```
var context = dnaism.context()
                                                                                            we are interested in exploring. We do that by setting the
           .start(1100000)
                                                                                             chromosome and the start and stop position of the
           .stop(1200000)
                                                                                             region of interest. In addition we have to specify the
           .size(1280)
                                                                                             space we have to visualize the data, in pixels. Finally
                                                                                             the step() method allows us to control the resolution.
           .chrm('chr17')
           .step(2);
                                                                                             The next two set of statements define the axis and the
d3.select("#demo").selectAll(".axis")
                                                                                             rules. Those will remain the same for other
   .data(["top", "bottom"])
                                                                                             visualizations so the user does not have to modify
                                                                                             them.
 .enter().append("div")
   .attr("class", function(d) { return d + " axis"; })
   .each(function(d) { d3.select(this).call(context.axis().ticks(12).orient(d)); });
                                                                                             We define a source. The interface of a source
d3.select("body").append("div")
                                                                                             component defines a contract that context uses to
                                                                                             requests data for a specific region. All the logic on how
   .attr("class", "rule")
                                                                                             to retrieve the data is encapsulated in that component.
   .call(context.rule());
                                                                                             Once the source is defined we instantiate metrics for all
var source_bedfile = context.bedfile();
                                                                                             the samples we want to incorporate in our visualization.
var metrics = [
   source bedfile.metric("18277.bed"),
  source_bedfile.metric("19466.bed"),
   source bedfile.metric("23138.bed"),
   ....];
                                                                                             Finally, we use the horizon component to render the
d3.select("body").selectAll(".horizon")
                                                                                             visualizations.
   .data(metrics)
 .enter().insert("div", ".bottom")
   .attr("class", "horizon")
 .call(context.horizon()
   .format(d3.format(".2")));
                                                                                             The final statement adds visual clarity to the visualization
context.on("focus", function(i) {
                                                                                             by changing the coordinates of the values of the metrics
 d3.selectAll(".value").style("right", i == null ? null : context.size() - i + "px");
                                                                                             to make sure they follow the rule as its moves along the
```

x-axis.

});

First we define the context of the region of the genome