**Legend:**

**Planned**

**Drafted**

**Recorded**

**Posted**

**Number Lesson**

**Introductory and overview materials**

1. **Welcome to the PhysiCell training materials**

<https://github.com/physicell-training/00-Welcome-to-training>

* 1. Include an overview, possible “paths”
  2. Getting help

1. **What you need to code in PhysiCell**

<https://github.com/physicell-training/01-What-you-need>

* 1. Working with the PhysiCell chuse environment in nanoHUB workspace

1. How to run a PhysiCell model on nanoHUB [in progress]

<https://github.com/physicell-training/02-How-to-nanoHUB>

1. What is an agent-based model?

<https://github.com/physicell-training/03-What-is-ABM>

1. Introduction to PhysiCell

<https://github.com/physicell-training/04-PhysiCell-intro>

1. PhysiCell codebase structure

<https://github.com/physicell-training/05-PhysiCell-codebase>

1. Microenvironment

<https://github.com/physicell-training/06-Microenvironment>

1. Cells

<https://github.com/physicell-training/07-Cells-intro>

* 1. Type, ID, …
  2. State
  3. Functions (more later)
  4. Custom data (more later)
  5. Phenotype (more later)

**Greater depth**

1. Phenotype

<https://github.com/physicell-training/08-Phenotype-intro>

08x: Phenotype subtopics

1. Custom Data
2. Cell Functions
3. Parameters
4. Globals
5. Cell Definition
6. General project structure (revisited)
7. SVG plotting (and custom color functions)

**Advanced topics**

1. Accessing all cells in a simulation
2. Metadata structures
3. PhysiCell time steps
4. Reading cell positions from a file

**Entering the PhysiCell Community**

1. PhysiCell-Tools
2. PhysiCell tutorials
3. Contributing to PhysiCell

0

1. What you need to run these
2. How to run

0 What you need to run these tutorials

opt1 What is an agent-based model

1. PhysiCell Overview

chemical processes, mechanical processes, phenotype / cell process

3 time scales

should have some cool motivating examples

2 How to use a PhysiCell-based nanoHUB app (integrate with 1?)

3 PhysiCell codebase / project structure

how to populate / depopulate / compile / run / find output

4 PhysiCell code structure

* Aneequa's domain map
* Overall strategy
  + set up environment (now in XML)
  + define cell types
    - including custom codes / variables/ models
  + adding cells to the environment
  + optional: custom coloring

5 Micronenvironment

6 Cell

7 Basic functionality (inherited from basic agents)

position, type, ….

7 Phenotype

7.n sub-phenotype training (e.g., motility)

8 Custom Data

9 State

10 Functions in PhysiCell (general form)

10 Cell.Functions

11 Parameters

11 Globals (for fine tuning)

15 Cell Definitions (templating the cells)

cell\_defaults

16 Initializing a simulation

12 Accessing all cells in a simulation, advanced topics

13 SVG plotting and coloring functions

14 metadata structures

optional / advanced

PhysiCell-Tools

examining data in Python

examining data in matlab

povray

…

Extra tricks for visualization

ImageMagick

mencoder

Creating a nanoHUB app with xml2jupyter

1. environment

go to chuse (right click)

* what needs to be in a new "PhysiCell" preset in chuse?
  + gcc , ImageMagick, meconder, text editor …
  + python 3.x, scikit-learn, keras

gedit, anaconda-7, image-magick-7.0.4, matlab-2018a, paraview-5.2.0, povray-3.6.1,

request:

nautilus, mplayer (with mencoder), an image viewer (e.g., eog)

* write a script that:
  + fetches most recent PhysiCell from github
  + unzips it in a directory called "PhysiCell" in users' root

<https://nanohub.org/tools/workspace>