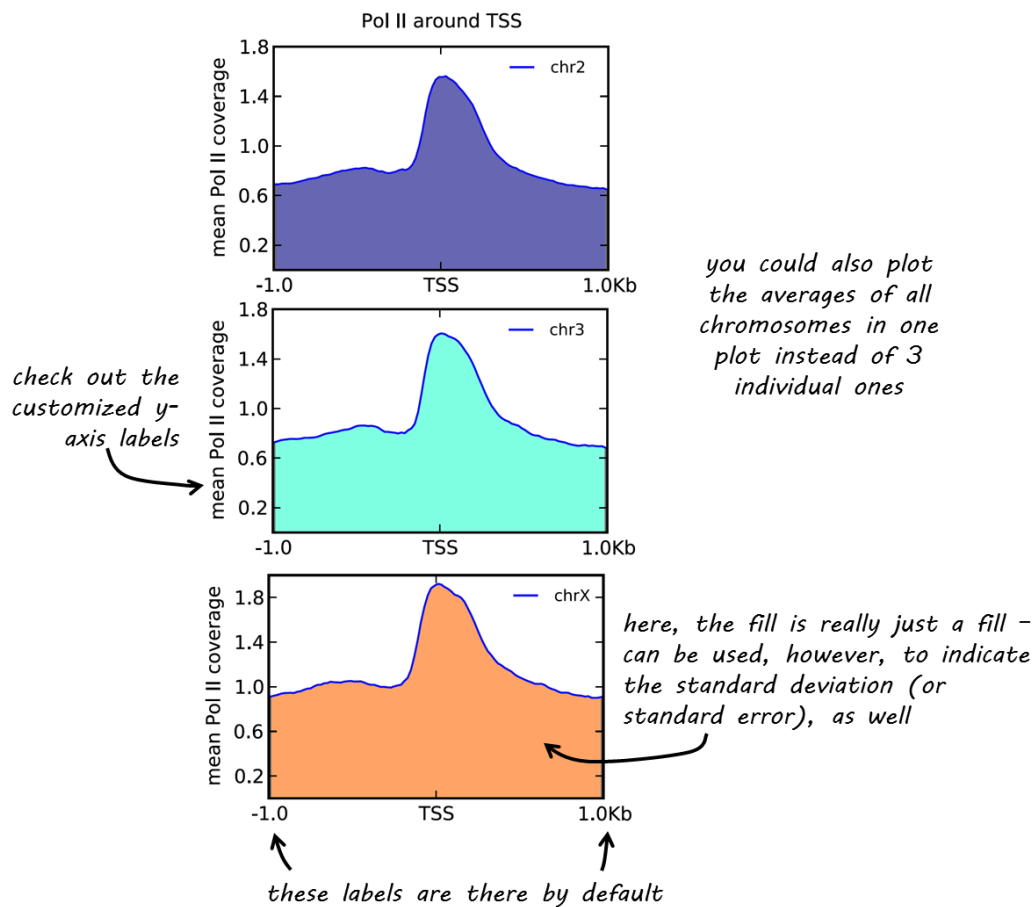


2nd example: Summary plots with all genes scaled to the one size and user-specified groups of genes

Here's the **profiler** plot corresponding to the heatmap above. There's one major difference though - do you spot it?



We used the same BED file(s) as for the heatmap, hence the 3 different groups (1 per chromosome). However, this time we used `computeMatrix` not with `scale-regions` but with `reference-point` mode.

```
$ /deepTools-1.5.2/bin/computeMatrix reference-point --referencePoint TSS \
--regionsFileName Dm.genes.indChromLabeled.bed --scoreFileName PolII.bw \
--beforeRegionStartLength 1000 --afterRegionStartLength 1000 \
--binSize 10 --outFileName PolII_matrix_indChr_refPoint \
--missingDataAsZero --sortRegions no

$ /deepTools-1.5.2/bin/profiler --matrixFile PolII_matrix_indChr_refPoint \
--outFileName profile_PolII_indChr_refPoint.pdf
--plotType fill --startLabel "TSS" \
--plotTitle "Pol II around TSS" --yAxisLabel "mean Pol II coverage" \
--onePlotPerGroup
```

When you compare the profiler commands with the heatmapper commands, you also notice that we made use of many more labeling options here, e.g. `--yAxisLabel` and a more specific title via `-T`

This is how you would have obtained this plot in Galaxy (only the part that's *different* from the above shown command for the `scale-regions` version is shown):

computeMatrix

The reference point for the plotting:**Discard any values after the region end:**☐

This is useful to visualize the region end when not using the scale-regions mode and when the reference-point is set to the TSS.

Distance upstream of the start site of the regions defined in the region file:

If the regions are genes, this would be the distance upstream of the transcription start site.

Distance downstream of the end site of the given regions:

If the regions are genes, this would be the distance downstream of the transcription end site.

profiler

profiler (version 1.0.2)

Matrix file from the computeMatrix tool:**The input matrix was computed in scale-regions mode:****Show advanced output settings:****Show advanced options:****Determine the type of statistic that should be used for the profile.:****Plot height:**

Height in cm. The default for the plot height is 5 centimeters. The minimum value is 3 cm.

Plot width:

Width in cm. The default value is 8 centimeters. The minimum value is 1 cm.

Plot type:

For the summary plot (profile) only. The "lines" option will plot the profile line based on the average type selected. The "fill" option fills the profiles. The "std" option colors the region between the profile and the standard deviation of the data. As in the case of fill, a semi-transparent option only works if "one plot per group" is set.

Labels for the regions plotted in the heatmap:

If more than one region is being plotted a list of labels separated by comma and limited by quotes, is required. For example, "label1, label2".

Title of the plot:

Title of the plot, to be printed on top of the generated image. Leave blank for no title.

Do one plot per group:☒

When the region file contains groups separated by "#", the default is to plot the averages for the distinct plots in one plot. If this option is set, a separate plot is generated for each group.

Minimum value for the Y-axis of the summary plot. Leave empty for automatic values:**Maximum value for Y-axis of the summary plot. Leave empty for automatic values:****Description for the x-axis label:****Description for the y-axis label for the top panel:**