Accessing and using underlying cBioPortal data

Introduction to cBioPortal

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4 Recognise the process for accessing and analysing cBioPortal data

Why bother?

"under-the-hood" dataset has more information than displayed publicly

analyse lists of genes quickly

"improve" the plot quality

perform more advanced statistical testing (e.g. DEA, GSEA)

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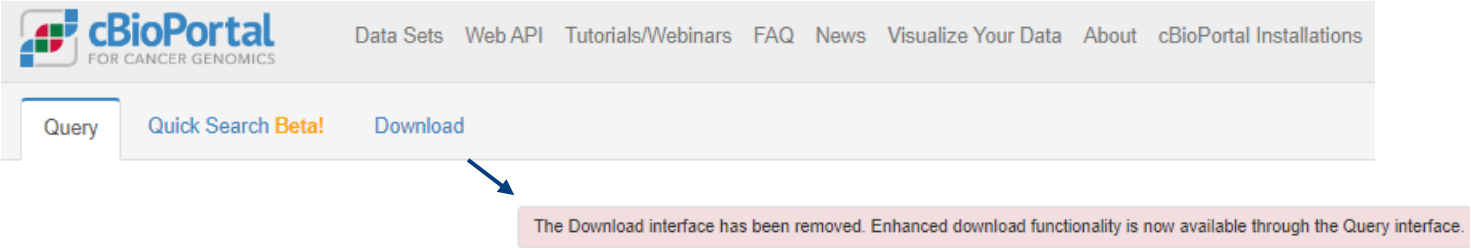
Downloading data



Unhelpful starting point.

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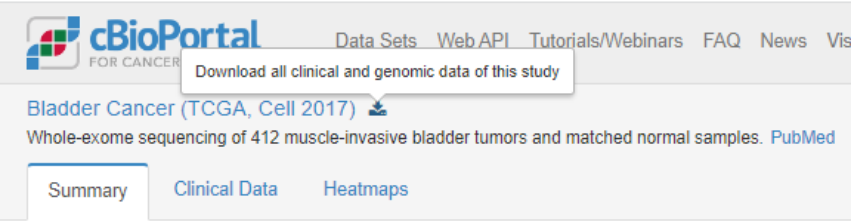
Downloading data

Explore your dataset first, and then download.



Download will start and give a `.tar.gz` file

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Downloading data

blca_tcga_pub_2017 | Search blca_tcga_pub_2017

Name	Date modified	Type	Size
case_lists	25/03/2022 19:07	File folder	
data_clinical_patient.txt	25/03/2022 19:15	TXT File	355 KB
data_clinical_sample.txt	25/03/2022 19:15	TXT File	103 KB
data_cna.txt	25/03/2022 19:15	TXT File	22,499 KB
data_linear_cna.txt	25/03/2022 19:15	TXT File	64,382 KB
data_methylation_hm450.txt	25/03/2022 19:15	TXT File	119,597 KB
data_mrna_seq_v2_rsem.txt	25/03/2022 19:15	TXT File	69,336 KB
data_mrna_seq_v2_rsem_zscores_ref_all_samples.txt	25/03/2022 19:15	TXT File	60,450 KB
data_mrna_seq_v2_rsem_zscores_ref_diploid_samples.txt	25/03/2022 19:15	TXT File	59,941 KB
data_mutations.txt	25/03/2022 19:15	TXT File	264,752 KB
data_mutsig.txt	25/03/2022 19:15	TXT File	2,083 KB
data_rppa.txt	25/03/2022 19:15	TXT File	643 KB
data_rppa_zscores.txt	25/03/2022 19:15	TXT File	569 KB
LICENSE	25/03/2022 19:07	File	1 KB
meta_clinical_patient.txt	25/03/2022 19:07	TXT File	1 KB
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meta_study.txt	25/03/2022 19:07	TXT File	1 KB

For each assay, 1 data file and 1 metadata/information file

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Understanding the data

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TSV – feature x patient ID (many missing values, cancer-specific features)

Patient information

Sex, height, weight, race, ethnicity, diagnosis age, survival status

Occupation history, smoking status, family history

Tumour information

Stage, grade, disease codes, metastasis status

Tumour-specific categories (e.g. for bladder, rate of prostate cancer)

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Understanding the data

data_cna.txt	25/03/2022 19:15	TXT File	22,499 KB

tumour x gene using GISTIC scale (TSV)

- -2 homozygous "deep" deletion
- -1 shallow deletion (anything that isn't total loss)
- 0 diploid
- 1 gain ("a few" extra copies)
- 2 amplification (often in focal sets)

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tumour x gene, normalised gene expression data (TSV)

- Normalised counts
- Can feed into differential expression pipelines (DESeq2 *etc*), if careful!

- Good for comparisons of <u>one</u> gene across samples
- Harder to compare expression between genes of same sample

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Understanding the data

data_mutations.txt	25/03/2022 19:15	TXT File	264,752 KB

TSV – list of all mutations, sorted by tumour ID

- Includes synonymous mutations as well as non-synonymous
- Data structure is rubbish, requires lots of parsing to find hotspots *etc.*

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Working with the data

Existing UG training and extensive core bioinformatic support

Python support available too – pandas package is versatile

Doable…! But. Memory intensive, and watch delimiters when importing.

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Working with the data… final thoughts

The data is not always complete

- Inconsistent column usage between datasets
- Watch 'whitespace' vs 'tab space' vs comma delimiters

Biological vs Statistical significance

Limited by previous bioinformatic analysis pipelines, genome version *etc.*

- More advanced questions can go back to the raw data

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Introduction to cBioPortal

Course complete!

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