

Module 4: Vascular Patterning

Author:

- Walter de Back

Aim:

- Learn to distinguish between alternative hypothesis/mechanisms explaining the same phenomenon
- When two different mechanisms can reproduce the same phenomenon, how can modeling help to distinguish between these mechanisms?

Description:

- Introduce problem and provide examples:
 - multiple mechanism, same result
- Introduce CPM/PDE hybrid/multiscale models
 - coupling model formalisms (through production + chemotaxis)
- Introduce vasculogenesis
 - Isolated cells into vascular network
- Provide two models: A.xml and B.xml that show the same behavior
- Assignment 1: What biological processes do these models reflect?
 - Autocrine model: angioblasts produce their own chemoattractant (VEGF)
 - Paracrine model: paracrine chemoattractant is bound to angioblasts-produced matrix molecules
- Assignment 2: How can you determine which one is more plausible?
 - Theoretically?
 - Explore differences in parameter sensitivity:
 - Sensitivity analysis: ParamSweep (see "[parameter sweep](#)" in FAQ)
 - Experimentally?
 - Explore how the models produce different predictions:
 - Inhibit VEGF binding (use nonbinding isoform VEGF121)
 - Change cell densities
 - Administer fluorescent VEGF
 - Quantitative analysis?
 - Quantify parameters:
 - FRAP: diffusion
 - FRAP: rate of binding/unbinding
 - ELISA: decay
 - Microfluidic device: chemotactic strength

Paper:

- Köhn-Luque A, de Back W, Starruß J, Mattiotti A, Deutsch A, J-M Perez-Pomares, HA Hererro. (2011) Early Embryonic Vascular Patterning by Matrix-Mediated Paracrine Signalling: A Mathematical Model Study. PLoS ONE 6(9): e24175. [link](#)

Documents:

- [Assignment \(handout, pdf\)](#)
- [Diff \(handout, pdf\)](#)

Morpheus models:

- [Example: Vascular patterning](#)
- [h A.xml \(autocrine chemotaxis\)|h](#)

```
<MorpheusModel version="1">
  <Description>
    <Title>ModelA</Title>
  </Description>
  <Space>
    <Lattice class="square">
      <Size value="200 200 0"/>
      <BoundaryConditions>
        <Condition boundary="x" type="periodic"/>
        <Condition boundary="y" type="periodic"/>
      </BoundaryConditions>
      <NodeLength unit="micron" value="2"/>
      <Neighborhood>
        <Order>2</Order>
      </Neighborhood>
    </Lattice>
  </Space>
  <Time>
    <StartTime value="0"/>
    <StopTime value="4000"/>
    <SaveInterval value="0"/>
    <RandomSeed value="56"/>
  </Time>
  <CellTypes>
    <CellType class="biological" name="Angioblasts">
      <VolumeConstraint>
        <Strength value="25"/>
        <Target value="90"/>
      </VolumeConstraint>
      <Property symbol="cell" value="1.0" name="cell"/>
      <Property symbol="s" value="2000" name="chemotactic
strength"/>
      <ConnectivityConstraint/>
      <Chemotaxis>
        <Layer symbol-ref="u"/>
        <Strength symbol-ref="s"/>
      </Chemotaxis>
    </CellType>
  </CellTypes>
</MorpheusModel>
```

```

    <CellType class="medium" name="medium">
      <Property symbol="cell" value="0" name="cell"/>
    </CellType>
  </CellTypes>
  <CPM>
    <Interaction default="0">
      <Contact type1="medium" type2="Angioblasts" value="80"/>
      <Contact type1="Angioblasts" type2="Angioblasts"
value="160"/>
    </Interaction>
    <MetropolisKinetics temperature="50" stepper="edgelist">
      <Neighborhood>
        <Order>2</Order>
      </Neighborhood>
    </MetropolisKinetics>
    <MCSDuration value="1.0"/>
  </CPM>
  <PDE>
    <Layer symbol="u" name="VEGF">
      <Diffusion rate="1e-6" unit="µm²/s"/>
    </Layer>
    <System solver="runge-kutta" time-step="1.0">
      <Constant symbol="gamma1" value="1e-3" />
      <Constant symbol="delta" value="1e-3" />
      <DiffEqn symbol-ref="u">
        <Expression>cell*gamma1 - (1-cell)*delta*u
</Expression>
      </DiffEqn>
    </System>
  </PDE>
  <CellPopulations>
    <Population size="0" type="Angioblasts">
      <InitRectangle cells="200" type="regular">
        <Dimensions size="200 200 0" origin="0 0 0"/>
      </InitRectangle>
    </Population>
  </CellPopulations>
  <Analysis>
    <Gnuplotter clean="true" interval="50" timename="false">
      <Terminal opacity="0.65" name="png"/>
      <Cells flooding="true">
        <ColorMap>
          <Color value="1" color="gray"/>
          <Color value="0" color="grey"/>
        </ColorMap>
      </Cells>
      <PDE symbol-ref="u" superimpose="true" isolines="3">
        <ColorMap>
          <Color value="1.0" color="red"/>
          <Color value="0.5" color="yellow"/>
          <Color value="0.0" color="white"/>
        </ColorMap>
      </PDE>
    </Gnuplotter>
  </Analysis>

```

```
        </ColorMap>
    </PDE>
</Gnuplotter>
</Analysis>
</MorpheusModel>
```

- h B.xml (paracrine chemotaxis)|h

```
<MorpheusModel version="1">
  <Description>
    <Title>ModelB</Title>
  </Description>
  <Space>
    <Lattice class="square">
      <Size value="200 200 0"/>
      <BoundaryConditions>
        <Condition boundary="x" type="periodic"/>
        <Condition boundary="y" type="periodic"/>
      </BoundaryConditions>
      <NodeLength unit="micron" value="2"/>
      <Neighborhood>
        <Order>2</Order>
      </Neighborhood>
    </Lattice>
  </Space>
  <Time>
    <StartTime value="0"/>
    <StopTime value="4000"/>
    <SaveInterval value="0"/>
    <RandomSeed value="56"/>
  </Time>
  <CellTypes>
    <CellType class="biological" name="Angioblasts">
      <VolumeConstraint>
        <Strength value="25"/>
        <Target value="90"/>
      </VolumeConstraint>
      <Property symbol="cell" value="1.0" name="cell"/>
      <Property symbol="s" value="2000" name="chemotactic
strength"/>
      <ConnectivityConstraint/>
      <Chemotaxis>
        <Layer symbol-ref="w"/>
        <Strength symbol-ref="s"/>
      </Chemotaxis>
    </CellType>
    <CellType class="medium" name="medium">
      <Property symbol="cell" value="0" name="cell"/>
    </CellType>
  </CellTypes>
</MorpheusModel>
```

```

    </CellType>
  </CellTypes>
  <CPM>
    <Interaction default="0">
      <Contact type1="medium" type2="Angioblasts" value="80"/>
      <Contact type1="Angioblasts" type2="Angioblasts"
value="160"/>
    </Interaction>
    <MetropolisKinetics temperature="50" stepper="edgelist">
      <Neighborhood>
        <Order>2</Order>
      </Neighborhood>
    </MetropolisKinetics>
    <MCSDuration value="1.0"/>
  </CPM>
  <PDE>
    <Layer symbol="u" name="VEGF">
      <Diffusion rate="10" unit="µm²/s"/>
    </Layer>
    <Layer symbol="v" name="ECM">
      <Diffusion rate="1e-3" unit="µm²/s"/>
    </Layer>
    <Layer symbol="w">
      <Diffusion rate="1e-3" unit="µm²/s"/>
    </Layer>
    <System solver="runge-kutta" time-step="1.0">
      <Constant symbol="gamma1" value="1e-3" />
      <Constant symbol="gamma2" value="1e-3" />
      <Constant symbol="alpha" value="1e-1" />
      <Constant symbol="delta" value="1e-2" />
      <DiffEqn symbol-ref="u">
        <Expression>gamma1 - delta*u - alpha*u*v </Expression>
      </DiffEqn>
      <DiffEqn symbol-ref="v">
        <Expression>gamma2*cell - alpha*u*v</Expression>
      </DiffEqn>
      <DiffEqn symbol-ref="w">
        <Expression>alpha*u*v</Expression>
      </DiffEqn>
    </System>
  </PDE>
  <CellPopulations>
    <Population size="0" type="Angioblasts">
      <InitRectangle cells="200" type="regular">
        <Dimensions size="200 200 0" origin="0 0 0"/>
      </InitRectangle>
    </Population>
  </CellPopulations>
  <Analysis>
    <Gnuplotter clean="true" interval="50" timename="false">
      <Terminal opacity="0.65" name="png"/>
    </Gnuplotter>
  </Analysis>

```

```
<Cells flooding="true">
  <ColorMap>
    <Color value="1" color="gray"/>
    <Color value="0" color="grey"/>
  </ColorMap>
</Cells>
<PDE symbol-ref="w" superimpose="true" isolines="3">
  <ColorMap>
    <Color value="1.0" color="red"/>
    <Color value="0.5" color="yellow"/>
    <Color value="0.0" color="white"/>
  </ColorMap>
</PDE>
</Gnuplotter>
</Analysis>
</MorpheusModel>
```

From:
<https://imc.zih.tu-dresden.de/wiki/morpheus/> - **Morpheus**

Permanent link:
<https://imc.zih.tu-dresden.de/wiki/morpheus/doku.php?id=documentation:course:module4&rev=1355563949>

Last update: **10:32 15.12.2012**

