

FAANG metadata - analysis specification

This document describes the specification for all analysis metadata. You can find an overview of our metadata and archival plans in the overview document ([faang_metadata_overview.md](#)) . The experiment ([faang_experiment_metadata.md](#)) and sample ([faang_sample_metadata.md](#)) documents are also in this git repo (<https://github.com/FAANG/faang-metadata>) .

Raw data produced by each experiment will be analysed, producing *analysis results*. For example :

1. ChIP-seq experiment will generate reads.
2. Reads are aligned to the genome.
3. Normalized signal plots and QC metrics will be produced from the alignments.
4. ChIP-seq & ChIP input alignments are used for peak calling.

Steps 2-4 produce analysis results. For each of these analysis results we should record which data, reference data and protocol were used to produce them.

Metadata requirements

Process attributes

Analysis metadata needs to contain the following process attributes

1. Input data – a list of files used as input and references to the experiment records in a data archive
2. Reference data – genome assembly, gene set, etc
3. Analysis protocol – a precise description of the analysis protocol, including the following information:
 - URLs and version numbers for all software used (including in-house scripts)
 - Full command line used to run the analysis
 - Link to any VM or containers used, if applicable

The analysis must be reproducible based on the protocol document.

QC attributes

The analysis metadata will also contain QC attributes. These will vary based on the experiment type, but for sequencing work should always include mapping statistics as a bare minimum.

Required:

- `total_reads` (*number*) the number of reads used in mapping

- mapped reads (*number*) the number of reads that can be mapped. Care should be taken that reads with multiple mappings are only counted once
- percentage reads mapped (*number*) the percentage of reads that can be mapped. As with mapped reads, care should be taken that reads with multiple mappings are only counted once.

File naming

Each file should be uniquely identifiable with a human readable name, giving sufficient information to understand what it contains. We expect analysis to be repeated at intervals, as reference data and protocols are updated, so a data freeze date is included.

Short names based on the following, separated with a dot ('.'):

- species / assembly version
- sample name
- sample description (tissue or cell type)
- assay type
- experiment target
- experiment ID
- analysis protocol name
- results type (e.g. genotypes vs. sites for 1000genomes vcf files)
- data freeze date
- file format

e.g

OAR3_1.OA_Roslin001.liver.H3K27ac.ERX053278.FAANGUK_chipv3.peaks.20150617.bb

So this hypothetical example represents a liver H3K27ac ChIP-Seq experiment for the Roslin's first Sheep sample using the FAANG v3 peak calling pipeline on the Sheep Assembly OAR_v3.1