

RFC20: Patient View Clinical Attributes Customization

Central problem(s) this view would like to address:

We show clinical attributes of a patient and the associated samples on the patient view at the top of the page. See for instance:

[P-0001104](#) Female, 75 years old, Colorectal Cancer, Adenocarcinoma with mucinous features, **LIVING**, **Recurred/Progressed** (27 months)
└ **❶ P-0001104-T03-IM3** Primary (Ascending Colon), Driver Mutation: BRAF, **❷ P-0001104-T02-IM3** Metastasis (Liver), **❸ P-0001104-**

Currently all these referred attributes are hardcoded. See also:

https://rawgit.com/inodb/3711693a6210c3d81536/raw/clinical_attributes_in_code.html

It is impossible to change the format for other instances of the portal without changing the code. Furthermore it's not possible at the moment to change what is displayed per cancer type or study.

This RFC proposes to:

- Move current JS formatting to CSS
 - Most of the formatting logic in JS can be styled in CSS instead
- Add a data cleaning step
 - Current clinical attributes at MSKCC are not strict, some data cleaning needs to be done in JS to keep more advanced logic out of CSS

Questions for the Group

- 1) Is CSS styling the proper solution to this problem? Or should we use templating or some other front end framework (ReactJS/Angular) with subclassing?
- 2) What kind of problems could arise from using CSS?
- 3) Are there any other pages in the portal that could follow similar principles for styling per cancer_type/study, is this solution generalizable?

Proposed Solutions

CSS styling

There is a PR open that implements this solution:

<https://github.com/cBioPortal/cbioportal/pull/1015>

Python style templating

For both the patient and the sample we use a template string similar in style to [Python formatting](#). A JavaScript implementation is [available](#).

Patient:

“({OTHER_SAMPLE_ID}) {OS_STATUS} ({AGE})”

Sample:

“({SAMPLE_TYPE}) {DRIVER_MUTATIONS}”

Parentheses without any value in it can be filtered out post replacement of the clinical attributes. Currently we have some logic that if the SAMPLE_TYPE is Primary, we will display PRIMARY_SITE and METASTASIS_SITE if the SAMPLE_TYPE is Metastasis. The Python style templating solution would require one to move this logic to the code i.e. keeping some limited set of hardcoded clinical attributes.

Another idea would be to use a templating language that allows for slightly more logic such as [Mustache](#) (although called logic-less there is some if condition possible) or even [Dust](#). Here is an example of a mustache template for the patient info:

https://gist.github.com/inodb/26014d55599342af06e6b5ace8db8190#file-patient_template-mustache

Key Ideas

- Portal maintainers can change what clinical attributes are shown on the patient view for both the patient and the sample
- The styling can be changed per study or cancer type