
g3d

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CHAPTER 1

Introduction

g3d is a binary file format for storing genomic 3D structure data, g3d is short for genomic 3D format.

We have one [github repository](#) hosts the g3d toolsets:

1. g3dv - the online g3d visualization platform
2. g3dtools - the command line tool to generate or query *.g3d* file
3. g3djs - the JavaScript API for reading *‘.g3d’* file

If you have any question, please contact us by [submit an Issue request](#).

A frontend library based on [Vue.js](#) display .g3d file using [three.js](#) engine.

Features:

1. Single mesh mode, all meshes mode
2. Customization (color, line width etc)
3. Walk mode
4. Clickable label to highlight
5. Screenshot (w/ and w/o label)
6. Performance (high FPS)

2.1 Start from a g3d file

Prepare your 3D genomic structure data in .g3d format, you can then put it on a web server for remote access or just save on your local drive.

Open the g3dv website at: <https://g3dv.now.sh/>

Genomic 3D Visualizer

About

Remote file Local file

Input a G3D file URL

G3D file url

Genome assembly

hg19

Select a resolution

200K

Select a gene or region

gene symbol or region

Chosen region:

Choose display region

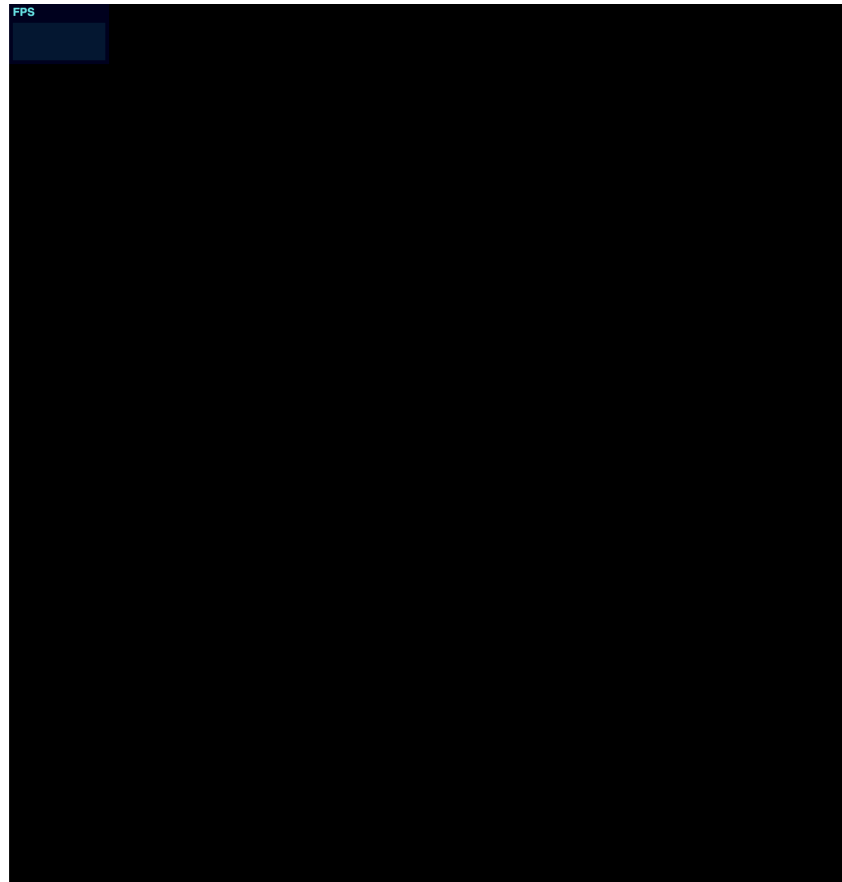
☒ Input region

☐ Whole Chromosome

☐ Whole Genome

Example

Go



Click the `Remote file` or `Local file` tab to switch from using a file from web server or a local file from your hard drive.

We have provide example file and region for your to take a quick look, just click the `Example` button and then the `Go` button, the 3D structure for the default region will be displayed:

Genomic 3D Visualizer

About

Remote file Local file

Input a G3D file URL

https://wangftp.wustl.edu/~dli/tm

Genome assembly

hg19

Select a resolution

200K

Select a gene or region

chr7:27053397-27373765

Chosen region: chr7:27053397-27373765

Choose display region

☒ Input region

☐ Whole Chromosome

☐ Whole Genome

Example Go

3D FPS (0-40)

chr7:27053397-27373765_p

Background 0x0

Show label ☒

Show all ☐

Regions

region chr7:27053397-27373765

color rgb(152,154,80)

scale 1

Camera

Walk mode ☐

Look ahead ☐

speed Slow

Remove selection

Screenshot

Close Controls

If you want to see whole chromosome structure, choose `Whole Chromosome` as display region, submit again:

Choose display region

☐ Input region

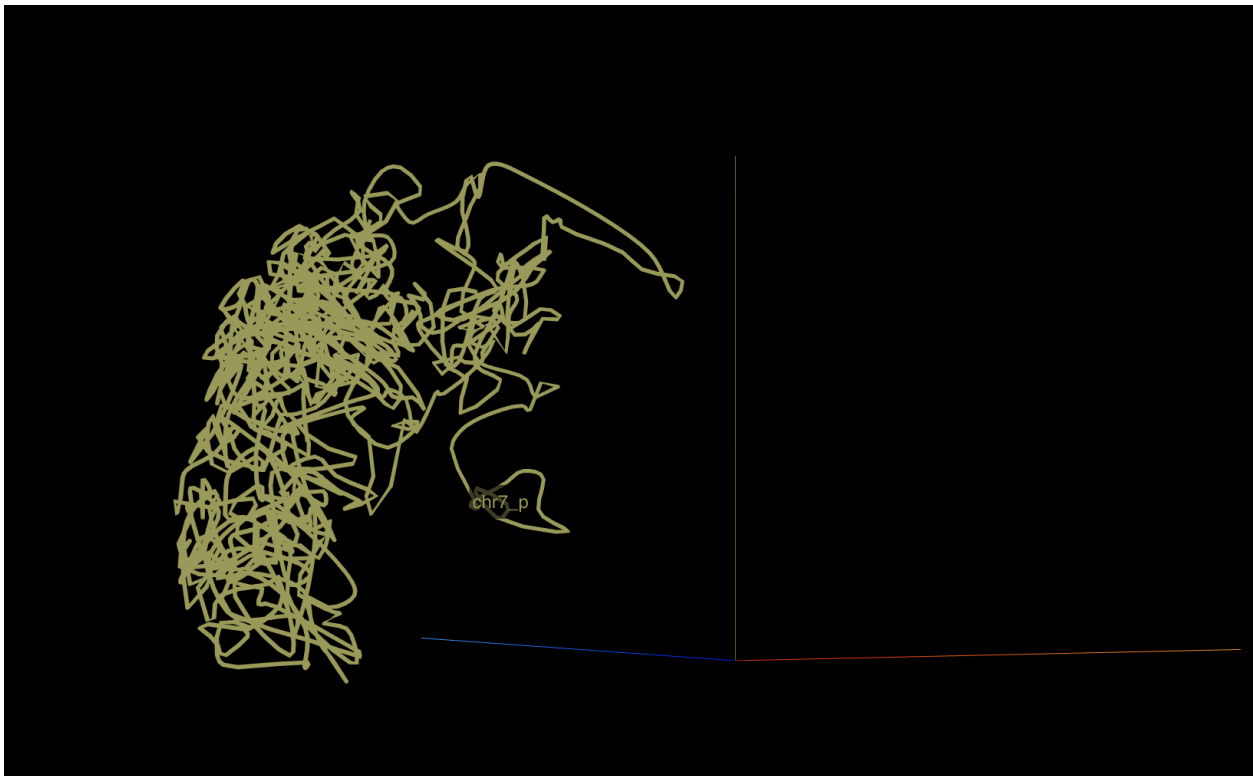
☒ Whole Chromosome

☐ Whole Genome

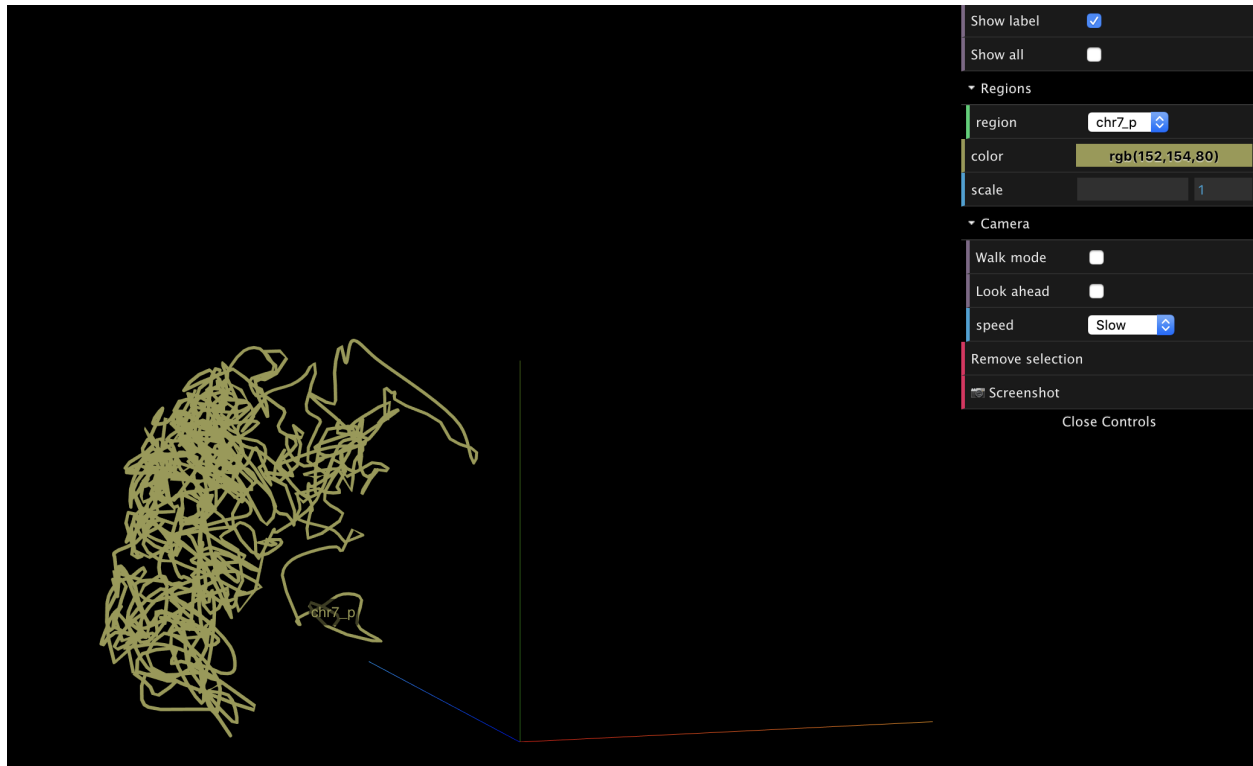
Example

Go

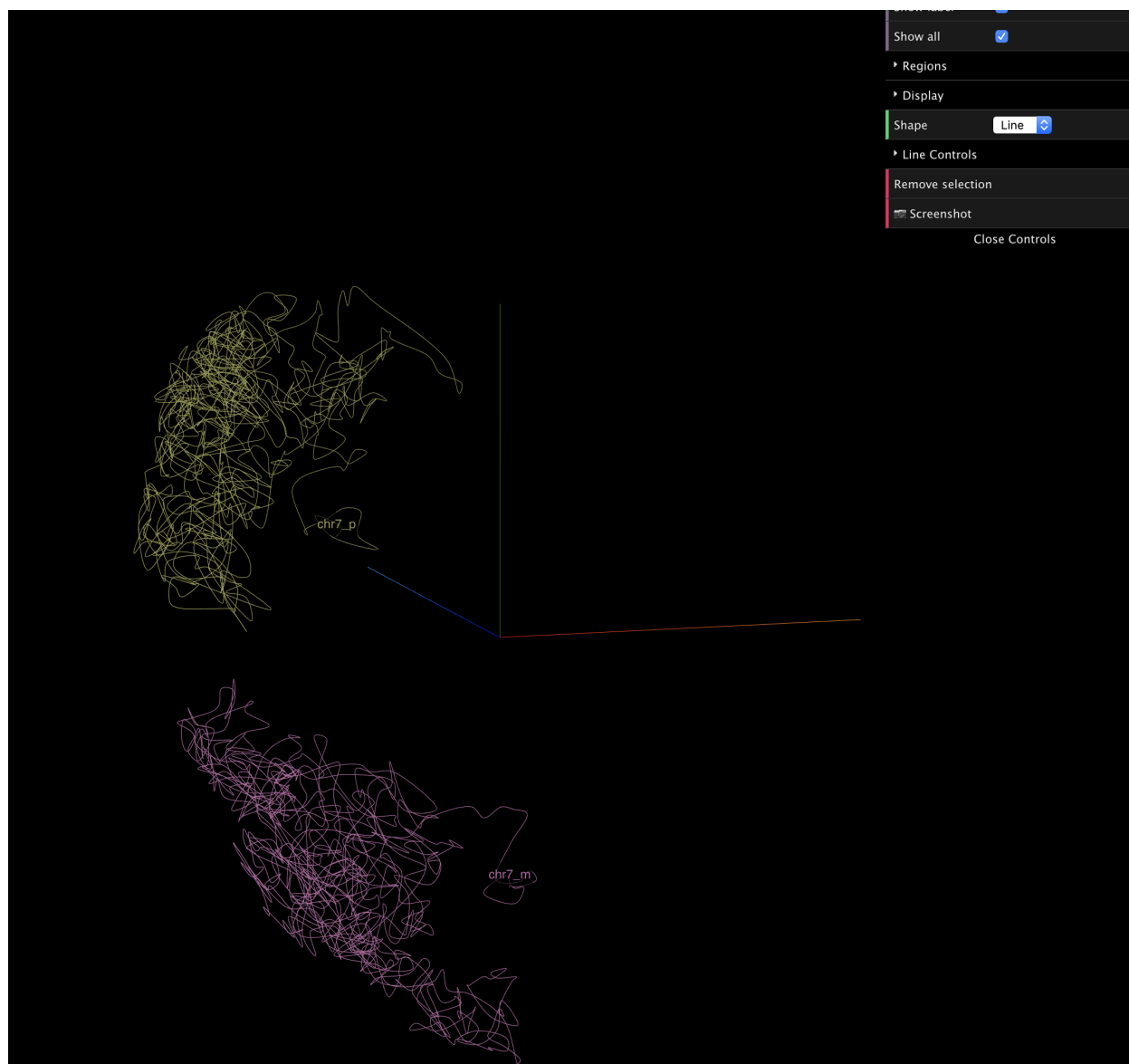
The display will update:



By default, only one 3D model will be displayed, either from maternal or paternal, or from one chromosome. One the display scene, the right part shows the configuration menu for single mode:

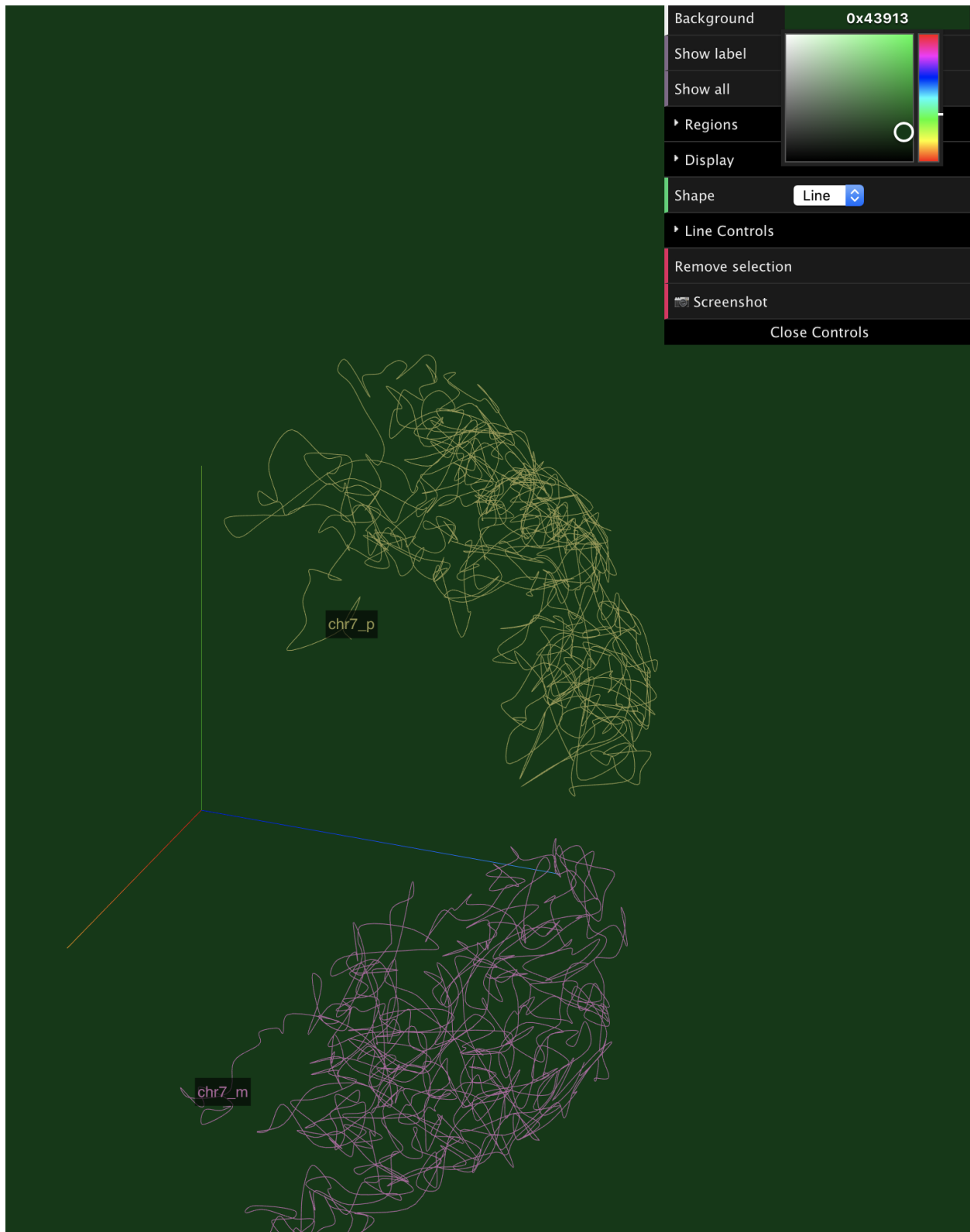


The Show all checkbox toggles single model mode or multiple models mode:

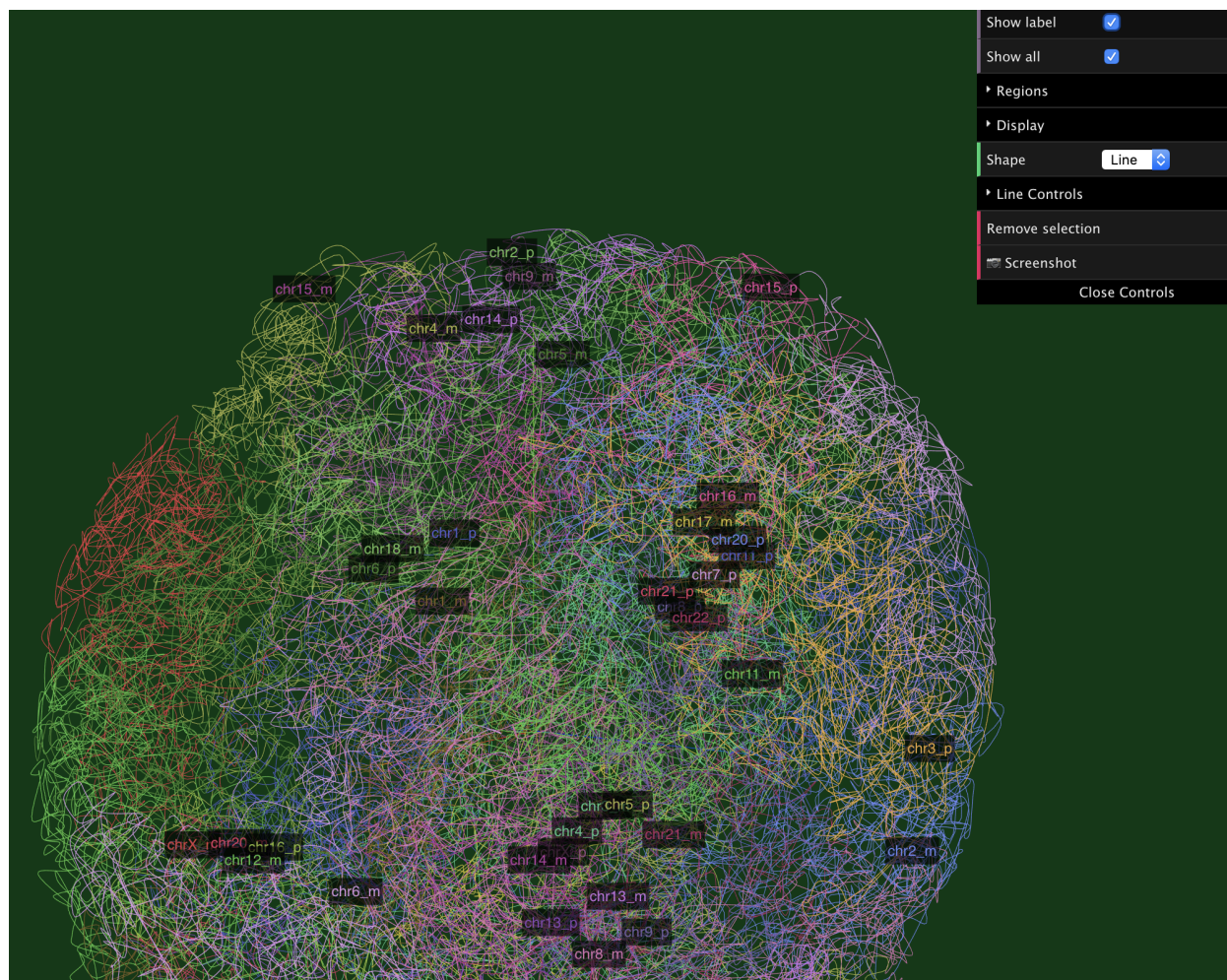


2.1.1 Display configurations

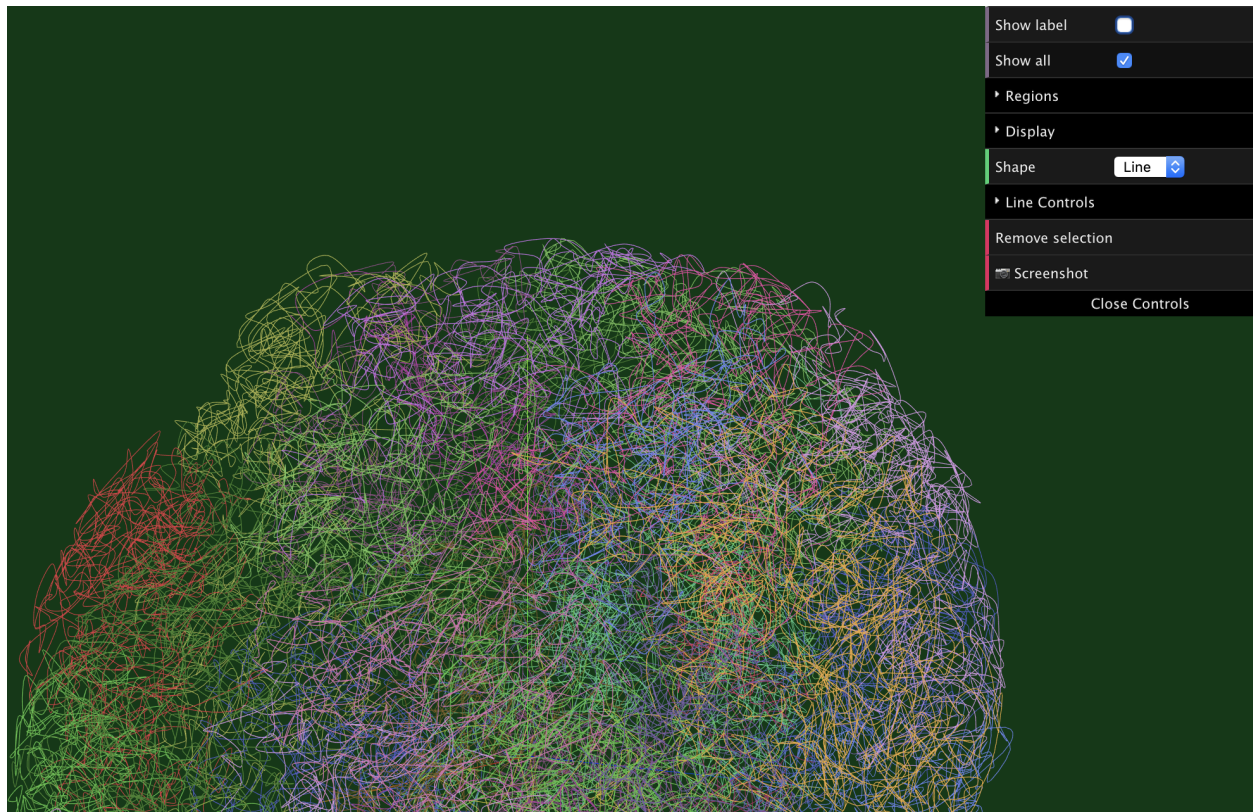
The Background color can be changed if you move mouse over to the `Background` menu item, click the palette to change the color you liked:



The label for each chromosome or region will be displayed by default:

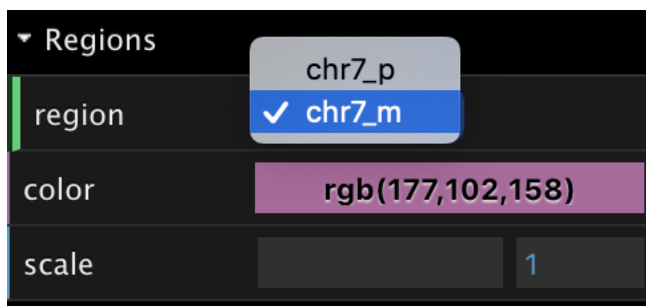


You can make them invisible by uncheck the `Show label` menu item:

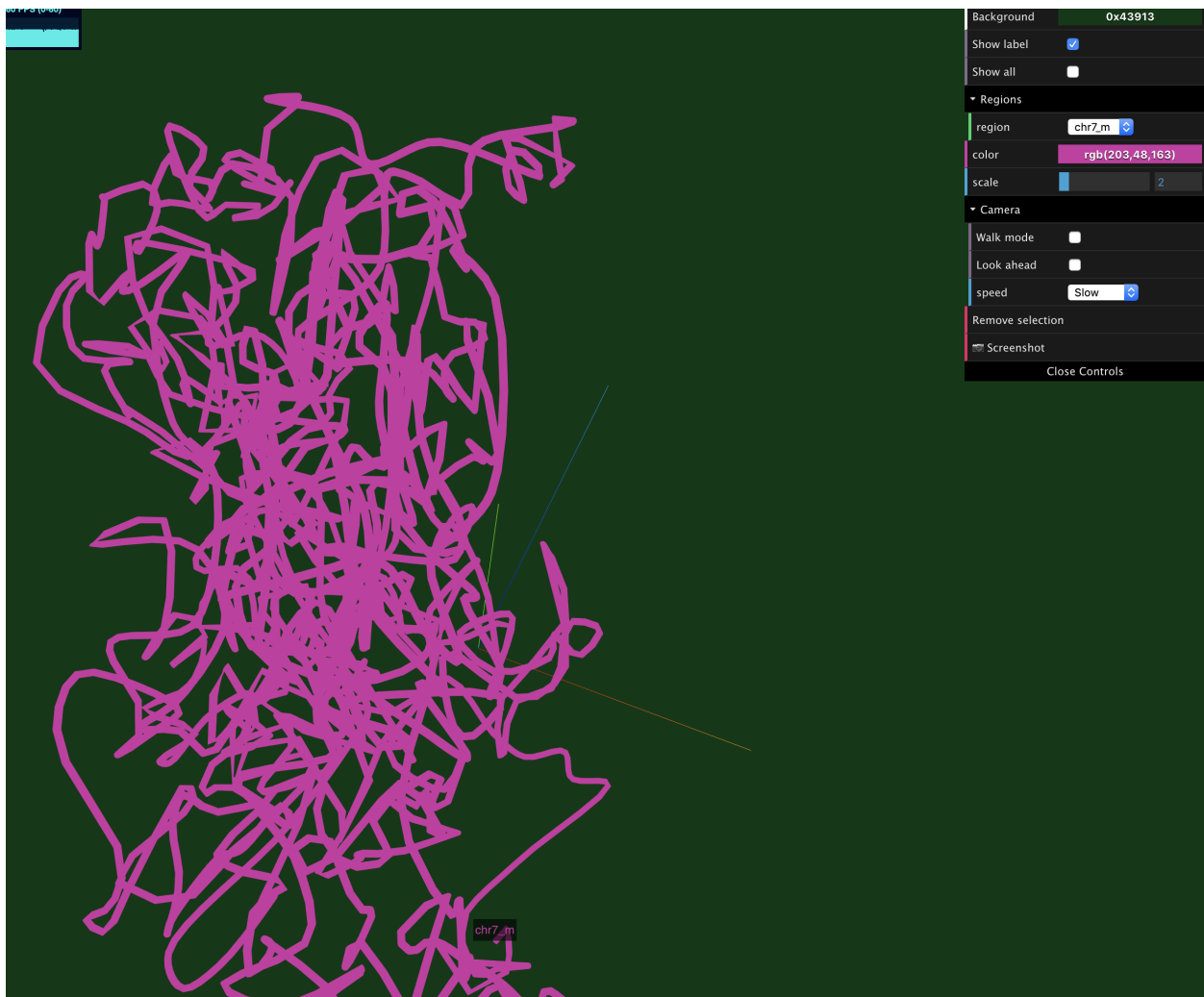


2.1.2 Single model mode

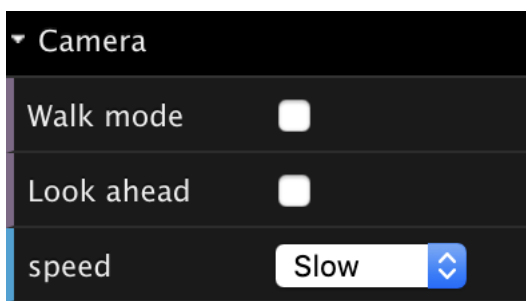
While at single model mode, there is a dropdown menu for selection which region/chromosome to display, we can also change the color and scale:



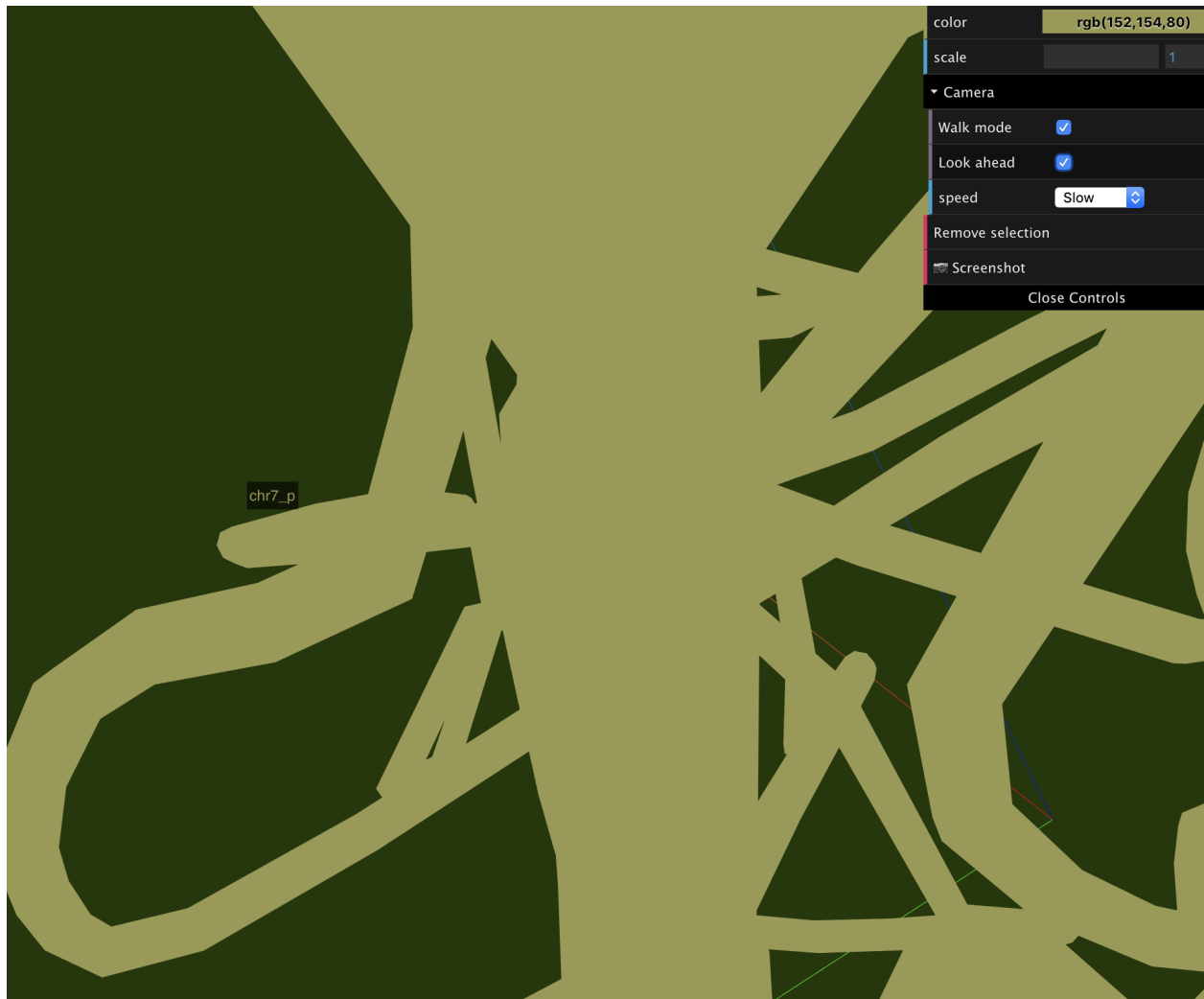
After adjusted region, color and scale:



On single model mode, there is a walking camera provided to mimic the walk/run along with the reigon/chromosome:

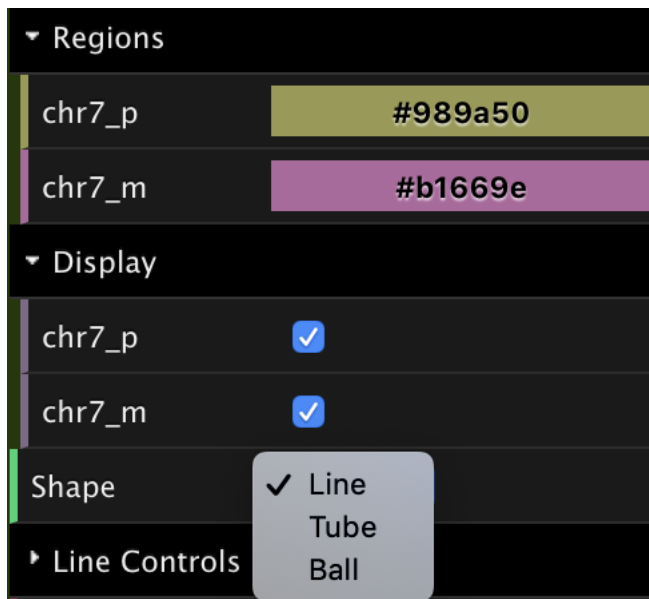


By checking the `Walk mode` checkbox, the view will start to move/walk. The speed can be adjusted as well.

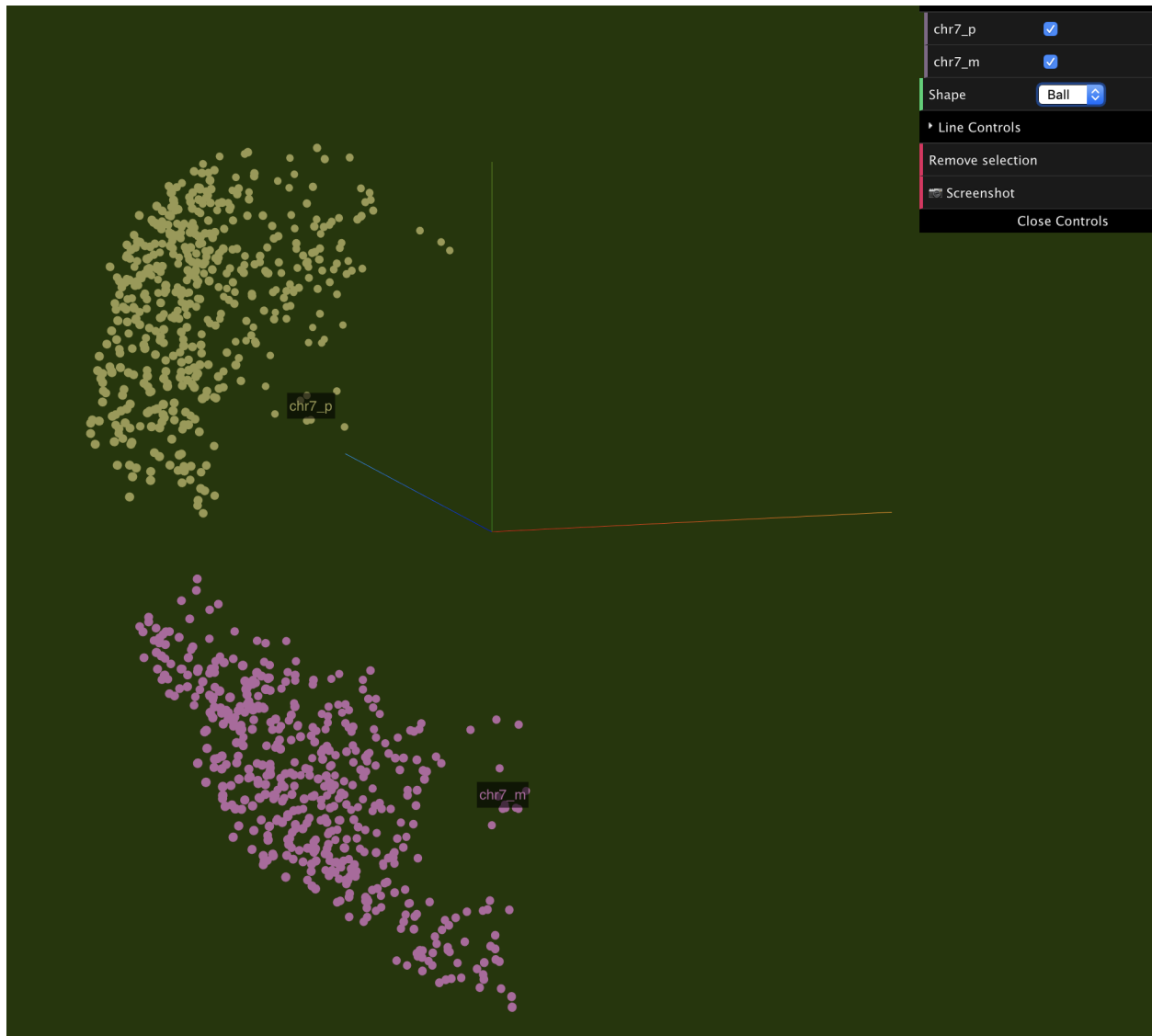


2.1.3 Multiple models mode

Multiple models mode displays all 3D models, both from paternal and maternal, and from all chromosomes/regions. There are two dropdown menus to change the color of each model, and toggle the display of each model. Also you can change the shape type to *line*, *tube* or *ball*.

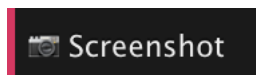


The image below shows while we changed shape type to *ball*:



2.1.4 Screenshot

Use the screenshot button (shown below) to take a screenshot, the generated screenshot will be the same as the time when you clicked the button.



2.2 Try genomics 3D structure in AR mode

- Please use your phone's camera point the QR code in the image below, Safari will popup and try to open our website, and will ask if allow to use the camera, please *Allow*



Genomics
3D AR

- then point the camera again to the Marker part (St. Louis Arch), and you will see the 3D structure in AR.

AA



g3dv.now.sh

`markersAreaEnabled :false`

CHAPTER 3

g3dtools

A tool for operating .g3d (genome 3D structure) format.

Require: **Python** (Recommend version 3 and above).

example input, 6 columns bed-like text file:

| | | | | | |
|------|----------|----------------|----------------|---------------|---|
| chr7 | 16760000 | -14.3866688728 | -36.3919302029 | 19.8483965881 | m |
| chr7 | 16760000 | -24.9116268071 | 50.0521268287 | 9.91073185128 | p |
| chr7 | 25160000 | -10.1170055526 | -34.8975763469 | 20.2401719179 | m |
| chr7 | 25160000 | -21.8210915649 | 27.1128556621 | 13.4856945965 | p |
| chr7 | 33540000 | -4.11059384846 | -54.4940083464 | 4.21321135564 | m |
| chr7 | 33540000 | -12.0040359857 | 31.5960497183 | 26.6925954134 | p |
| chr7 | 41940000 | 5.75342635105 | -55.4976428728 | 8.65307697332 | m |
| chr7 | 41940000 | -23.7372022413 | 36.0614692267 | 31.919119243 | p |
| chr7 | 50320000 | -10.7099779927 | -38.0214001171 | 25.8308473821 | m |
| chr7 | 50320000 | -28.5142098162 | 26.6468499001 | 28.8634805533 | p |
| chr7 | 26200000 | -11.5800097945 | -37.9903257744 | 16.2461100893 | m |
| chr7 | 26200000 | -15.9552426623 | 27.016940724 | 17.5722080595 | p |
| chr7 | 27260000 | -14.1883124179 | -44.7860807973 | 12.4104162757 | m |
| chr7 | 27260000 | -20.0857754297 | 30.9204143041 | 18.4774635708 | p |
| chr7 | 28300000 | -18.0160836669 | -39.398544495 | 12.811858164 | m |
| chr7 | 28300000 | -14.9383020843 | 39.1464516779 | 17.3743509519 | p |
| chr7 | 29360000 | -11.8032470923 | -47.3595095319 | 13.2828128833 | m |
| chr7 | 29360000 | -12.2445277916 | 41.2431968179 | 14.8844908717 | p |
| chr7 | 30400000 | -12.8674349856 | -45.0752589744 | 9.15498568359 | m |

columns are:

- chromosome
- start position
- X (coordinates in 3D)
- Y
- Z

- haplotype (optional), *m* for *maternal*, *p* for *paternal*, *s* for *shared*, if omitted, *s* will be used

3.1 Generate a new .g3d file using the format listed above

```
g3dtools load ../test/test.g3d.bed.gz -o ../testOut/test -s 2,3,4,5,6,7,8,9,10
```

3.2 Generate a new .g3d file from .3dg format

Input a file with high resolution, let the tool calculate lower resolutions:

```
g3dtools 3dg ../test/GSM3271347_gm12878_01.impute3.round4.clean.3dg.txt.gz -o  
../testOut/GSM3271347_gm12878_01.impute3.round4.clean -s 2,3,4,5,6,7,8,9,10
```

or prepare different resolution files in advance:

3.3 Query

By region:

```
g3dtools query testOut/test.g3d -c chr7 -s 27053397 -e 27373765
```

change resolution:

```
g3dtools query testOut/test.g3d -c chr7 -s 27053397 -e 27373765 -r 100000
```

when resolution not exists:

```
g3dtools query testOut/test.g3d -c chr7 -s 27053397 -e 27373765 -r 130000  
[Query] Error, resolution 130000 not exists for this file,  
available resolutions: [20000, 40000, 60000, 80000, 100000, 120000, 140000, 160000,   
↪180000, 200000]
```

Javascript API for reading .g3d genomic 3D structure files.

4.1 Installation

Requires [Node](#).

```
npm install g3djs
```

4.2 Examples

Example code below to fetch data from a .g3d file hosted on a webserver.

```
import G3dFile from 'g3djs';

const url = 'https://wangftp.wustl.edu/~dli/tmp/test.g3d';
const file = new G3dFile({ url });
// get metadata
// metadata contains information about genome assembly, dataset name, resolutions etc.
file.readHeader().then(() => console.log(file.meta));

// get 3D data from a specific region, under a specific resolution
// parameters: chrom, start, end, resolution
file.readData('chr7', 27053397, 27373765, 20000).then(data => console.log(data));

// get data for a chromosome, 200000 is the resolution
file.readDataChromosome('chr7', 200000).then(data => console.log(data));

// get data for the genome, 200000 is the resolution
file.readDataGenome(200000).then(data => console.log(data));
```


CHAPTER 5

Indices and tables

- `genindex`
- `modindex`
- `search`