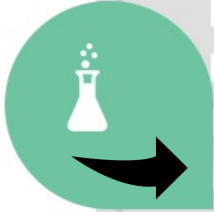
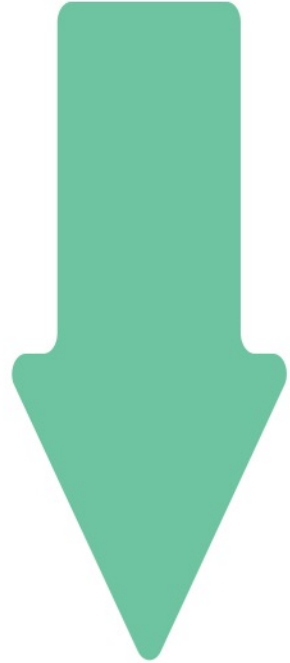
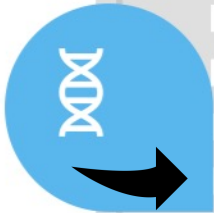


# Building monocyte derived macrophage behavior



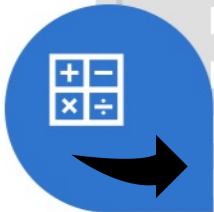
## Experimental steps

This tab includes data related to wet-lab experiments, such as laboratory protocols and FASTQ files, done on monocyte derived macrophages to calibrate and validate intracellular models of monocyte derived macrophages.



## Bioinformatics steps

This tab includes data related to bioinformatics analysis, such as scripts and pipelines, used to analyze data gathered in the wet-lab part.



## Modeling steps

This tab includes data related to the intracellular mathematical model of macrophages, including literature used to build the models, links to scripts, results, etc.

# Experimental flow for coculture experiment

Monocyte derived macrophage

Sample metadata

Get Nextflow pipeline

PBMC Isolation Protocol

Differentiation and Protocol

M-CSF

A. fumigatus

Transcriptome

Proteome

Collect at 0, 2,4,6,8 hours

Blot assays

ELISA

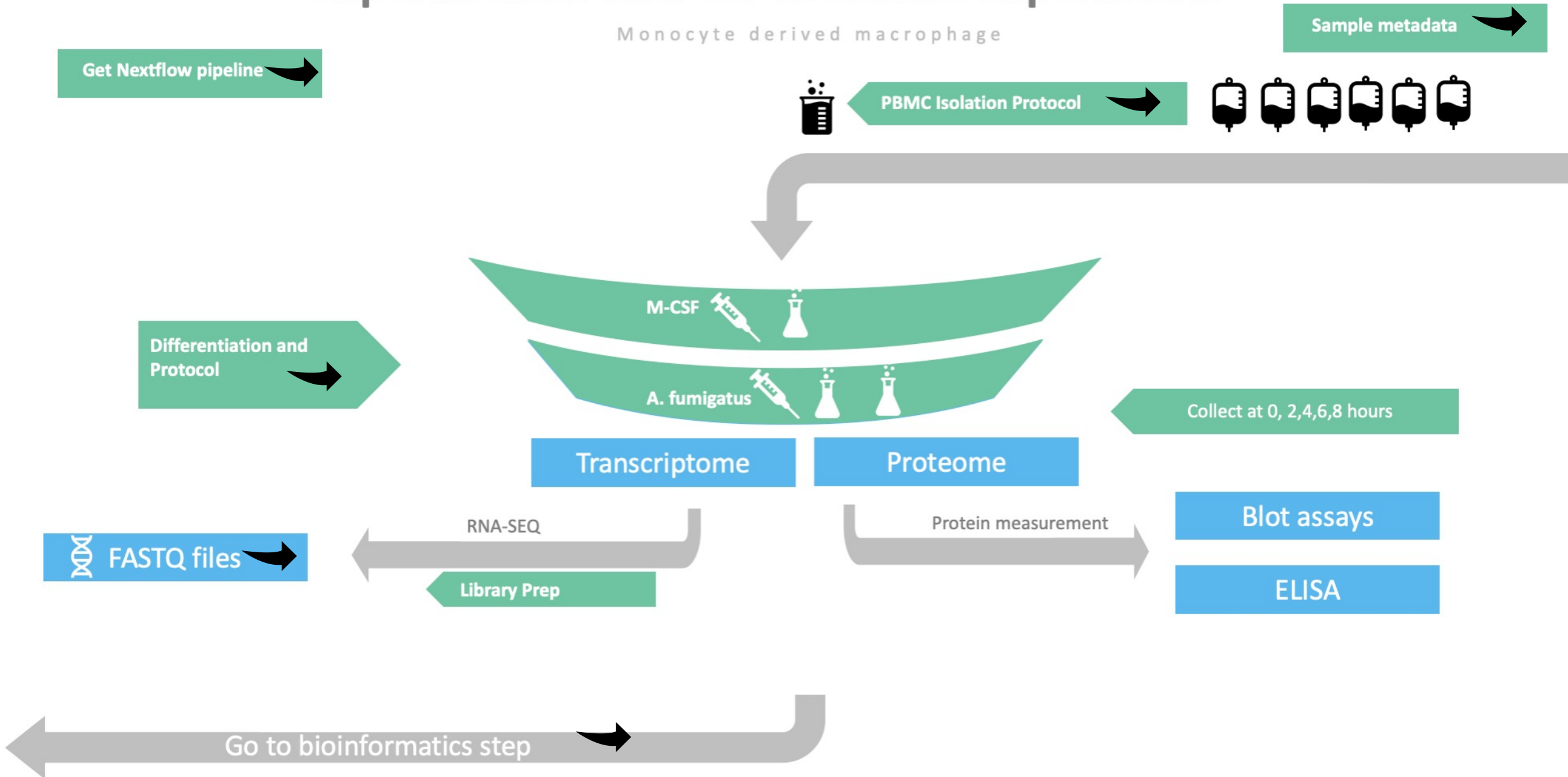
FASTQ files

RNA-SEQ

Library Prep

Protein measurement

Go to bioinformatics step



# Bioinformatics pipeline

Monocyte derived macrophage

FASTQ files for monocyte derived macrophage

MultiQC pretrim

Adapters FASTA file

Get reference genome

Analysis scripts

Pool samples from different runs

Cut adapters (Trimmomatic)

STAR aligner (index and align)

Qualimap, SAM tools  
MultiQC

DESEQ2, CHEA3,  
enrichment

Aligned reads

Results

Go to modeling step

# Mathematical modeling pipeline

Monocyte derived macrophage