# PhysiBoSS 2.0 Intracellular model

# Vincent Noël1

<sup>1</sup>Computational Systems Biology of Cancer, Institut Curie, INSERM U900, Université PSL, Paris

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#### Introduction

We want a cell to have an intracellular model

› Intracellular models can be of different types : SBML, MaBoSS, FBA, ...

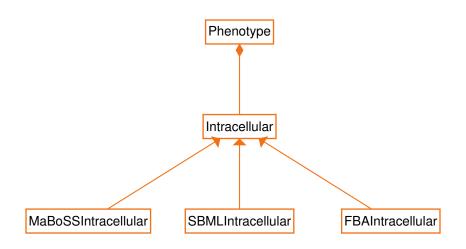
We want to be able to describe them in the XML Cell Definitions



#### Introduction

```
<cell definitions>
   <cell definition name="default" ID="0">
        <phenotype>
            <intracellular type="maboss">
                <bnd filename>./config/boolean network/model 0.bnd</bnd filename>
                <cfg filename>./config/boolean network/model.cfg</cfg filename>
                <time step>1</time step>
                <initial values>
                    <initial value node="A">1</initial value>
                    <initial value node="C">0</initial value>
                </initial values>
            </intracellular>
        </phenotype>
        <custom data/>
   </cell definition>
   <cell definition name="other" parent type="default" ID="1">
        <phenotype>
            <intracellular type="maboss">
                <bnd filename>./config/boolean network/model 1.bnd</bnd filename>
            </intracellular>
        </phenotype>
        <custom data/>
   </cell definition>
```







#### Phenotype

```
class Phenotype
private:
public:
   bool flagged for division;
   bool flagged for removal;
   Cycle cycle;
   Death death:
   Volume volume:
   Geometry geometry;
   Mechanics mechanics:
   Motility motility:
   Secretion secretion:
   Molecular molecular;
   // We need it to be a pointer to allow polymorphism
   // then this object could be a MaBoSSIntracellular, or a SBMLIntracellular
   Intracellular* intracellular:
   Phenotype(): // done
   void operator=(const Phenotype &p );
   void operator=(Phenotype &p );
   void sync to functions( Cell Functions& functions ); // done
```



#### Intracellular virtual class

```
class Intracellular
private:
public:
   std::string type;
   // This function returns a copy of the intracellar object
   virtual Intracellular* clone() = 0;
   // This function parse the xml cell definition
   virtual void initialize intracellular from pugixml(pugi::xml node& node) = 0;
   // This function initialize the model, needs to be called on each cell once created
   virtual void start() = 0:
   // This function update the model for the time step defined in the xml definition
   virtual void update() = 0:
   // This function checks if it's time to update the model
   virtual bool need update() = 0;
   // This function checks if a node exists
   virtual bool has node(std::string name) = 0;
   // Access value for boolean model
   virtual bool get boolean node value(std::string name) = 0:
   // Set value for boolean model You, 4 months ago * Added virtual methods for getting and s
```

virtual void set boolean node value(std::string name, bool value) = 0;



#### MaBoSSIntracellular implementation

```
class MaBoSSIntracellular : public PhysiCell::Intracellular {
 private:
 public:
    static long counter;
    std::string bnd filename;
    std::string cfg filename;
    double time step = 12;
    bool discrete time = false:
    double time tick = 0.5:
    double scaling = 1.0;
    std::map<std::string, double> initial values;
    std::map<std::string, double> mutations;
    std::map<std::string, double> parameters;
   MaBoSSNetwork maboss:
    double next physiboss run = 0;
   MaBoSSIntracellular();
   MaBoSSIntracellular(pugi::xml node& node);
   MaBoSSIntracellular(MaBoSSIntracellular* copy):
```



#### MaBoSSIntracellular implementation

```
Intracellular* clone() {
    return static cast<Intracellular*>(new MaBoSSIntracellular(this));
Intracellular* getIntracellularModel() {
    return static cast<Intracellular*>(this);
void initialize intracellular from pugixml(pugi::xml node& node);
void start() {
    this->maboss.restart node values();
void update() {
    this->maboss.run simulation();
    this->next physiboss run += this->maboss.get time to update();
bool need update() {
    return PhysiCell::PhysiCell globals.current time >= this->next physiboss run;
bool has node(std::string name) {
    return this->maboss.has node(name);
bool get boolean node value(std::string name) {
    return this->maboss.get node value(name);
```



#### XML Cell definition parsing

```
// intracellular
    node = cd node.child( "phenotype" );
    node = node.child( "intracellular" );
   if( node )
        std::string model type = node.attribute( "type" ).value();
#ifdef ADDON PHYSIBOSS
        if (model type == "maboss") {
            // If it has already be copied
            if (pParent != NULL && pParent->phenotype.intracellular != NULL) {
                pCD->phenotype.intracellular->initialize intracellular from pugixml(node);
            // Otherwise we need to create a new one
            } else {
                MaBoSSIntracellular* pIntra = new MaBoSSIntracellular(node);
                pCD->phenotype.intracellular = pIntra->getIntracellularModel();
#endif
```



#### Usage

```
// Creating a new intracellular model
pC = create cell(get cell definition("default"));
// Updating an intracellular model
if (pCell->phenotype.intracellular->need update())
    set input nodes(pCell);
    pCell->phenotype.intracellular->update();
    from nodes to cell(pCell, phenotype, dt);
// Get node value
bool value = pCell->phenotype.intracellular->get boolean node value("Apoptosis");
// Modify node value
pCell->phenotype.intracellular->set boolean node value("TNF", 1):
```



#### Conclusion

Developed with Master student Marco Ruscone from University of Turin

Available at https://github.com/sysbio-curie/PhysiBoSSa, sample project : physiboss-cell-lines

 We might want several intracellular models within a cell (and they might communicate)

We also added PhysiBoSS specific components in the Jupyter Notebook GUI

