File Management

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"Managing your Research Data: Best practices in Research Data Management for Biological Sciences"

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- Data Management Principles
 - Research Data Life-cycle
 - Data Management Checklist
- Techniques to help organize your research data
 - File Organization
 - File Naming
 - Version Control
 - Meta Data (ReadMe)
 - Running Low in Storage Space?

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Research Data Lifecycle



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Data Management Checklist

- What types of data and how long?
- Who will be responsible for which aspect?
 - Roles & Responsibilities.
- How to document/store/back-up/share data?
 - @Study-level @Data-level @File-level
 - Restrictions?
 - Ethical Obligations & Copyright/Intellectual Property.
 - Wet lab: Electronic Lab Notebook (ELN)

Data Types Recommended by UK Data Archive

Type of data	Recommended formats
Tabular data with extensive metadata variable labels, code labels, and defined missing values	SPSS portable format (.por) delimited text and command ('setup') file (SPSS, Stata, SAS, etc.) structured text or mark-up file of metadata information, e.g. DDI XML file
Tabular data with minimal metadata column headings, variable names	comma-separated values (.csv) tab-delimited file (.tab) delimited text with SQL data definition statements
Geospatial data vector and raster data	ESRI Shapefile (.shp, .shx, .dbf, .prj, .sbx, .sbn optional) geo-referenced TIFF (.tif, .tfw) CAD data (.dwg) tabular GIS attribute data Geography Markup Language (.gml)
Textual data	Rich Text Format (.rtf) plain text, ASCII (.txt) eXtensible Mark-up Language (.xml) text according to an appropriate Document Type Definition (DTD) or schema
Image data	TIFF 6.0 uncompressed (.tif)
Audio data	MPEG-4 (.mp4) OGG video (.ogv, .ogg) motion JPEG 2000 (.mj2)
Video data	MPEG-4 (.mp4) OGG video (.ogv, .ogg) motion JPEG 2000 (.mj2)
Documentation and scripts	Rich Text Format (.rtf) PDF/UA, PDF/A or PDF (.pdf) XHTML or HTML (.xhtml, .htm) OpenDocument Text (.odt)

For a full table including Acceptable formats:

https://www.ukdataservice.ac.uk/manage-data/format/recommended-formats.aspx

Data Management Checklist

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- How to document/store/back-up/share data?
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<u>Data Management Checklist – 13 Core Questions to Consider</u>

- What data will you collect or create?
- How will the data be collected or created?
- What documentation and metadata will accompany the data?
- How will you manage any ethical issues?
- How will you manage copyright and Intellectual Property Rights (IPR) issues?
- How will the data be stored and backed up during the research?
- How will you manage access and security?
- What is the long-term preservation plan for the dataset?
- Which data should be retained, shared, and/or preserved?
- How will you share the data?
- Are any restrictions on data sharing required?
- Who will be responsible for data management?
- What resources will you require to deliver your plan? (people, time, hardware)

Full Checklist with Guidance can be downloaded here: https://www.dcc.ac.uk/news/new-checklist-data-management-plan https://www.dcc.ac.uk/sites/default/files/documents/resource/DMP/DMP Checklist 2013.pdf

Your needs to think about when choosing Electronic Note Book

- Cost? One-time or subscription(monthly/yearly)?
- Access control. Other Users? Collaborators?
- Types of information to record and storage space required.
- Any specialized functionality you require?
- Data protection for sensitive data.
- What happens if someone leaves the lab?
- What happens when you stop using this ELN?

Further readings about how to choose an ELN

- Kwok, Roberta. 2018. "How to pick an electronic laboratory notebook."
 Nature 560 (7717): 269-270. https://doi.org/10.1038/d41586-018-05895-3
- The Electronic Lab Notebook in 2020: A comprehensive guide with a short list of 5 ELNs. https://www.labfolder.com/electronic-lab-notebook-eln-research-guide
- A Comprehensive and Up-to-date Comparison Grid from Harvard Data Management including over 30 ELNs comparing over 50 features. https://datamanagement.hms.harvard.edu/analyze/electronic-lab-notebooks

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File Structure

- Ways to organize electronic files

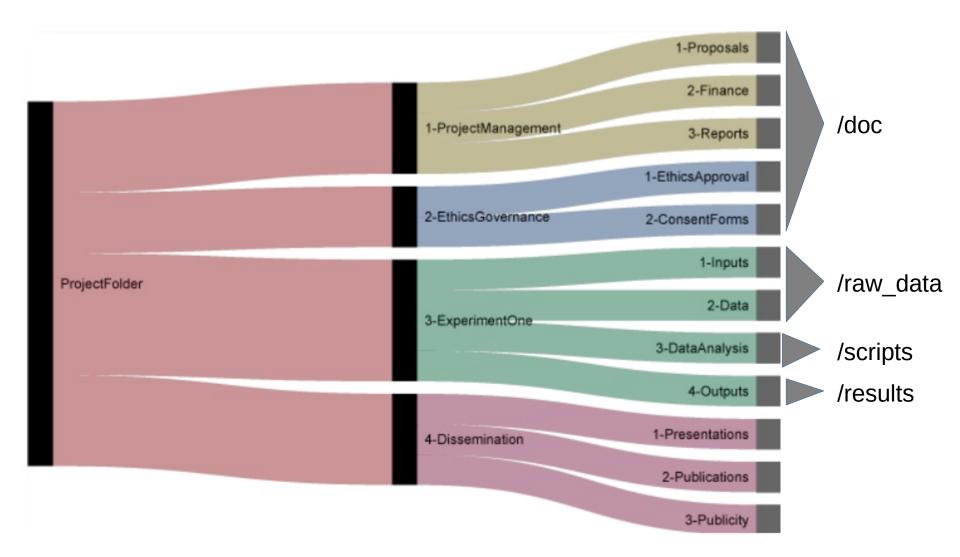
Hierarchical

Files organized in folders and sub-folders

Tag-based

Each file assigned one or more tags

<u>Folder Structure Examples – Hierarchical</u>



Folder Structure Examples – Tag-based

```
TagSpaces Desktop
TagSpaces v3.8.4
TAG LIBRARY
                                              26_R1_001.fastq
> Smart Tags 

                                                               mutation_calling_benchmark integrated_analysis_breast_Cancer

→ Patient ID

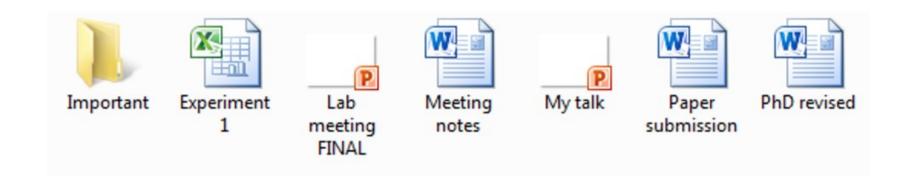
                                              0 B - 2021.03.17
P01 P02 P03
                                              27_R1_001.fastq
Data Type
                                                               integrated_analysis_breast_Cancer
                                              P02 RNA_seq
                                              0 B - 2021.03.17
RNA_seq DNA_genome
                                              28_R1_001.fastq
expression_array ChIP_seq BS_seq
                                              P03 RNA_seq
                                                               integrated_analysis_breast_Cancer
Project
                                              0 B - 2021.03.17
mutation_calling_benchmark
                                              29_R1_001.fastq
integrated_analysis_breast_Cancer
                                               P01 DNA_genome
                                                                   integrated_analysis_breast_Cancer
                                              0 B - 2021.03.17
                                              30_R1_001.fastq
                                               P02 DNA_genome integrated_analysis_breast_Cancer
```

Note: Tags themselves can have hierarchical structure.

More about Tagging: https://libguides.mit.edu/metadataTools/

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File Naming – does it matter?



In 3 years' time would you know what these are?

File Naming – 3C principles

Can your collaborator (or yourself 5 years from now) identify the content without opening the file?

Clear

- Objective: my, current, latest, final
- Meaningful: He?

Concise

• the, and

Consistent

Systematic naming/Standard

File Naming – Other Tips

- Use underscores "_ " to separate elements
 - avoid special characters, e.g., "@" and spaces " "
 - Periods ". " only before the file extension
- Use leading zero for consistent sorting

Without Leading Zero

Name	
datafile_number_1.txt	qw254@qw254-desktop:~/t
datafile_number_2.txt	datafile_number_10.txt
datafile_number_3.txt	datafile_number_11.txt
datafile_number_4.txt	<pre>datafile_number_12.txt datafile_number_13.txt</pre>
datafile_number_5.txt	datafile_number_14.txt
datafile_number_6.txt	datafile number 15.txt
datafile_number_7.txt	datafile_number_16.txt
datafile_number_8.txt	datafile_number_17.txt
datafile_number_9.txt	datafile number 18.txt
datafile_number_10.txt	datafile_number_19.txt
datafile_number_11.txt	datafile_number_1.txt
datafile_number_12.txt	datafile_number_20.txt
datafile_number_13.txt	datafile_number_2.txt
datafile_number_14.txt	datafile_number_3.txt
datafile_number_15.txt	datafile_number_4.txt
datafile_number_16.txt	datafile_number_5.txt
datafile_number_17.txt	datafile_number_6.txt
datafile_number_18.txt	datafile_number_7.txt
datafile_number_19.txt	datafile_number_8.txt
datafile_number_20.txt	datafile_number_9.txt

Not consistent sorting.

With Leading Zero

qw254@qw254-desktop:~/t Name datafile number 01.txt datafile_number_01.txt datafile number 02.txt datafile_number_02.txt datafile number 03.txt datafile number 03.txt datafile number 04.txt datafile number 04.txt datafile number 05.txt datafile number 05.txt datafile number 06.txt datafile number 06.txt datafile number 07.txt datafile_number_07.txt datafile number 08.txt datafile_number_08.txt datafile number 09.txt datafile_number_09.txt datafile_number_10.txt datafile number 10.txt datafile number 11.txt datafile number 11.txt datafile number 12.txt datafile number 12.txt datafile_number_13.txt datafile number 13.txt datafile number 14.txt datafile number 14.txt datafile number_15.txt datafile_number_15.txt datafile_number_16.txt datafile number 16.txt datafile_number_17.txt datafile number 17.txt datafile number 18.txt datafile number 18.txt datafile_number_19.txt datafile_number_19.txt datafile_number_20.txt datafile number 20.txt

Consistent!

File Naming Examples

How about the following file name?

my Data @DryValley November 15 2010.v2.dat

How would you revise it?

(type your proposal in zoom chat window)

Reminder to check:

- Clear
 - Objective
 - Meaningful
- Concise
- Consistent
 - standard

File Naming Examples - revised

Original:

my Data @DryValley November 15 2010.v2.dat

Revised (one of the possibilities):

DV_ICPOES_20101115_JDS_v02.dat

- DV: site code (Dry Valley)
- ICPOES: instrument name
- 20101115: date of data generation
- JDS: initial of the scientist
- V02, second version (leading zero)

Batching Renaming Tools

Windows:

- Ant Renamer: http://www.antp.be/software/renamer
- Bulk Rename Utility: http://www.bulkrenameutility.co.uk/
- PSRenamer: http://www.powersurgepub.com/products/psrenamer.html

Mac:

- PSRenamer: http://www.powersurgepub.com/products/psrenamer.html
- Renamer4Mac : http://renamer4mac.com/
- Name Mangler: http://manytricks.com/namemangler/

Linux/Unix:

- GNOME Commander: http://www.nongnu.org/gcmd/
- PSRenamer: http://www.powersurgepub.com/products/psrenamer.html
- Use *grep*, *sed and awk* to search for and change

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Version Control

Why?

- Track changes
- Enable reversing to earlier version

How?

- File naming (maually)
 - Date

```
Template_soil _testing_20120319.xlsx
```

- Author's name

```
Template_soil _testing_by_AS.xlsx
```

- Version number

```
v01, v02 for major edit; v01_0, v01_1, v01_2 for minor edit
Template_soil _testing_v03_02.xlsx
```

- Version control tools (automatically)
 - Wet lab

Electronic Lab Notebooks(ELN)

Laboratory Information Management System(LIMS)

- Dry labGit (GitHub/GitLab)

Version Control Example

VERSION CONTROL TABLE FOR A DATA FILE	
Title:	Vision screening tests in Essex nurseries
File Name:	VisionScreenResults_00_05
Description:	Results data of 120 Vision Screen Tests carried out in 5 nurseries in Essex during June 2007
Created By:	Chris Wilkinson
Maintained By:	Sally Watsley
Created:	04/07/ 2007
Last Modified:	25/11/ 2007
Based on:	VisionScreenDatabaseDesign_02_00

VERSION	RESPONSIBLE	NOTES	LAST AMENDED
00_05	Sally Watsley	Version 00_03 and 00_04 compared and merged by SW	25/11/2007
00_04	Vani Yussu	Entries checked by VY, independent from SK	17/10/2007
00_03	Steve Knight	Entries checked by SK	29/07/2007
00_02	Karin Mills	Test results 81-120 entered	05/07/2007
00_01	Karin Mills	Test results 1-80 entered	04/07/2007

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Why meta data?

- What is metadata?
 - Description that help someone else understand the contents and organization of your files *in your absence*
 - Usually stored in top-level folders
- What does metadata include?
 - What?
 - Who?
 - How?
 - Where & When?

What are in meta data? (I)

DCC DATA RELEASES

DCC / Filter by file name...

- What?
- Who?
- How?
- Where & When?



README.txt

ICGC - DCC DATA RELEASES

These are the DCC Data Releases of the International Cancer Genome Consortium (ICGC). Release 28 also contains PCAWG mutation data. Please see below for more information on the **PCAWG publication policy and embargo status**.

Current DCC Data Releases

Directory	Contents	Release Date
Release_28	DCC Data Release 28	03/27/2019
Release_27	DCC Data Release 27	04/30/2018
Release_26	DCC Data Release 26	12/08/2017
Release_25	DCC Data Release 25	06/08/2017
Release_24	DCC Data Release 24	05/17/2017

ICGC Publication and Embargo Policy

Contact

What are in meta data? (II)

DCC / release 28 / Filter by file name...

Name	File Size	Date
■ README.txt	3.23 KB	Nov 26, 2019
		Nov 26, 2019
➢ Projects		Nov 26, 2019

README.txt

CORRECTIONS <



LICA-FR sequencing-based expression data

November 26, 2019

The current sequencing expression data (exp_seq.LICA-FR_corrected.tsv.gz) at https://dcc.icgc.org/releases/current/Projects/LICA-FR_corrected.tsv.gz) FR contains incorrect raw read count values. Please download the corrected "exp_seq.LICA-FR.tsv.gz" file at https://dcc.icgc.org /releases/Supplementary/LICA-FR/corrected data.

ICGC DATA PORTAL RELEASE 28

This is the Data Portal data Release 28 of the International Cancer Genome Consortium (ICGC). NOTE: This Release also contains PCAWG mutation data. Please see below for more information on the PCAWG publication policy and embargo status.

March 27, 2019

Summary

This release includes:

86 Cancer Projects

22 Cancer primary sites

22,330 Donors with molecular data in DCC

24,289 Total Donors

81,782,588 Simple Somatic Mutations

57,905 Mutated genes

https://dcc.icgc.org/releases

What are in meta data? (III)

DCC / release_28 / Projects / Filter by file name...

Name

README.txt

[ALL-US] Acute Lymphoblastic Leukemia - TARGET, US

[AML-US] Acute Myeloid Leukemia - TARGET, US

[BLCA-CN] Bladder Cancer - CN

[BLCA-US] Bladder Urothelial Cancer - TCGA, US

[BOCA-FR] Soft Tissue cancer - Ewing sarcoma - FR

□ [BOCA-UK] Bone Cancer - UK

[BPLL-FR] B-Cell Prolymphocytic Leukemia

[BRCA-EU] Breast ER+ and HER2- Cancer - EU/UK

What?

• Who?

How?

• Where & When?

ALL-US Acute Lymphoblastic Leukemia - TARGET, US

AML-US Acute Myeloid Leukemia - TARGET, US

BLCA-CN Bladder Cancer - CN

BLCA-US Bladder Urothelial Cancer - TCGA, US

BOCA-FR Soft Tissue cancer - Ewing sarcoma - FR

BOCA-UK Bone Cancer - UK

BPLL-FR B-Cell Prolymphocytic Leukemia - FR

BRCA-EU Breast ER+ and HER2- Cancer - EU/UK

File Descriptions

Open-access analyzed data:

clinical.[ICGC project code].tsv.gz: contains aggregated clinical donor, specimen and sample information exp_array.[ICGC project code].tsv.gz: gene expression measured at the transcriptional level (mRNA) using array-based platforms exp_seq.[ICGC project code].tsv.gz: gene expression measured at the transcriptional level (mRNA) using sequencing-based platforms

File Formats

Controlled-Access Analyzed Data

Access to Raw Data (ie. BAM, FASTQ files)

What are in meta data? (IV)

Details of the columns in Table S3: 1. sample_id tumor sample id (aliquot id) 2. ttype Tumor type name 3. chr Chromosome number 4. position Chromosome position 5. ref Reference allele 6. alt Alternate allele 7. gene Gene name 8. driver information related to 'mutational' driver type, in particular whether the driver mutation is in [promoters_core, 5utr, 3utr, enhancers, cds, ncRNA, mirna_pre, Incrna_promoters_core, splice_sites] 9. driver statement information related to 'mutational' drivers, whether the driver mutation is known driver, driver by rank, driver by rule or germline pathogenic variant 10. category subclasiffication of driver alteration types: CNA:[coding_amplification, coding_deletion], SV:[cis-activating_SV, coding_tsg_breakpoint, gene_fusion], mutational:['coding', 'noncoding'] 11. top_category driver alteration types: somatic copy number alterations (CNA), somatic structural variant (SV), somaic point mutations, or germline pathogenic variants.

What if your file transfer

got interrupted

without any warning message?

What are in meta data? (V)

- Avoid pitfalls in data transfer using md5sum check

file name	md5sum
PCAWG16.consensus.virus.genus.normal.2out3.v3.icgc.controlled.tsv.gz	854b6a4dce3b46891c8cc4afc65a40d3
PCAWG16.consensus.virus.genus.normal.3out3.v3.icgc.controlled.tsv.gz	82f20aa61129522672fb8e1d7036cdfc
PCAWG16.consensus.virus.genus.tumour.2out3.v3.icgc.controlled.tsv.gz	1787e28e61651b19701cfbb9c108b908
PCAWG16.consensus.virus.genus.tumour.3out3.v3.icgc.controlled.tsv.gz	054200b756d059fc435c6f39ae9646b3
PCAWG16.consensus.virus.genus.normal.2out3.v3.tcga.controlled.tsv.gz	bba31c95dad98dc3b796c6937969a4e7
PCAWG16.consensus.virus.genus.normal.3out3.v3.tcga.controlled.tsv.gz	af0d91d2be2263f68c40e10a7780aced
PCAWG16.consensus.virus.genus.tumour.2out3.v3.tcga.controlled.tsv.gz	f5c5c6b6b09a2f2eb1372cdfd85077b9
PCAWG16.consensus.virus.genus.tumour.3out3.v3.tcga.controlled.tsv.gz	8e1352617fff430d5bedfcaa8fd3362f

- Md5sum output are "fingerprints" to files. They are hash values derived using the whole file as input.
- Changes to a file will cause md5sum output to change. Conversely, if md5sum outputs are the same the files are identical.

Note: If you are worried that the data is maliciously altered instead of accidental corruption, there are more advanced options: SHA-256 (sha256sum), SHA-512 (sha512sum) or BLAKE2(b2sum).

Further reading about meta data:

Cornell University has excellent README file guidelines: https://data.research.cornell.edu/content/readme

Putting It Together

```
Project_20190102_SuJ_BC_RNASeq_5490/
       README
       meta/
              ExperimentalDesign_20190105.doc
              Platelayout.doc
              SampleSheet.csv
              FileList.csv
              MeetingNotes 20190114.doc
       data/
          bam/
             Sample1.aligned.bam

    Sample2.aligned.bam

           fastq/
             - Sample1_R1.fg
             Sample1_R2.fg
             Sample2_R2.fg
             Sample2 R2.fg
        reference/
         - human/
            Grch38_genome.fa
             Gencode26_genes.gtf
       scripts/
           1.subread_align_grch38.sh
           2.featureCounts_mRNA.sh
           - 3.edgeR_DE.R
           4.GSEA_mSigDB13.sh
           5.backup_scratca_to_nas.sh
      - results/
           - counts/
             └─ count_files.txt
           DE_genelists
              — PrimaryTumour_v_normal_DE_genelist.csv
               - Metastatic v Primary DE genelist.csv
```

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- File Naming
- Version Control
- Meta Data

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Running out of Space – Do we need all the files?

Five steps to decide what data to keep:

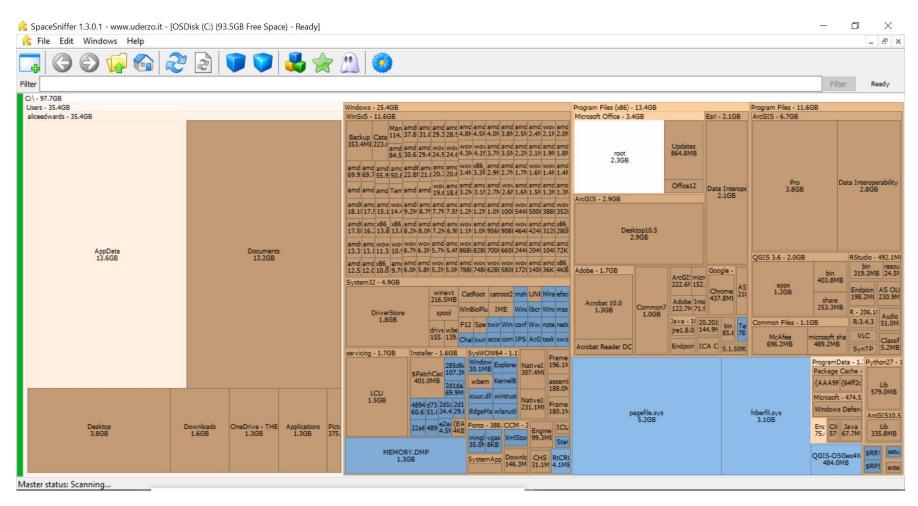
- 1. Identify purposes that the data could fulfill
- 2. Identify data that **must** be kept
- 3. Identify data that **should** be kept
- 4. Weight up the costs
- 5. Complete the data appraisal

For more details:

https://www.dcc.ac.uk/guidance/how-guides/five-steps-decide-what-data-keep

Running out of Space - for Windows

SpaceSniffer (http://www.uderzo.it)



Running out of Space – for Mac & other Linux?

For Mac:

Disk Inventory X (http://www.derlien.com/)

Linux command line (bash):

du -sh # shows you how much disk space the current folder takes

du -h -d 1 | sort -h # sort all folders in the current directory by size

Summary

The Complete Research Data Life-cycle

Can someone else (as well as yourself years from now) understand the contents and organization of your files *in your absence*.

- Data Management Checklist
 - What?
 - Who?
 - **How?**
- Data Management Techniques
 - File Structure & ReadMe & File Name (3C)
 - add Where and When
 - Keep track of changes with Version Control
 - Avoid pitfalls in data transfer using md5sum check

Further readings:

Good Practice in Bioinformatics Analysis

Wilson, G. (2017). Good enough practices in scientific computing. PLoS Computational BiologyS Computational Biology. (https://doi.org/10.1007/BF02378113)