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Session 5: Custom variables, parameters, microenvironment, and cell def searches, dictionaries

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Agenda

- Working with C++ code
  - Defining Custom variables
  - Querying cell definitions
  - Querying for microenvironment
  - Boundary conditions
  - Dictionaries for signals and behaviors

Need and Files to edit

- Always add something later
- Custom Functions
- File to edit
  - custom.cpp
  - custom.h
  - PhysiCell_settings.xml

Custom Variables

- Two ways to add custom variables to Model
  - Quick builder
  - Add in C++ file

Defining and Initializing Custom Variables

- Where?

custom_modules/custom.cpp

- How?

- cell_defaults.custom_data.add_variable("energy", "dimensionless" , 0.5);

- cell_defaults.custom_data.add_variable("energy", "dimensionless" , parameters.doubles("cell_default_inital_energy"));

- cell_defaults.custom_data.add_variable("alpha", "none" , parameters.doubles("cell_default_aplha"));

Accessing custom Vriables

- Where ?
  - custom.cpp
- How?
  - static int nE = pCell->custom_data.find_variable_index("energy");
  - pCell->custom_data[nE]

Cell definition search

- By index
- Cell_Definition* pCD = cell_definitions_by_index[n];

- By Human readable name
- pCD = find_cell_definition("blood vessel");

Boundary conditions microenvironment

Sampling the microenvironment (1)

- There is a global microenvironment called **microenvironment.** You can access it anywhere from inside a PhysiCell model.

- Each cell is in some computational voxel in the microenvironment.
  - pCell->get_current_voxel_index(void);
    - Get the index of the voxel

- You can query the microenvironment to determine which index corresponds to a variable.
  - microenvironment.find_density_index("resource"); // Find the index of "resource".
    - This function returns -1 if it can't find your substrate.

- Each cell can access the vector of chemical substrates in its voxel
  - pCell->nearest_density_vector();
    - Vector of all the substrates
  - pCell->nearest_density_vector()[2]
    - substrate with index 2 in the cell's voxel
    - often, you'll want to use the search above to figure out which index

Sampling the microenvironment (2)

- Each cell can access the gradients of the substrates in its voxel
  - `pCell->nearest_gradient(2);`
    - ♦ gradient of substrate #2

- We can access the mesh
  - `microenvironment.mesh`
  - `microenvironment.mesh.voxels`

- We can iterate through all voxels

```
for( int i=0; i < microenvironment.mesh.voxels.size() ; i++ )
{ std::cout << microenvironment.mesh.voxels[i].center << std::endl; }
```

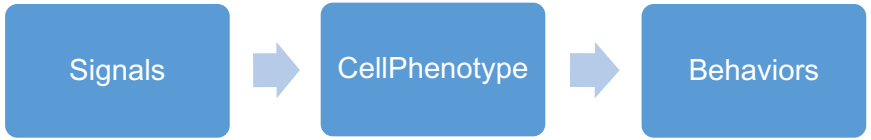
Dirichlet's nodes

- void Microenvironment::add_Dirichlet_node(int voxel index, std::vector<double>& value)
- `microenvironment.add_dirichlet_node( n,bc_vector);`

- Where n is the voxel number and bc_vector is double vector of size n where n is number of substrates in the environment.

Signal and Behavior Dictionaries

- a "dictionary" of standard signals
  - inputs to intracellular and rule-based models.



- A "dictionary" of standard behaviors that can be used as outputs to intracellular and rule-based models.
- This dictionaries are automatically constructed at the start of each simulation based upon the combinations of signaling substrates and cell types.

Common Signals

- extracellular and intracellular substrate concentrations
- substrate gradients
- contact with dead cells
- contact with cells (of type X)
- damage
- Pressure
- Use `display_signal_dictionary()` to quickly display a list of available signals.

Functions to access signals

- int find_signal_index(std::string signal_name) : get the index of the named signal
- std::vector<int> find_signal_indices(std::vector<std::string> signal_names); get a vector of indices for a vector of named signals
- std::string signal_name(int i); display the name of the signal with the given index
- std::vector<double> get_signals(Cell* pCell); get a vector of all known signals for the cell
- std::vector<double> get_cell_contact_signals(Cell* pCell); get a vector of the cell contact associated signals for the cell
- std::vector<double> get_selected_signals(Cell* pCell , std::vector<int> indices); get a vector of signals for the cell, with the supplied indices
- std::vector<double> get_selected_signals(Cell* pCell , std::vector<std::string> names); get a vector of signals for the cell, with the supplied human-readable names of th
- double get_single_signal(Cell* pCell, int index); get a single signal for the cell with the indicated index
- double get_single_signal(Cell* pCell, std::string name); get a single signal for the cell with the indicated human-readable name

Behaviors Dictionary

- We introduced a "dictionary" of standard behaviors that can be used as outputs to intracellular and rule-based models. This dictionary is automatically constructed at the start of each simulation based upon the combinations of signaling substrates and cell types.

Major classes of behaviors

- secretion, secretion target, uptake, and export rates
- cycle progression
- death rates
- motility parameters
- chemotactic parameters
- cell-cell adhesion and repulsion parameters
- cell adhesion affinities
- cell-BM adhesion and repulsion parameters
- phagocytosis rates
- attack rates
- fusion rates
- transformation rates
- Use `display_behavior_dictionary()` to quickly see a list of possible behaviors.

get and set Functions for behavior

- int find_behavior_index(std::string response_name) :
  get the index of the named behavior
- std::vector<int> find_behavior_indices(std::vector<std::string> behavior_names)
  get the indices for the given vector of behavior names.
- std::string behavior_name(int i);
  get the name of the behavior with the given index
- std::vector<double> create_empty_behavior_vector();
  create an empty vector for the full set of behaviors
- void set_behaviors(Cell* pCell , std::vector<double> parameters);
  write the full set of behaviors to the cell's phentoype
- void set_selected_behaviors(Cell* pCell , std::vector<int> indices , std::vector<double> parameters);
  write the selected set of behaviors (with supplied indices) to the cell's phenotype
- void set_selected_behaviors(Cell* pCell , std::vector<std::string> names , std::vector<double> parameters);
  write the selected set of behaviors (with supplied names) to the cell's phenotype
- void set_single_behavior(Cell* pCell, int index , double parameter);
  write a single behavior (by index) to the cell phentoype
- void set_single_behavior(Cell* pCell, std::string name , double parameter);
  write a single behavior (by name) to the cell phentoype

Example (interaction sampler project)

// contact with a differentiated cell reduces proliferation

// high rate of proliferation unless in contact with a differentiated cell

```
static double stem_cycling_halfmax = pCD->custom_data["cycling_contact_halfmax"]; // 0.1;


        base_val = pCD->phenotype.cycle.data.exit_rate(0); // 0.002;
        max_val = 0.0;
        signal = num_differentiated;
        half_max = stem_cycling_halfmax; //  0.1;
        hill = Hill_response_function( signal, half_max , 1.5 );
        phenotype.cycle.data.exit_rate(0) = base_val + (max_val-base_val)*hill;
```

Best Practices

- In any customized cell function, you can access the microenvironment at its location.

- For best practices, you *don't* want to hard-code the index substrate. If somebody adds a substrate to the XML or reorders them, it could break your code.
- Instead, search for the index of the substrate and store the result in a static variable.
- Dictionaries are recommended way to add behaviors to signals

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