**2022-07-15 | seqNdisplayR bugs – last bugs before publication**

**SLA’s suggested improvements**

1. Pick your own colors in-app
2. Accept annotations of gtf-type
3. Add sequence at sufficient zoom level

***Reported bugs***

**Bug #1** (Kristoffer)

Bug discovered in app, and could be reproduced in R version.

xl\_fname = system.file('extdata', 'seqNdisplayR\_sample\_sheet\_elaborate2.xlsx',

package='seqNdisplayR')

session = load\_excel(xl\_fname, load\_annotations = T)

plot(session, feature='LMO4')

session[['parameters']][['3-seq']][['calcMean']] = FALSE

plot(session, feature='LMO4')

Error in .panel.word.widths[, .n.level] <- .common.font.size \* (nchar(names(panels\_list[[.dataset]][[.n.level - :

number of items to replace is not a multiple of replacement length

**FIXED: 2022-09-16**

**Bug #2** (Jerome/Patrik)

Bug discovered in app, and could be reproduced in R version.

Make the app ignore extra lines in the dataset option sheet of the excel.

Like if I have only and 'RNA-seq' dataset in the samples sheet but 4 lines with 'tt-seq', 'RNA-seq', 'Chip-seq' and 'random-seq' in the dataset option, that it only gets the relevant one (potentially with a warning).

**FIXED: 2022-09-19**

**Bug #3** (Jerome/others)

Bug in app only

The app going 'epileptic' when a wrong excel was put in. In every case the problem did come from the excel, but in every case the reaction was kind of the same: it looks 'scary' in a way (like everyone going 'WTF' and not being sure what to do).

In the 3 different cases the excel issue was different:

√ Matti had unproperly filled the sample sheet (absence of name in subset1)

√ Kat first used an excel with no '.xls' extension, and then one with the 'samples sheet' empty

√ Torben used a template from the template folder that was outdated (we actually need to update these)

**FIXED: 2022-09-19**

**Bug #4** (Jerome)

I had to make some SeqNDisplay yesterday and I notice a few things that need to be specified in the manuscript:

if you are plotting from an online path, it cannot contain white spaces (maybe it works if it get replaced by these '%20%' symbols you see on website paths but I haven't tried it yet)

only use latin alphabet. No Δ or such, the text will display correctly but the tracks won't be picked (and I think it fucks up the app for future plotting and then requires a full R restart, like there is no error returned but the displays are not good)

using indexes or superscript won't impair plotting but will be ignored

use only one time each name for a specific subset, like you can't have 2 'WT' within the same subset of the same dataset, it will only display one (not sure if the second one gets ignored of if they get pulled)

**REMEMEBER TO ADD TO MANUSCRIPT 2022-09-19**

**Bug #5** (Jerome/others)

Finally, the 'display panel text horizontal' option currently does not work

**FIXED: 2022-09-19 (rather: seems to work ok)**

**Bug #6** (Jerome)

Plotting does not take place (and returns a problem of 'time' argument, but without crashing) when both 'display both strand\* and 'intermingled display' are unticked. Reticking 'intermingled' solves the issue and plots properly since there is only one strand but it would be nice to be able to switch directly from both strand intermingled to single strand by just ticking/unticking 'display both strand' rather than having to play with both buttons – that’s a minor point though

**FIXED: 2022-09-23 (rather: seems to work ok)**

**Bug #7** (Jerome)

I think I discovered a limitation based on the name of the tracks while trying to plot the Iasillo data where files are named like this 'Ars2-tot-3-\_plus\_hg38.bw'. I think R does not like to handle these types of characters '-'. The error took the form of displaying all the plot perfect, excepts there was not a single text. The error persisted when changing excel template to another one that previously worked and when simply restarting the app. A full restart of R solved it though. The same tracks plotting worked perfectly after they were renamed. I guess there is nothing to do here except make a very strict warning that these cannot be in the track names. Unless you want to include a function that checks names for 'annoying characters' but while it would be convenient that might be a bit of work.

Last, seeing Toshi Group meeting today I had the tough if a future version (not for publication) could add a display of genomic sequence upon high zooming (like IGV) or if it would be difficult to implement.

**From workshop:**

* Log2 indication (FIXED 2022-09-23)
* save settings on empty app (?)
* xtension on .xlsx file (? There is now a check for the extension and an error message)
* customizable 'enhance' signals (increased from 2x to 5x, customizable later)

**Future:**

* customizable 'enhance' signals
* include sequence at certain zoom levels