Hands-on exercise on integrative analysis using iCoMut on FireBrowse
BTEP Data Integration Workshop
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Prepared by: Parthav Jailwala, CCBR

Comut plot is often seen in cancer research publications as a visual summary of genetic variations/mutations in cancer cohorts. The plot itself is essentially an ensemble of multiple smaller and simpler plots (e.g. heat maps and bar graphs) aligned and interconnected via a common X or Y axis. This form of grid-like graphical summary is particularly suitable for presenting data with an intricate and associative nature. iCoMut aims to further transform the static image into an interactive data exploring experience that is flexible and versatile, and through a web-enabled user interface, provides greater public access.

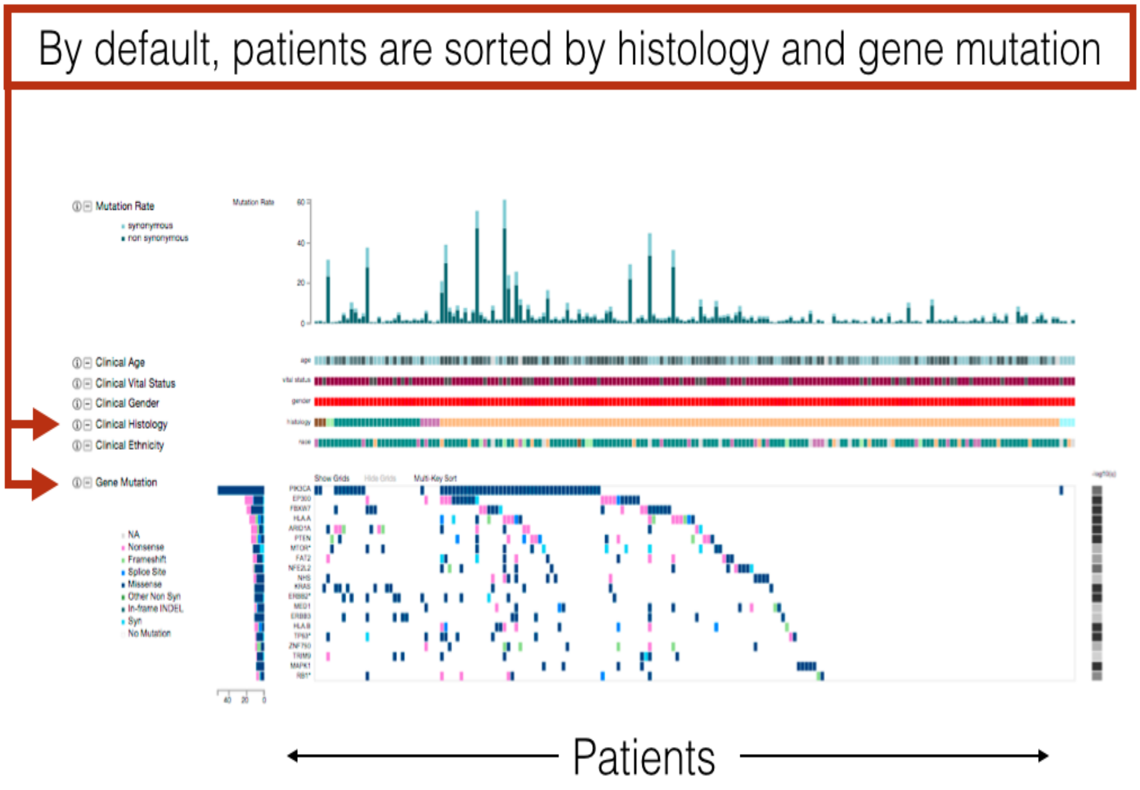
Step 1: Access the iCoMut page on firebrowse.org

http://firebrowse.org/iCoMut/

Step 2: Select 'CESC – Cervical and Endocervical cancers' under 'Select a TCGA cancer cohort'. You will now visualize the iCoMut plot for all GBM samples in TCGA, with various tracks for clinical and genomic data associated with these samples

Step 3: Explore different ways of sorting the tracks

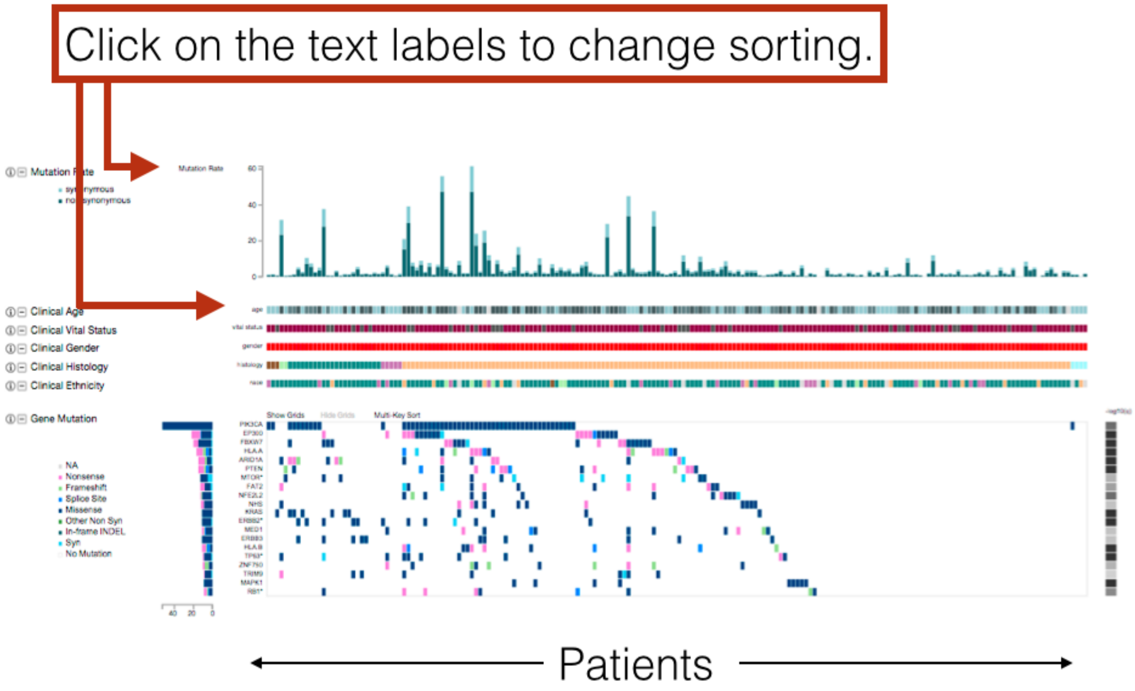
By default, patients in a cancer cohort are sorted first by the histological subtypes (if available), then by the gene mutations.



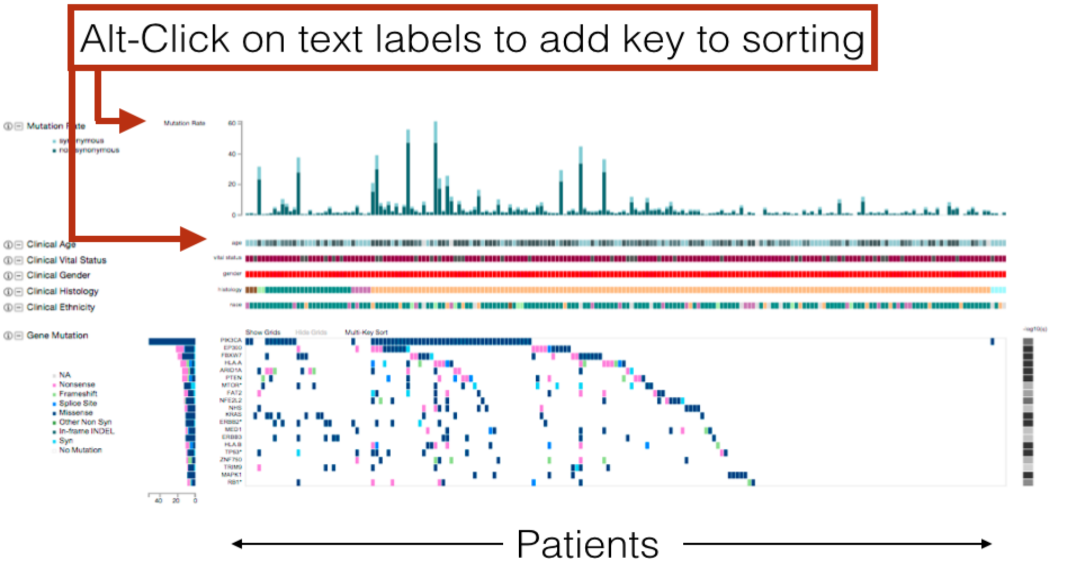
By default, patients are sorted by histology and gene mutation

Patients

Data can be sorted by clicking on the text labels of the axes and the heat maps. To perform a multi-key sorting, **alt-click** on a text label to add a key.

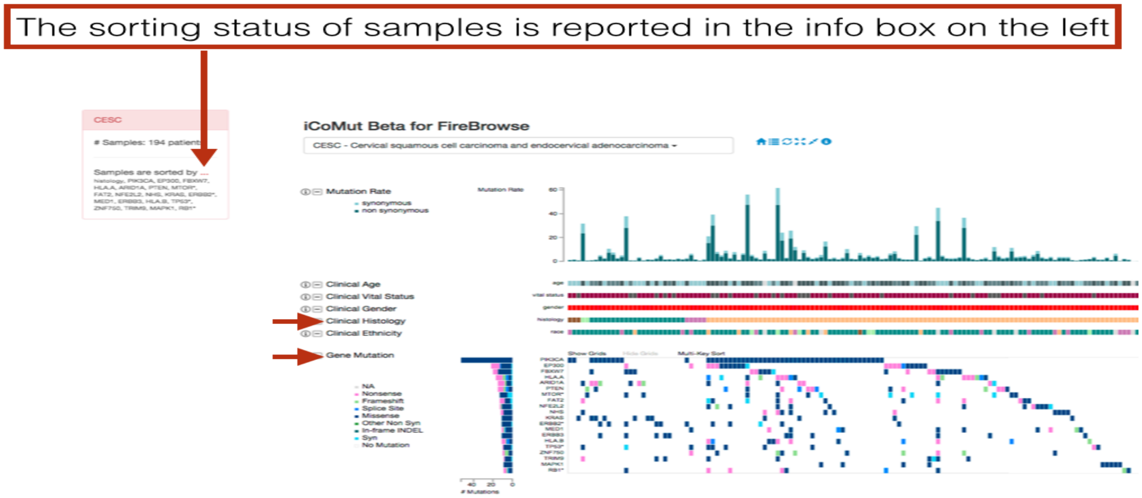


Click on the text labels to change sorting.



Alt-Click on text labels to add key to sorting

The info box located on the left reports the sorting status of the patients.



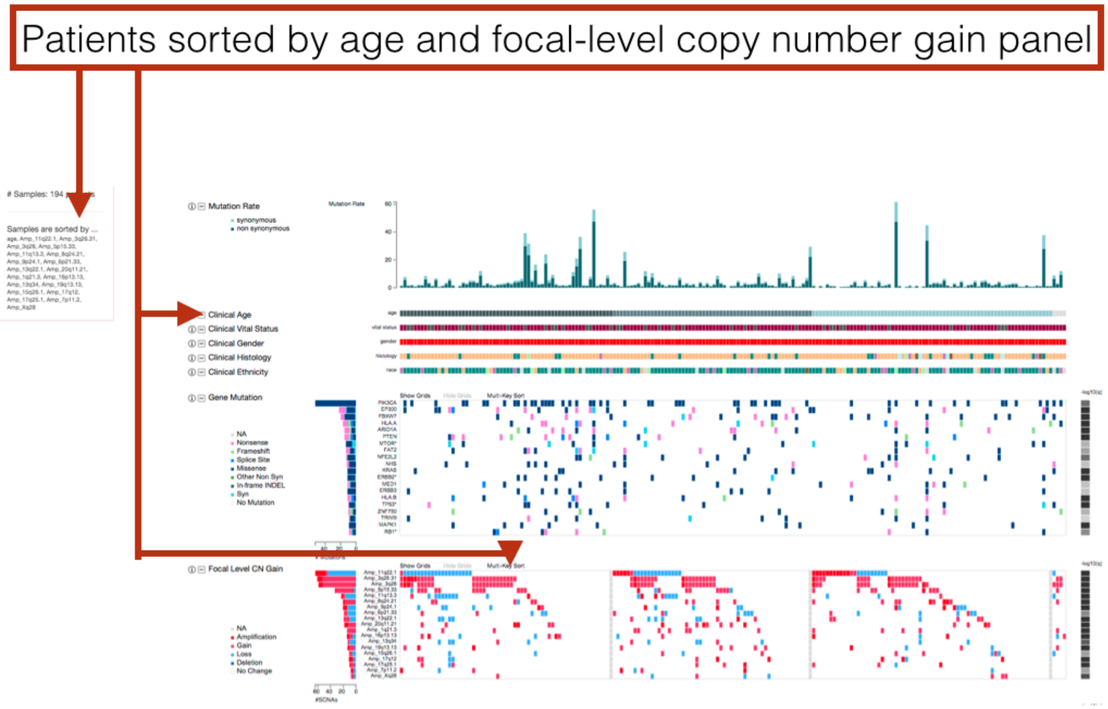
The sorting status of samples is reported in the info box on the left

CESC

Samples: 194 patients

Samples are sorted by ...
histology, PIK3CA, EP300, FBXW7, HLA.A, ARID1A, PTEN, MTOR*, FAT2, NFE2L2, NHS, KRAS, ERBB2*, MED1, ERBB3, HLA.B, TP53*, ZNF750, TRIM9, MAPK1, RB1*

Many options to sort patients can be done by mouse clicking. Here, for example, patients are sorting by age (click) then by focal-level copy number gain (alt-click on "Multi-Key Sort" located above the copy number heat map).



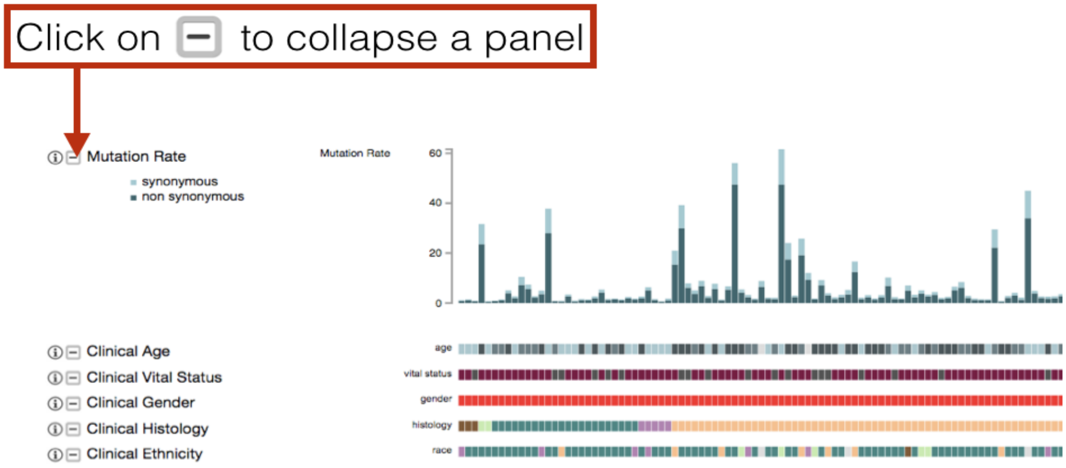
Patients sorted by age and focal-level copy number gain panel

Samples: 194 patients

Samples are sorted by ...
age, Amp_11q22.1, Amp_3q26.31, Amp_3q28, Amp_5p15.33, Amp_11q13.3, Amp_8q24.21, Amp_9p24.1, Amp_6p21.33, Amp_13q22.1, Amp_20q11.21, Amp_1q21.3, Amp_16p13.13, Amp_13q34, Amp_19q13.13, Amp_15q26.1, Amp_17q12, Amp_17q25.1, Amp_7p11.2, Amp_Xq28

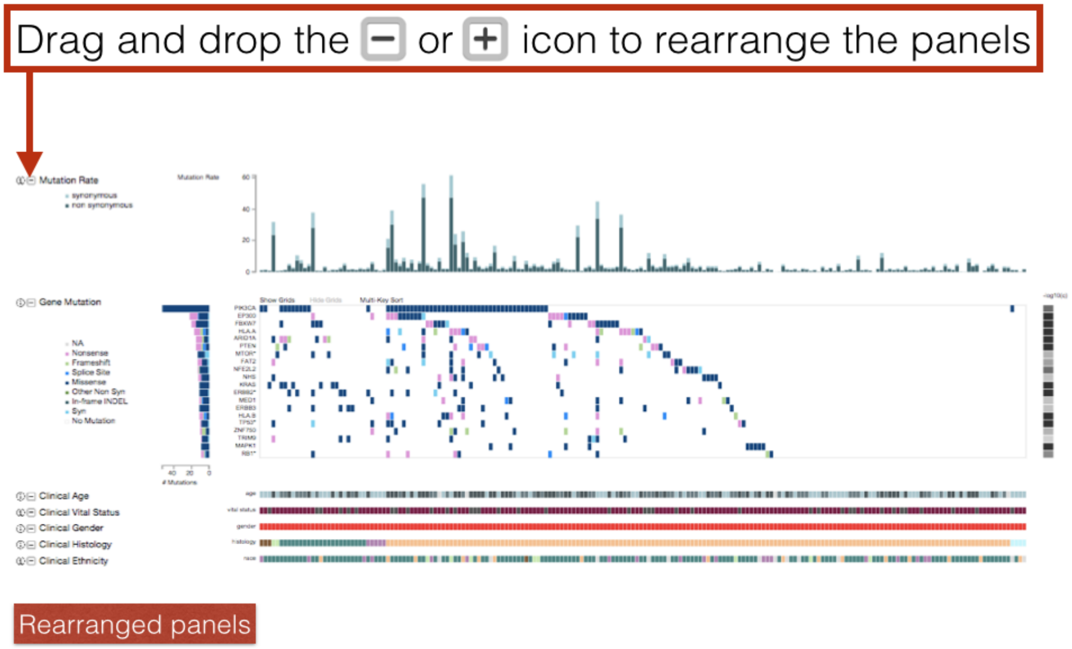
Step 4: Explore rearranging the panel layout

A panel can be collapsed by clicking on the minus icon.



Click on ⊟ to collapse a panel

Horizontal panels can be rearranged by drag and drop using the minus/plus icons located on the left of the panel titles.



Drag and drop the ⊟ or ⊞ icon to rearrange the panels

Rearranged panels

Collapse and Expand All

Control buttons, for collapsing and expanding all panels, are conveniently provided at the top of the comut plot. Additionally, by first collapsing all panels, the rearrangement of the layout order of panels can be done more easily by drag and dropping the plus sign next the panel title.

Click ⤢ to collapse all panels

iCoMut Beta for FireBrowse

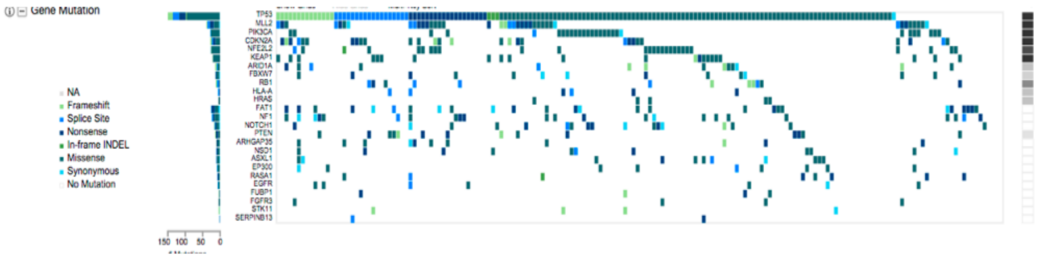
CESC - Cervical squamous cell carcinoma and endocervical adenocarcinoma ▾

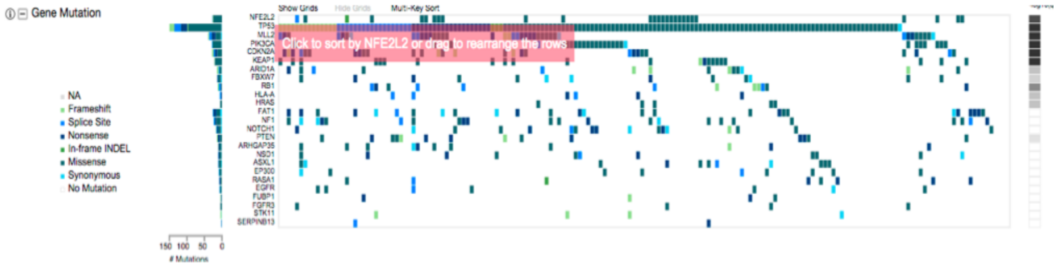
- Mutation Rate
- Clinical Age
- Clinical Vital Status
- Clinical Gender
- Clinical Histology
- Clinical Ethnicity
- Gene Mutation
- Focal Level CN Gain
- Focal Level CN Loss
- CN cNMF
- Methylation cNMF
- RPPA cNMF Clusters
- RPPA cHierarchical
- mRNAseq cNMF
- mRNAseq cHierarchical
- miRseq cNMF
- miRseq cHierarchical
- miRseq Mature cNMF
- miRseq Mature cHierarchical

Step 5: Explore sorting rows within an interactive Heat Map

Clicking (or alt-clicking) a row name will sort the columns (i.e. patients) by the row. The sorting order is toggled by clicking the same row name again.
Additionally, users can easily rearrange the order of rows by dragging and dropping the row names.

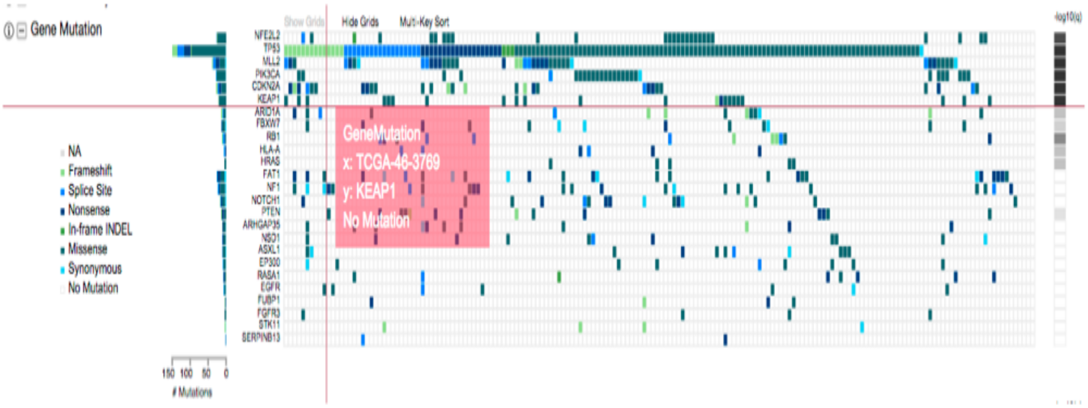
Drag and drop the row names to rearrange the row order





Clicking 'Show Grids' will show all the rectangles in a heat map, including the ones with no data. When in this mode, the cross-hair cursor is also shown. The cursor can be locked in at a rectangle by double-clicking. The locked cross-hair cursor will appear double-lined. To unlock the cursor, click again. Click 'Hide Grids' to hide the grids and cross-hair cursor. By not showing all the graphical elements in a heat map, the visual rendering is faster.

Cross hair mode



GeneMutation
x: TCGA-46-3769
y: KEAP1
No Mutation