



OICR MISO Tutorial

Samples



miso[™]
managing information
for sequencing operations



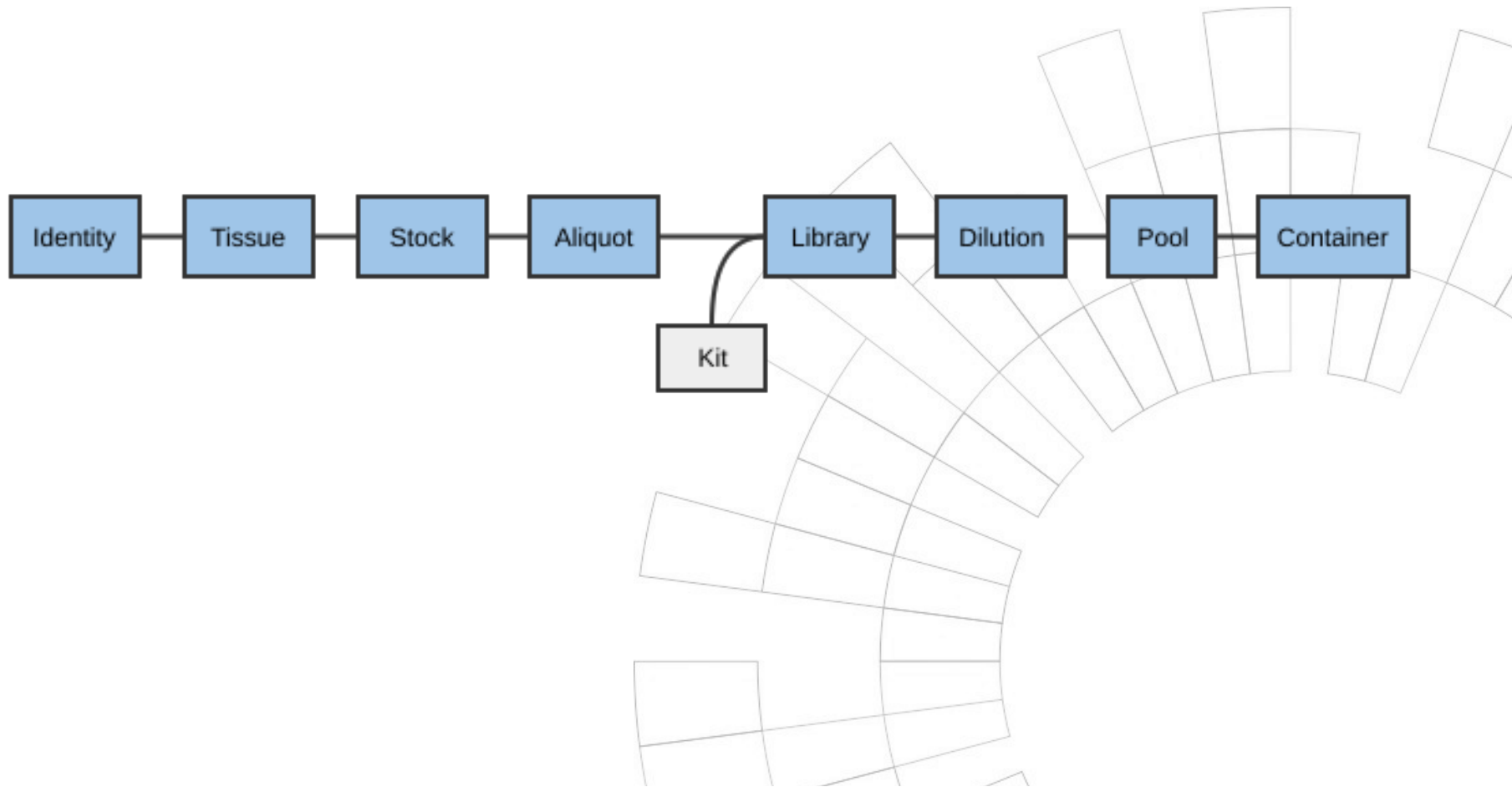
Genome
Sequencing
Informatics

Outline

- ▶ Logging in
- ▶ Receiving samples
 - ▶ Tissues
 - ▶ Tissue Processing
 - ▶ Stocks
 - ▶ Aliquots
- ▶ Propagating samples
- ▶ Adding Sample Qcs

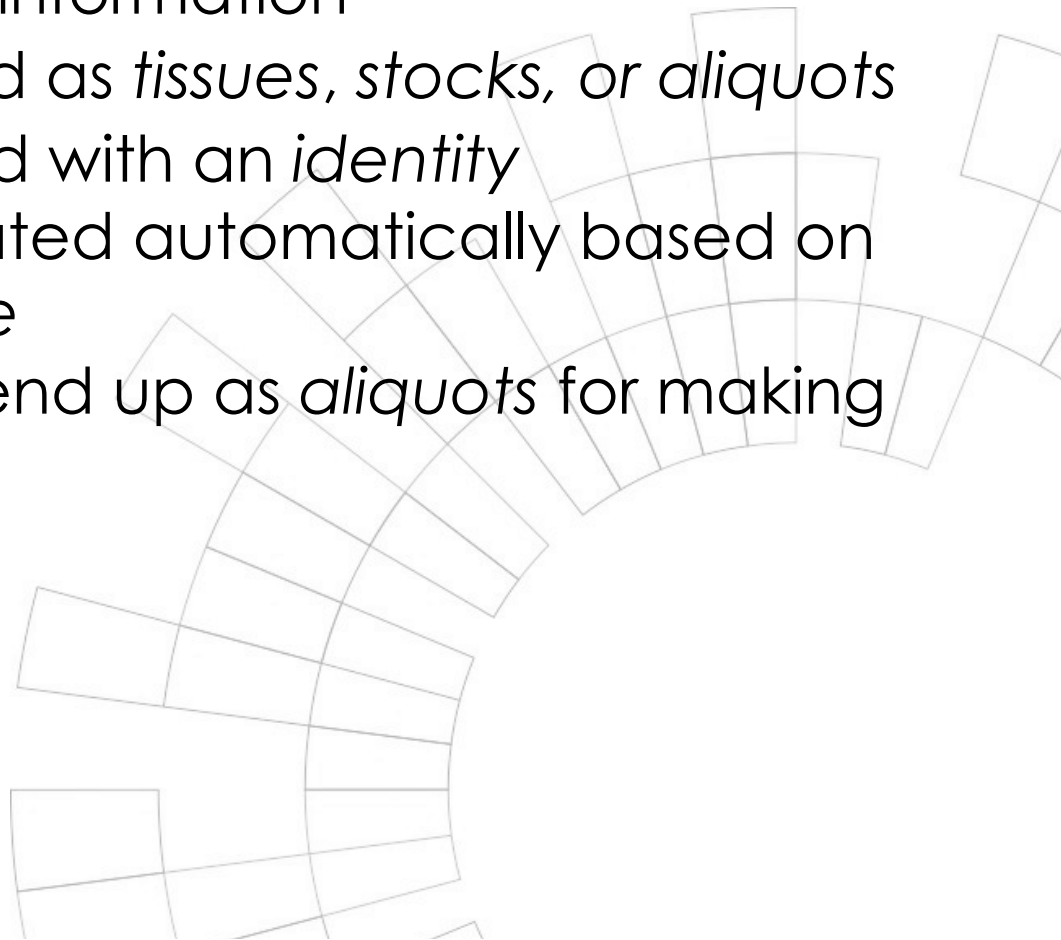


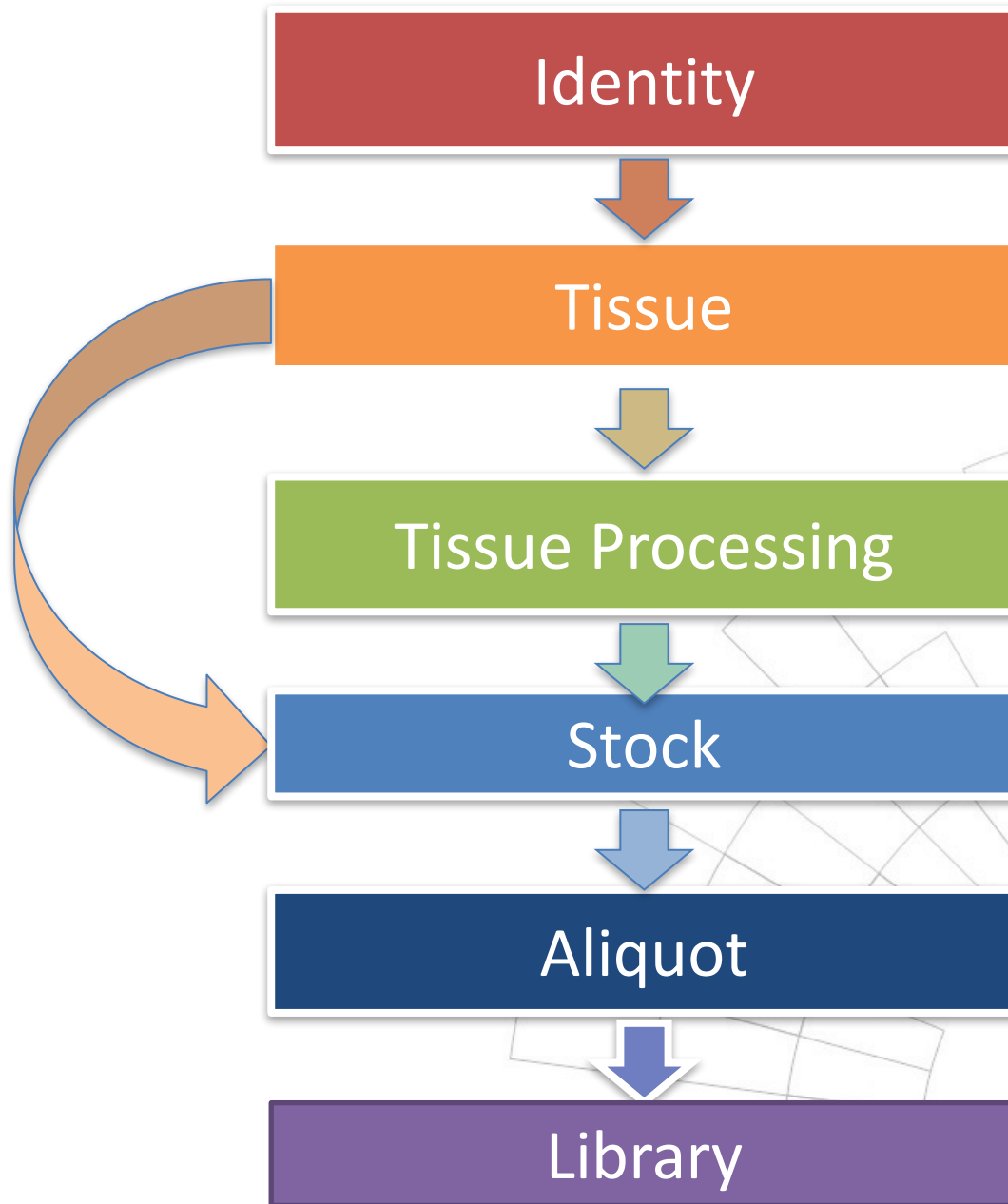
General MISO Flow



Samples

- ▶ Most collaborator-provided and tissue information is part of the *sample* information
- ▶ *Samples* are received as *tissues*, *stocks*, or *aliquots*
 - ▶ Each is connected with an *identity*
 - ▶ *Identities* are created automatically based on the *external name*
- ▶ Eventually, *samples* end up as *aliquots* for making *libraries*





Identity



- ▶ Represents a donor (person)
- ▶ The **external name** is the name used by the external institute to keep track of which donor gave that particular sample.
- ▶ The **alias** is the name OICR uses to keep track of which samples come from that donor.
- ▶ e.g. external name = Morgan; alias = MORG_0001.
- ▶ MISO has an Identity Search tool
 - ▶ Find existing Identities and list samples related to them

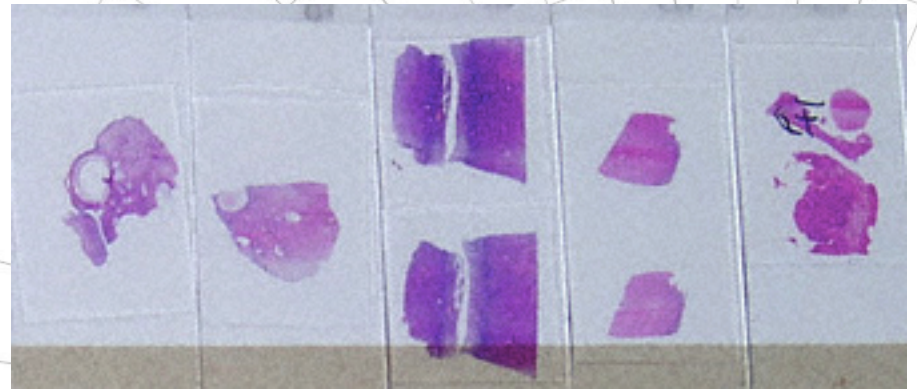
Tissue

- ▶ A piece of tissue direct from the donor
- ▶ Tissue Types:
 - ▶ Reference Tissue
 - ▶ Primary Tumor Tissue
 - ▶ Metastatic Tumor Tissue
 - ▶ Xenograft Tissue
 - ▶ Cell Line



Tissue Processing

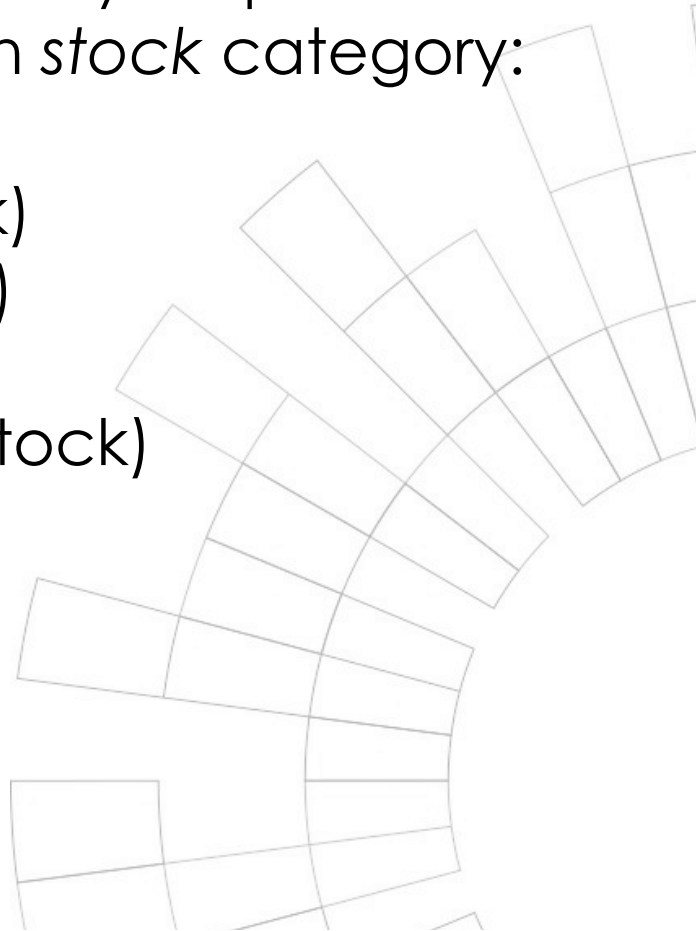
- ▶ Workflow steps as tissue samples get processed
- ▶ *Sample Classes* within Tissue Processing category:
 - ▶ Slides
 - ▶ Curls
 - ▶ LCM Tube
 - ▶ Single Cell



Stock

Extracted material that is ready to be separated into one or many aliquots

- ▶ *Sample Classes within stock category:*
 - ▶ gDNA (stock)
 - ▶ gDNA_wga (stock)
 - ▶ whole RNA (stock)
 - ▶ cDNA (stock)
 - ▶ Single Cell DNA (stock)

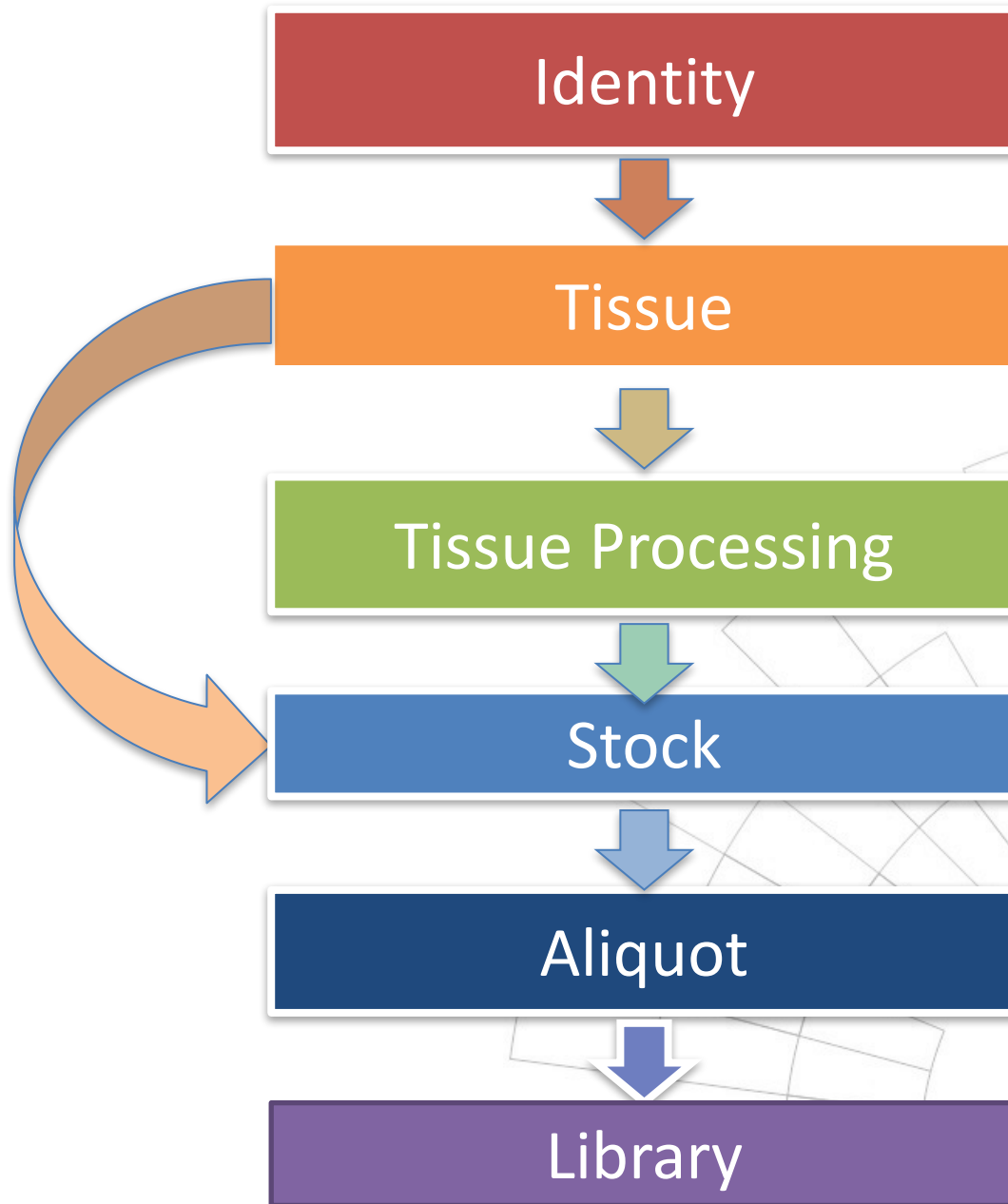


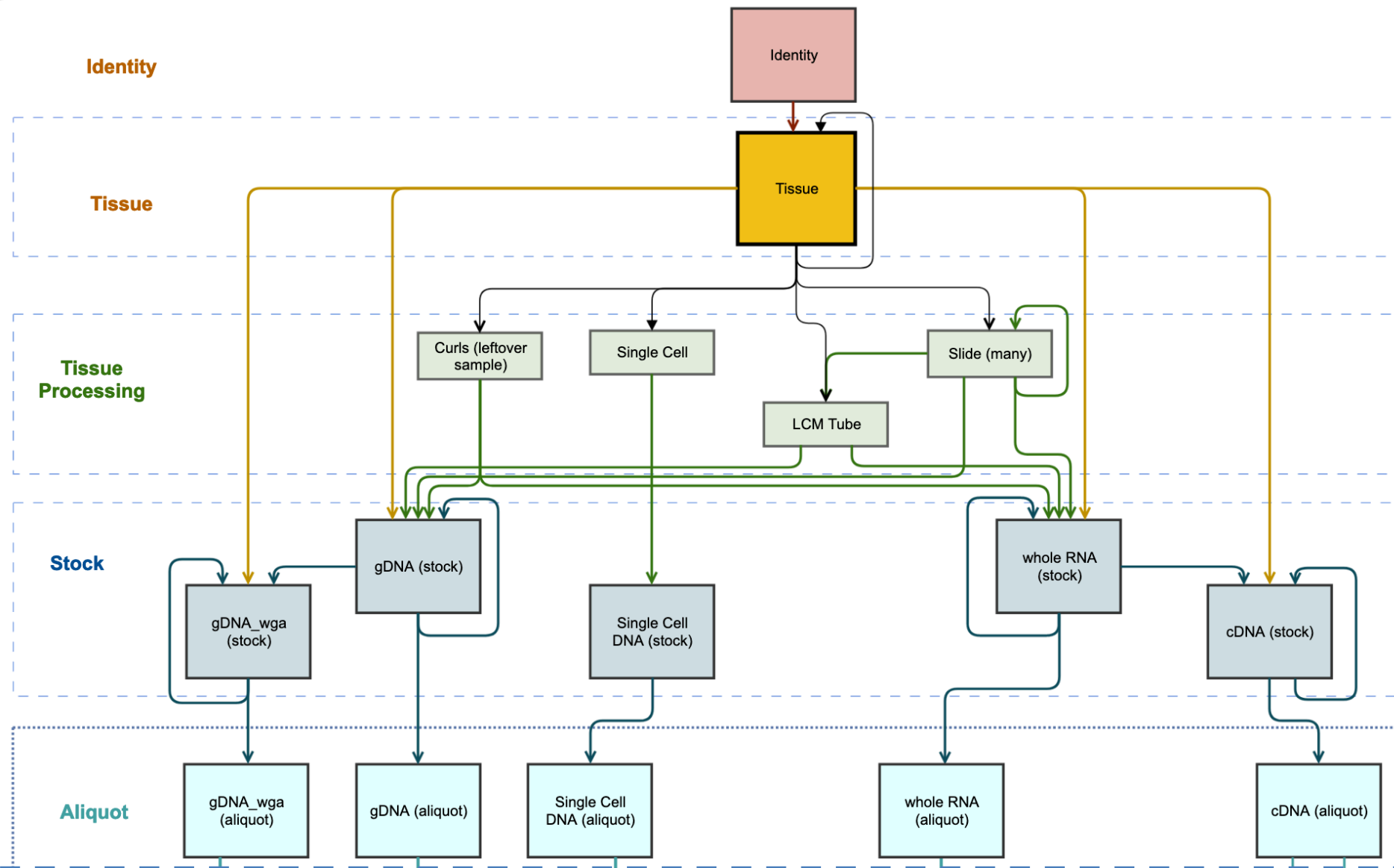
Aliquot

A portion of the extracted material to be made into a library or used for QC or other purposes

- ▶ *Sample Classes within aliquot category:*
 - ▶ gDNA (aliquot)
 - ▶ gDNA_wga (aliquot)
 - ▶ whole RNA (aliquot)
 - ▶ cDNA (aliquot)
 - ▶ Single Cell DNA (aliquot)







Troubleshooting

- ▶ How do you work with multiple samples derived from the same identity (i.e. DNA and RNA from one tissue slide, DNA from metastasis and control)
- ▶ How do I correct a sample that has the wrong information, e.g. wrong tissue type?
- ▶ What if I need to change the parent of a sample? (e.g. for swaps)
- ▶ What do I have to enter if receiving a pre-made library?
- ▶ How can I add a new tissue type, tissue origin, or add anything else in drop-down menus?
- ▶ How can I delete samples?



Done! Any further questions?

Exercise

Complete Tutorial 3: Samples

<https://oicr-gsi.github.io/miso-docs-oicr/>

