

## Data and simulation for stem cell amplification studies in prostate disease development and control

<sup>1</sup>Fiona Polack, <sup>1,2</sup>Alastair Droop, \*<sup>1</sup>Andrei Simionescu, \*<sup>1</sup>Livia Dia, \*<sup>2</sup>Emily Pollard, \*<sup>2</sup>Sarah Greener, <sup>2</sup>Fiona M Frame, <sup>2</sup>Norman J Maitland, <sup>1</sup>Susan Stepney

<sup>1</sup>Dept of Computer Science, YCCSA; <sup>2</sup>YCR CRU, Dept of Biology



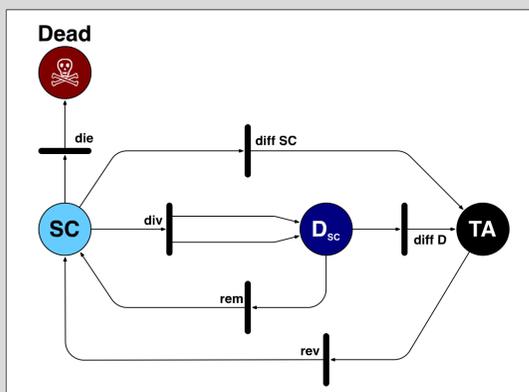
### Aims:

To produce a fit-for-purpose simulation of pathological changes in human prostate which will:

- (i) Extend and adapt to look at the effects of rare events
- (ii) Describe the cell dynamics of a range of different pathologies related to cell division and differentiation
- (iii) Use the parameters in the model to predict the outcome of treatments which target different cell types

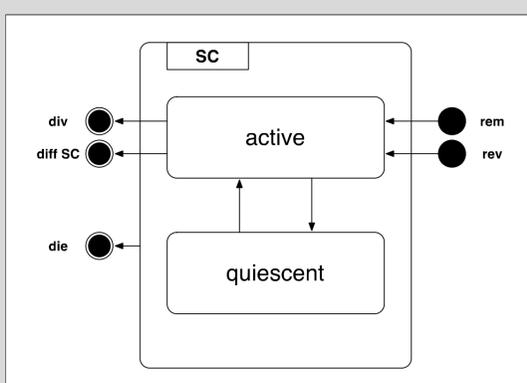
### Strategy

1. Produce a **Top level model** (Petri net) of cell division and differentiation, showing relevant outcomes for stem cells in prostate epithelium



SC = Stem Cell  
TA = Transit Amplifying Cell (place is black because the model continues, with division and differentiation of TA cell towards terminally differentiated luminal cell type)  
Transition labels containing:  
div = division diff = differentiation rev = reversion rem = remain

2. Generate a **State diagram** for a single stem cell showing the lower level states that govern when transition might occur



Terminal blobs are black for entry, annular for exit. Entry and exit labels refer to the transitions on the Petri net model that cause a cell to arrive in or leave the stem cell state.

3. Produce a **template** for converting the diagrams (Petri nets and associated state diagrams) to text, from which code can be generated.

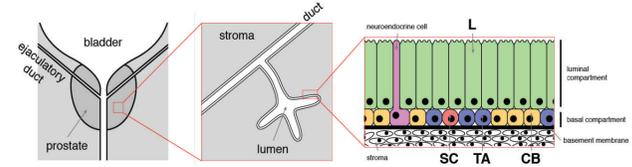
```
<model> ::= (<section>)*
<section> ::= "places:" (<place>)*
| "trans:" (<transition>)*
| "#" <commented-line>
<place> ::= <place-name> <start-count>
<transition> ::= <transition-name>
"in" <place-name>
"out" <place-name> ("," <place-name>)*
"rate" <number>
["mutability" <range>]
(<mutation>)*
<mutation> ::= "mutate" <transition-name> <range>
| "mutate_any" <range>
<range> ::= <number> "to" <number>
```

From this we can generate code in languages such as Python, Erlang, or, with some manipulation, Java.

### Biological data input

4. Generate cell proportion and cell fate data to provide numerical input for the model

#### Glandular architecture and cellular structure of the human prostate



The function of the prostate gland is to produce secretions which assist with sperm viability (and to act as a fibromuscular 'tap' to restrict urinary flow from the bladder). Secretory units are arranged as 'bunches of grapes' each draining via a collecting tubular duct into the urethra. The bilayered organisation of the epithelial cells surrounding each lumen is shown.

#### Immunofluorescence antibodies

Gene/antigen	Purpose
P63	Marks basal cell nuclei
NKX3.1	Marks luminal cell nuclei
Cytokeratin 18	Marks luminal cells
Cytokeratin 5	Marks basal cells
Ki67	Marks replicating cells
PCNA	Marks replicating cells
Caspase 8	Marks apoptotic (dying) cells
TUNEL	Marks apoptotic (dying) cells

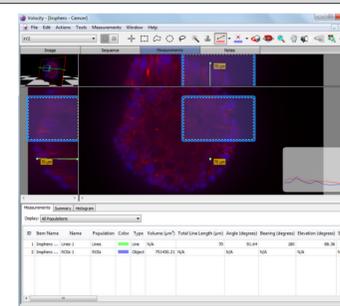
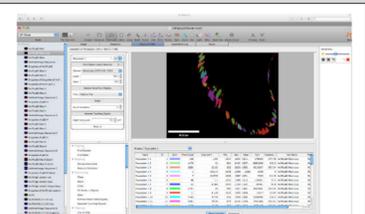


Image acquisition and recording in Volocity



Quantification of positive epithelial cell nuclei  
False colouring of positive basal cell population shown

#### Automated data recording/quantification of nuclei using digitised fluorescent images and Volocity

#### Glandular architecture of benign prostate

Basal layer marked by fluorescent immuno-histochemical detection of p63 (red) with nuclei counterstained in DAPI (blue)

#### Replicating cells in benign prostate

Replicating cells in the basal layer marked by fluorescent immuno-histochemical detection of Ki67 (cyan) with nuclei counterstained in DAPI (blue)

#### Glandular architecture of benign prostate

Luminal layer marked by fluorescent immuno-histochemical detection of NKX3.1 (green) with nuclei counterstained in DAPI (blue)

#### Cell phenotyping with cytokeratin antibodies

CK antibodies can identify cell types but irregular cell shapes limit quantification: We use antibodies against NUCLEAR proteins

#### Combined basal:proliferation image of Benign prostatic hyperplasia gland

Image indicates that BPH is driven by excessive basal cell proliferation: but we currently treat it by inhibiting the luminal cells!

Fluorescent images digitised to quantify  
(i) cell type proportions  
(ii) Dying and dividing cell numbers in each cell compartment  
Quantified from multiple glands and tissue samples  
Data used to feed model  
Iterative process of model building and refinement initiated

#### Further Reading:

Maitland N J (2013) Stem cells in the normal and malignant prostate. D J Tindall (Editor), Prostate Cancer: Biochemistry, Molecular Biology and Genetics, Protein Reviews 16, DOI 10.1007/978-1-4614-6828-8\_1 Mayo Clinic

#### C2D2 publication:

Choosing and adapting design notations in the principled development of complex systems simulations for research. Fiona A. C. Polack, In Modelling the Physical World Workshop, at Models 2012, Innsbruck, Austria, October 2012. ACM Digital Library

#### Acknowledgements:

Yorkshire Cancer Research and CIDCAT for providing student\* support for the project AD is supported by CRUK