# Modelling Natural Killer cell interactions with Tumour cells

#### David Rhodes





## Natural Killer (NK) cells

- Kill some tumour and virus infected cells
- Identify targets by change in expression levels of proteins normally found in healthy cells
- Have Inhibitory receptors (MHC Class I) and activating receptors (NKG2D and others)
- Unhealthy cells can reduce expression of inhibitory ligands and increase activating ligands
- Receptors and Ligands log normally distributed within population

#### NK Cells

- Each Receptor type on NK cells is expressed on only a proportion of NK cells
- Each NK cell therefore has a set of receptors each with its own unique level of expression
- Investigate how heterogeneous populations of NK cells can identify and target heterogeneous population of Tumour/Infected cells
- Without killing healthy cells in the process

## Model

- Explore different killing rules to help explain how NK cells determine which cells to kill
- Each agent in model is a cell, either NK or target
- Cells are spread across a 2D environment, mimicking in vitro testing
- Cells move around interacting for 4 virtual hours and number of target cells killed is monitored

#### Typical starting layout of 1000 cell model



250 Tumour cells (blue), 750 NK cells (green)

#### Model.XML

- Very simple model file
- 1 agent type Cell
- Agent can represent NK cells or target cells based on a 'Type' variable
- Majority of memory is for expression level of the different receptors/ligands
- 1 Message that sends all receptor/ligand data for evaluation in cell:cell interactions

#### **Functions File**

- Also quite simple
- Has functions for movement of cells
- Collision response if cells interact but one is not killed
- Evaluating the killing rule during NK:Target interactions
- Other minor functions such as keeping the cells within the bounds of environment

#### 0.XML

- Main complexity of tests
- Every cell has unique receptor/ligand expression
- NK cells have several other variables chosen from distributions
- Testing mainly focuses on creating different starting populations to see how they interact

🚰 Memory Variables											
Age	nt/Variable •	Var Type	Region 1		Region 2						*
	ell										
	id	int(SPECIAL)									
	type	int	0		1						
	kill_reserve	double	100000		0						
	max_reserve	double	normal(10000,25	00)	0						
	active	int	discrete((0.20,0),(	(0.80,1))	0						
	fatigue	int	0		0						
	х	double	rand(0,500)		rand(0,500)						
	У	double	rand(0,500)		rand(0,500)						
	Z	double	0		0						
	num_inhib1	double	normal(2.3,0.15)		normal(2.7,0.	27)					
	num_inhib2	double	discrete((0.2,0),(0	.8,normal(2.3,0.15)))	discrete((0.2,	0),(0.8,normal(	2.7,0.27)))				12
	num_inhib3	double	discrete((0.5,0),(0	0.5,normal(2.2,0.12)))	discrete((0.2,	0),(0.8,normal(	2.7,0.27)))				
	num_inhib4	double	discrete((0.5,0),(0	.5,normal(2.7,0.18)))	discrete((0.2,	0),(0.8,normal(	2.7,0.27)))				
	num_inhib5	double	discrete((0.5,0),(0	.5,normal(3,0.15)))	discrete((0.2,	0),(0.8,normal(	2.7,0.27)))				
	num_active1	double	normal(2.3,0.15)		normal(2.9,0.	25)					
	num_active2	double	discrete((0.1,0),(0	.9,normal(2.3,0.15)))	discrete((0.2,	0),(0.8,normal(	2.9,0.25)))				
	num_active3	double	discrete((0.1,0),(0	.9,normal(3.2,0.15)))	discrete((0.2,	0),(0.8,normal(	2.9,0.25)))				
	num_active4	double	discrete((0.5,0),(0	.5,normal(2.8,0.15)))	discrete((0.2,	0),(0.8,normal(	2.9,0.25)))				
	num_active5	double	discrete((0.5,0),(0	.5,normal(2.6,0.12)))	discrete((0.2,	0),(0.8,normal(	2.9,0.25)))				
	dir_x	double	rand(-1,1)		rand(-1,1)						
	dir_y	double	rand(-1,1)		rand(-1,1)						
	dir_z	double	0		0						~
				Evaluate expression	Syntax help	Region copy	Expand All	Validate	Update and close	Canc	el