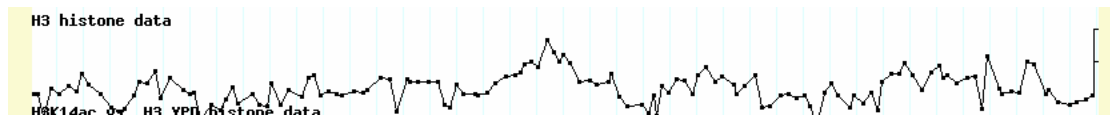


This is what I want to show my quantitative data: line with points.



Picture cut from http://frodo.wi.mit.edu/cgi-bin/yeast_histones/gbrowse.cgi/yeast_histones

This is my gff data:

I	POK H3_data	61	61	1.239895459	.	.	H3 Change
I	POK H3_data	2263	2263	0.620671591	.	.	H3 Change
I	POK H3_data	2858	2858	0.063376849	.	.	H3 Change
I	POK H3_data	3010	3010	0.110825165	.	.	H3 Change
I	POK H3_data	3174	3174	0.196825077	.	.	H3 Change
I	POK H3_data	3525	3525	-2.917006621	.	.	H3 Change
I	POK H3_data	3619	3619	-2.742709066	.	.	H3 Change
I	POK H3_data	3978	3978	-2.648177623	.	.	H3 Change
I	POK H3_data	4141	4141	-1.338767264	.	.	H3 Change
I	POK H3_data	4307	4307	0.440693117	.	.	H3 Change

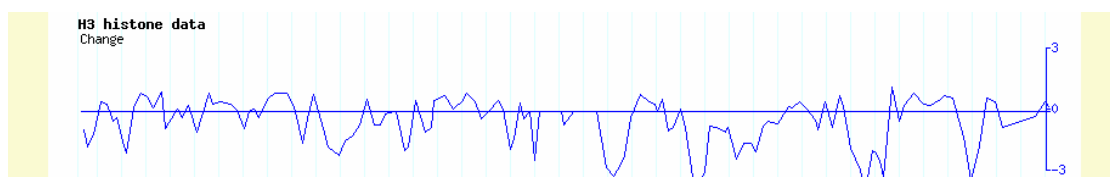
This is the modified part in my .conf file:

```

.....
aggregators = match
  BAC{left_end_read,right_end_read/BAC}
  processed_transcript
  coding
  H3_data{H3_data}
.....
[H3 histone data]
feature      = H3_data
fgcolor      = blue
bgcolor      = black
linewidth    = 1
glyph        = xyplot
graph_type   = linepoints
point_symbol = square
point_radius = 4
height       = 50
min_score    = -3
max_score    = 3
scale        = right
key          = H3 histone data

```

But, what I get is:



Question: How to configure the .conf file to get What I want?