFeedback.prototype.hide()  
    ui/userFeedback.js  
  
UserFeedback.prototype.bodyCopy(htmlString)  
    ui/userFeedback.js
```

## graphics

```
    igv-canvas.js  
  
graphics.setProperties(ctx, properties)  
    igv-canvas.js  
  
graphics.strokeLine(ctx, x1, y1, x2, y2, properties, linewidth)  
    igv-canvas.js  
  
graphics.fillRect(ctx, x, y, w, h, properties)  
    igv-canvas.js  
  
graphics.fillPolygon(ctx, x, y, properties)  
    igv-canvas.js  
  
graphics.strokePolygon(ctx, x, y, properties)  
    igv-canvas.js  
  
graphics.fillText(ctx, text, x, y, properties, transforms)  
    igv-canvas.js  
  
graphics.strokeText(ctx, text, x, y, properties, transforms)  
    igv-canvas.js  
  
graphics.strokeCircle(ctx, x, y, radius, properties)  
    igv-canvas.js  
  
graphics.fillCircle(ctx, x, y, radius, properties)  
    igv-canvas.js
```

```
graphics.drawArrowhead (ctx, x, y, size, lineWidth)
    igv-canvas.js

graphics.dashedLine (ctx, x1, y1, x2, y2, dashLen, properties)
    igv-canvas.js
```

## Color Helper Classes

```
class BinnedColorScale (cs)
    igv-color.js

    BinnedColorScale.prototype.getColor (value)
        igv-color.js

class GradientColorScale (scale)
    igv-color.js

    GradientColorScale.prototype.getColor (value)
        igv-color.js

class PaletteColorTable (palette)
    igv-color.js

    PaletteColorTable.prototype.getColor (key)
        igv-color.js

addAjaxExtensions ()
    igv-utils.js

addAlphaToRGB (rgbString, alpha)
    igv-color.js

attachDialogCloseHandlerWithParent ($parent, closeHandler)
    igv-utils.js

colorPickerMenuItem (popover, trackView)
    trackCore.js

configTrack (track, config)
    trackCore.js

constrainBBox ($child, $parent)
    igv-utils.js

createBrowser (parentDiv, config)
    igv-create.js

createColorString (token)
    igv-color.js

createGAVariant (json)
    variant/variant.js

createVCFVariant (tokens)
    variant/variant.js

dataRangeMenuItem (popover, trackView)
    trackCore.js

decodeGa4ghReadset (json)
    ga4gh/ga4ghAlignmentReader.js
```

**domElementRectAsString** (*element*)  
igv-utils.js

**encodeSearch** (*continuation*)  
encode/encodeSearch.js

**formatPopoverText** (*nameValueArray*)  
igv-utils.js

**ga4ghGet** (*options*)  
ga4gh/ga4ghHelper.js

**ga4ghSearch** (*options*)  
ga4gh/ga4ghHelper.js

**ga4ghSearchCallSets** (*options*)  
ga4gh/ga4ghHelper.js

**ga4ghSearchReadAndCallSets** (*options*)  
ga4gh/ga4ghHelper.js

**ga4ghSearchReadGroupSets** (*options*)  
ga4gh/ga4ghHelper.js

**ga4ghSearchVariantSets** (*options*)  
ga4gh/ga4ghHelper.js

**getCompositeColor** (*dest, src, alpha*)  
igv-color.js

**getQueryValue** (*name*)  
parseUtils.js

**getSpinnerObjectWithParentElement** (*parentElement*)  
igv-utils.js

**gotoLocusFeature** (*locusFeature, genome, browser*)  
browser.js

**greyScale** (*value*)  
igv-color.js

**guid** ()  
igv-utils.js

**hex2Color** (*hex*)  
igv-color.js

**isBlank** (*line*)  
parseUtils.js

**isComment** (*line*)  
parseUtils.js

**isNumber** (*n*)  
igv-utils.js

**isStringOrNumber** (*value*)  
igv-utils.js

**loadBamIndex** (*indexURL, config, tabix*)  
bam/bamIndex.js

**loadGenome** (*reference*)  
genome.js

**loadTribbleIndex** (*indexFile, config*)  
feature/tribble.js

**log** (*message*)  
igv-utils.js

**makeToggleButton** (*buttonOnLabel, buttonOffLabel, configurationKey, get\$Target, continuation*)  
igv-utils.js

**navigateKaryo** (*mouseX, mouseY*)  
karyo/karyo.js

**numberFormatter** (*rawNumber*)  
igv-utils.js

**numberUnFormatter** (*formattedNumber*)  
igv-utils.js

**paintAxis** (*ctx, pixelWidth, pixelHeight*)  
trackCore.js

**parseUri** (*str*)  
igv-utils.js

**presentAlert** (*string*)  
igv-utils.js

**prettyBasePairNumber** (*raw*)  
igv-utils.js

**random** (*min, max*)  
igv-utils.js

**randomGrey** (*min, max*)  
igv-color.js

**randomRGB** (*min, max*)  
igv-color.js

**randomRGBConstantAlpha** (*min, max, alpha*)  
igv-color.js

**removeBrowser** ()  
igv-create.js

**rgbColor** (*r, g, b*)  
igv-color.js

**rgbaColor** (*r, g, b, a*)  
igv-color.js

**setTrackColor** (*track, color*)  
trackCore.js

**setTrackLabel** (*track, label*)  
trackCore.js

**spinner** (*size*)  
igv-utils.js



**splitStringRespectingQuotes** (*string*, *delim*)  
igv-utils.js

**startSpinnerAtParentElement** (*parentElement*)  
igv-utils.js

**stopSpinnerAtParentElement** (*parentElement*)  
igv-utils.js

**throttle** (*fn*, *threshold*, *scope*)  
igv-utils.js

**trackMenuItem** (*popover*, *trackView*, *menuItemLabel*, *dialogLabelHandler*, *dialogInputValue*, *dialogClickHandler*, *doAddTopBorder*)  
trackCore.js

**trackMenuItemList** (*popover*, *trackView*)  
trackCore.js

**trackPopupMenuItemList** (*popover*, *viewport*, *genomicLocation*, *xOffset*, *yOffset*)  
trackCore.js

**translateMouseCoordinates** (*e*, *target*)  
igv-utils.js

**unbgzf** (*data*, *lim*)  
bam/bgzf.js



## CHAPTER 3

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### Indices and tables

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- `search`



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