

note:

timestamp: 2012-10-03 11:13:12.10 -7

intent: "test epibio quickextract kit with fish tissue"

project: "genelaser_test1"

Testing out genomic purification using EpiBio QuickExtract kit. Trying 6 samples to start:

samples[epibiotest1]:

lc: "left cheek, rubbed 10 sec"

ham: "hamachi sample from Moshi Moshi takeout order"

mak: "maki sample from Moshi Moshi takeout order"

neg: "negative control, nothing swabbing"

col: "positive control, 100 mg of frozen tuna tissue from sample:2122"

tab: "table top, 5cm streak rubbed 30 sec"

_file: "samples/2012-10-03_epibiotest1.csv"

First protocol! woot. This content is still part of the first block.

Above see sample data stored inline. Should this be the canonical place for it? Or should it reside in a more central json file and be included by reference? Which is less likely for users to screw up...?

[img:"data/2012-10-03_epibiotest1_sushi_samples.jpg"]

```
op[1]:
  timestamp: 2012-10-03 11:22:01.33 -7
  protocol: Epibio-quickextract-1@ceba48e
  samples: epibiotest1
  qc: op[2]
```

A new note block! This one is associated with the `Epibio-quickextract-1` operation block above. This is where we would write any notes about how the protocol went.

```
op[2]:
  timestamp: 2012-10-03 11:40:12.53 -7
  protocol: nanodrop_0D-260-280
  in: op[1]
  out: "data/qc/2012-10-03.csv"
```

Another Note (or is it operation?).

`[table:"data/qc/2012-10-03.csv"]` ← viewer renders inline

Quickextract seems to work; deviation in gDNA concentration might be a problem. Their whitepaper suggests a range of 7 - 25 ng / uL when it's working properly. `[ref:2012Weight]` .

Also see `[doi:10.1007/978-1-61779-591-6_6]` .

Notebook files have two kinds of top-level metadata blocks: <operation> and <note>. <note>s are associated with the closest preceding <operation>. <note>s can contain data tables, sample tables, protocol definitions, etc., represented inline or by reference via json or yaml blocks.

<note>s begin with `timestamp: <isodate>` metadata block. Additional metadata is inherited from the project.json file

render samples as table view;

TODO how is it automatically stored in samples/2012-10-03_genelaser-test1.csv?
organize content by experiment? i.e.

```
experiments/
├── 2012-10-03_genelaser-test1/
│   ├── index.md
│   ├── samples.csv
│   ├── images/
│   ├── data/
│   ├── notes/
│   ├── 2012-10-06_another-test1/
│   │   ├── index.md
│   │   ├── data/
│   │   └── notes/
│   └── index.md
├── private/
├── project.json
├── protocols/
├── plugins/
├── references/
│   ├── references.bib
│   └── 2010 weight DNA Barcoding Fishes.pdf
```

explicit in/out tags (no typerange tho) in <op> definition

op:

```
_id: 1
timestamp: 2012-10-03 11:22:01.33 -7
protocol: Epibio-quickextract-1@ceba48e
in: cells.tissue # <-- implicit
out: DNA.genomic # <-- implicit
samples: [epibiotest1, epibiotest1_rep2]
qc: op[2]
```