

Introduction to Cancer Systems Biology

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$$\frac{\partial n}{\partial t} = D_n \nabla^2 n - \chi \nabla \cdot (n \nabla f)$$

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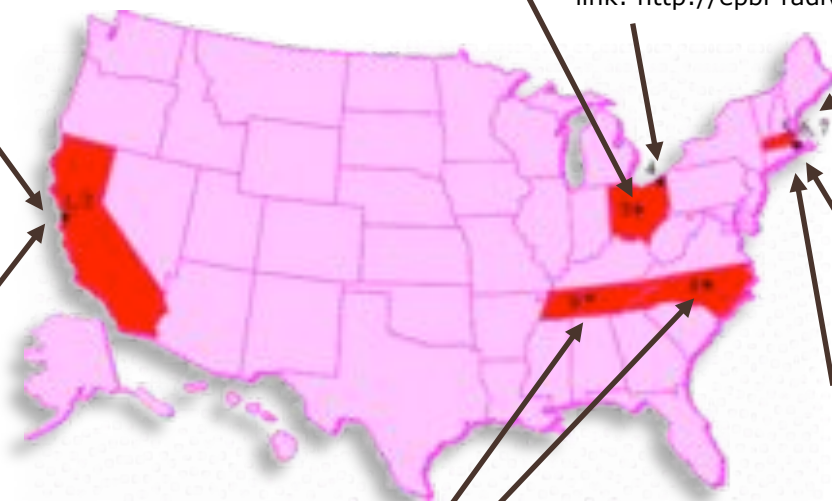
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What is Integrative Cancer Biology?

- It is the same as Cancer Systems Biology, or Systems Biology of Cancer

What is Systems Biology? *(Personal Definition, VQ)*

- A system of linked coordinates that slide along Biological Scales.
- SB practitioners still tend to work primarily at one particular biological scale, but their distinctive trait is a worry about connecting, or integrating, with scale levels above and below.

Biological Scales

ORGANISMS
(vertebrate model)



SYSTEMS
(angiogenesis)

ORGANS



($<10^7$)

TISSUE

(i.e., tumor fingering)



($\sim 10^6-10^9$)

($<10^7$)

MULTICELLULAR
(mammospheres)



($<10^7$)

CELLULAR

(i.e., single cell migration)



(1)

SUBCELLULAR

(i.e., actin networks, ECM structure)



MOLECULAR

(i.e., gene expression, signaling)



SB practitioners still tend to work primarily at one particular biological scale, but their distinctive trait is a worry about connecting, or integrating, with scale levels above and below.

Misconceptions about Systems Biology

- Mindless accumulation of data by some high-throughput means
- No hypothesis necessary prior to experimentation
- Large amounts of data automatically provide answers
- Can be comfortably ignored by “Conventional Biology”

Cancer Systems Biology: Why Bother?

“Enormous progress has been made in understandingthe critical cellular processes, such as cell cycle, DNA repair, apoptosis, transcription, cell migration, and matrix structure, [that are] so critical to our understanding and treatment of cancer.

However, cancer is not a disease only of cells. It is a disease of various systems and components that interact at both a molecular and cellular level to lead to initiation and progression of the disease.”

Cancer Systems Biology: Why Bother?

“These interacting systems include interactions between:

- genes in the cancer cells;
- signal transduction pathways within a cancer cell;
- cells in the tumor;
- tumor and its microenvironment;
- the individual and the macro-environment.”

Cancer Systems Biology: Why Bother?

“Furthermore, the changing interactions of these ... systems in a ... dynamic environment underscore the inherent complexity of the disease.

Until recently, it has been necessary to apply a reductionist approach to cancer research, focusing on a specific mutation, signaling pathway, or cell.

While there has been remarkable progress in understanding each of these component parts, further integration across components or scales has been limited primarily by the lack of technology and tools needed to interrogate at any higher level.”

Cancer Systems Biology: Why Bother?

“Within the past 10 years, new technologies have been developed that have generated extensive genomic, proteomic and other genome-wide datasets.

Other novel technologies have made possible vital imaging, isolation of rare cells, and organotypic culturing.

Together, these developments have afforded the possibility to expand the cancer research effort to include an integrative systems approach.”

Cancer Systems Biology: Why Bother?

Department of Health and Human Services

Participating Organizations

National Institutes of Health (NIH) (<http://www.nih.gov/>)

Components of Participating Organizations

National Cancer Institute (NCI) (<http://www.cancer.gov>)

Title: Collaborative Research in Integrative Cancer Biology and the Tumor Microenvironment (U01)

Announcement Type:

New

Program Announcement (PA) Number: PAR-09-026

Key Dates

Release/Posted Date: November 13, 2008

Opening Date: January 19, 2009 (Earliest date an application may be submitted to Grants.gov).

Why Bother with Computational and Mathematical Modeling of Cancer?

*Is this equivalent to saying that we need Theory in Cancer
Biology? Yes.*

Impact of theory in science (+)

“There is nothing more practical than a good theory”
James Clerk Maxwell

Music theory
JS Bach

Ok, theory in CB is good, but
why now, why me?

Science 20 December 1996:

Vol. 274, no. 5295, pp. 2039 – 2040

DOI: 10.1126/science.274.5295.2039

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PERSPECTIVES

Biologists Put on Mathematical Glasses

Torbjörn Fagerström, Peter Jagers, Peter Schuster, Eörs Szathmary

“No new principle will declare itself from below a heap
of facts”

Sir Peter Medawar

Assuming we must, how do we build a Theory of Cancer?

Short Answer: *Nobody knows. However, we can try.*

OPTIONS:

- *Armchair*
- *Take a page from other sciences: Physics and Engineering are recent and excellent examples of the power of computational/mathematical modeling*

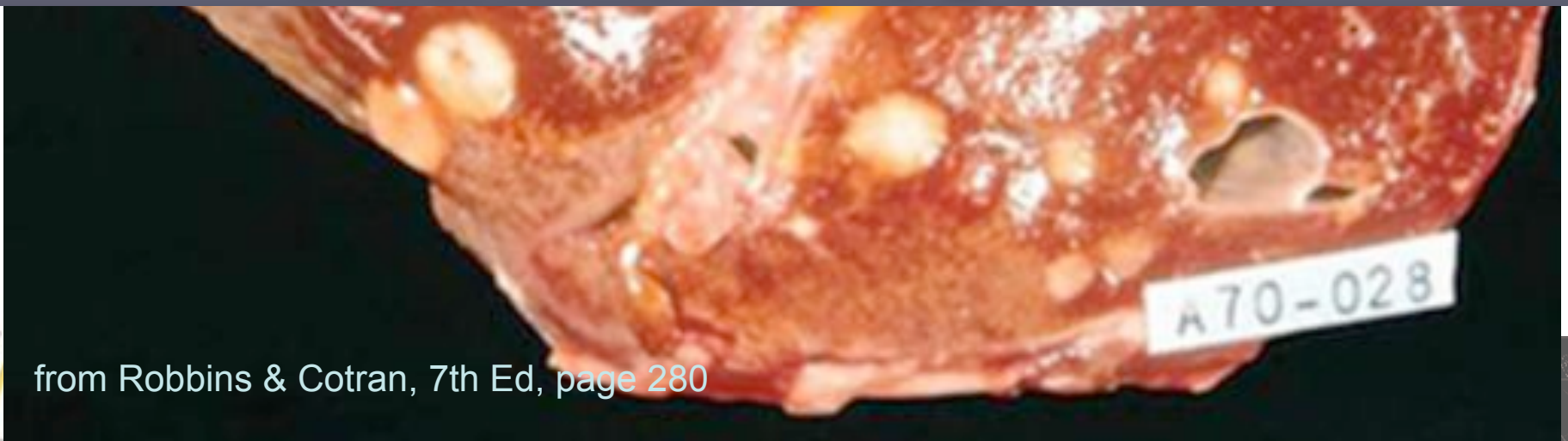
Outline

- A 4 minute course on Cancer: all you need to know to follow the remainder of this talk
- The interface between Oncology and Cancer Systems Biology
- How to practice Cancer Systems Biology
- Tangible examples of Cancer Systems Biology, including the experience in our own group (+AWW)

Macroscopic Appearance of Cancer Tissue



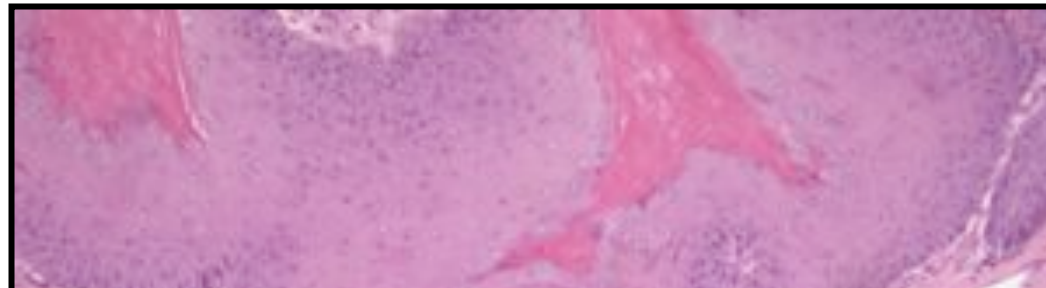
How we evaluate cancer disease in a patient
(Diagnosis and Prognosis): Pathologists
determine **STAGE** and.....



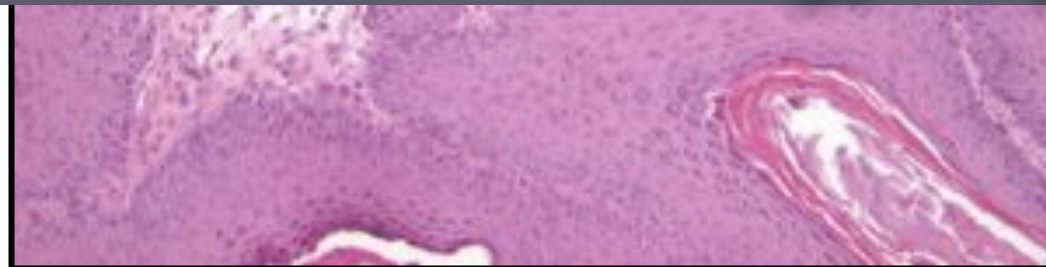
from Robbins & Cotran, 7th Ed, page 280



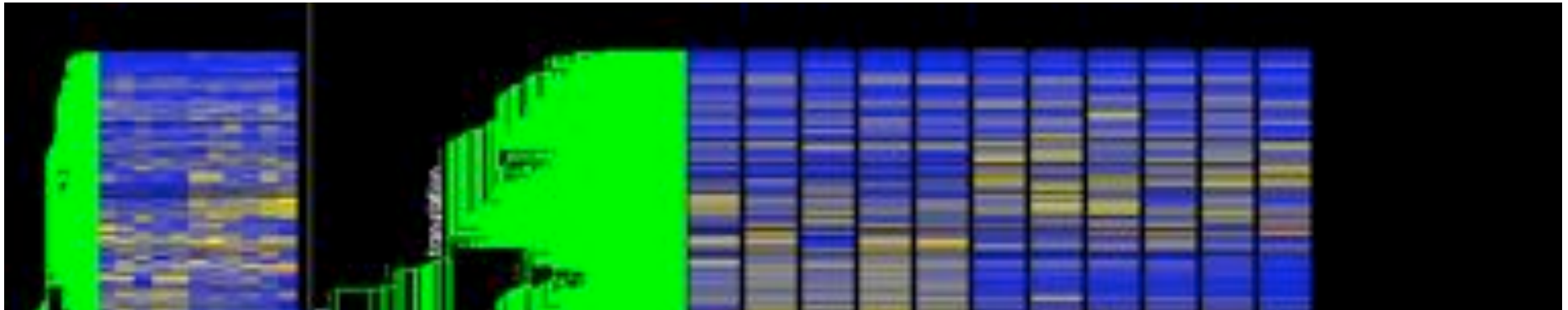
Microscopic Appearance of Cancer Tissue



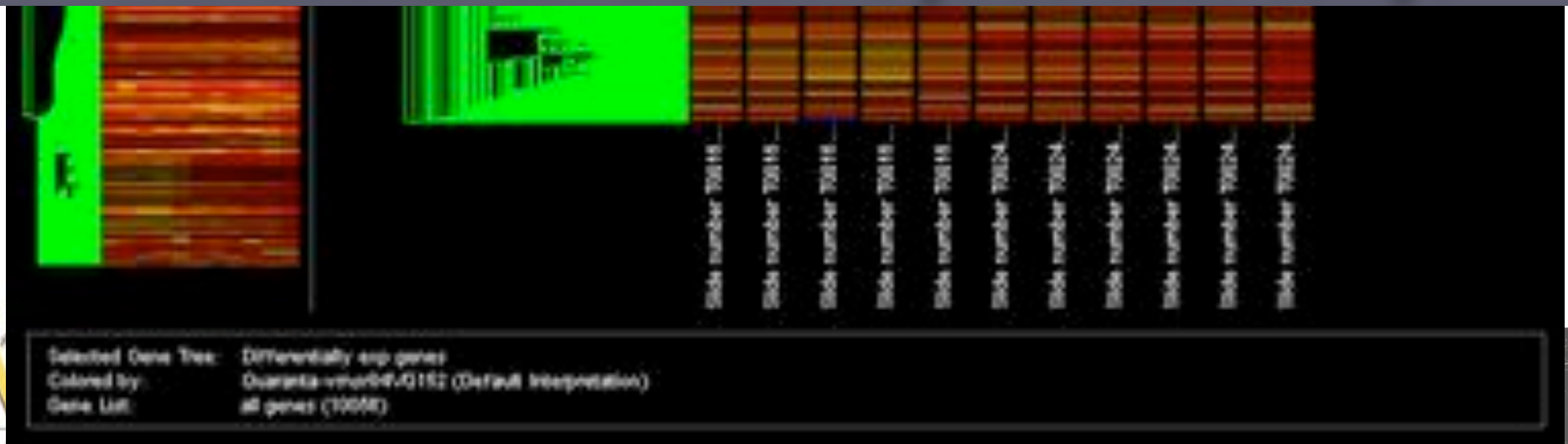
....**GRADE**: All subsequent clinical decision are based on the Pathology Report



Genes Expressed in Cancer Tissue



How we would like to evaluate cancer disease in a patient (Diagnosis and Prognosis):
Molecular or Genetic profiles. Why?



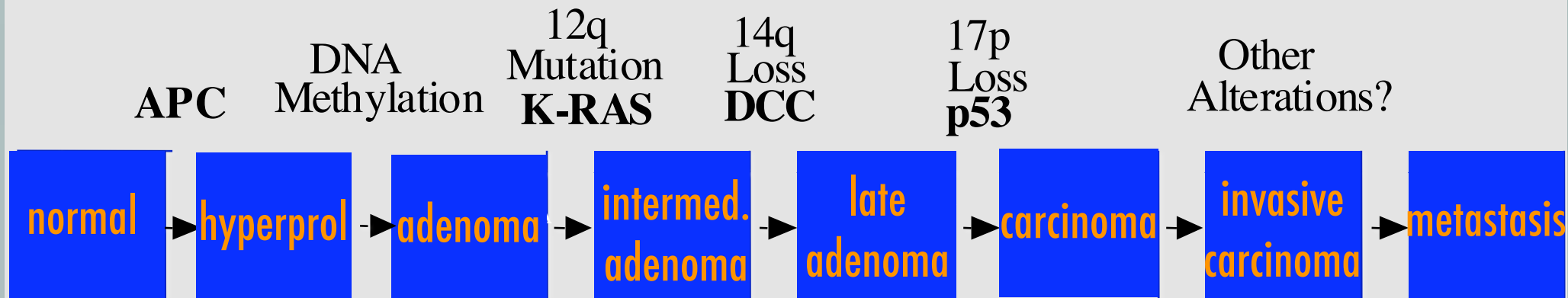
Multistage Tumor Progression: A Current Theoretical Framework

Cellular:

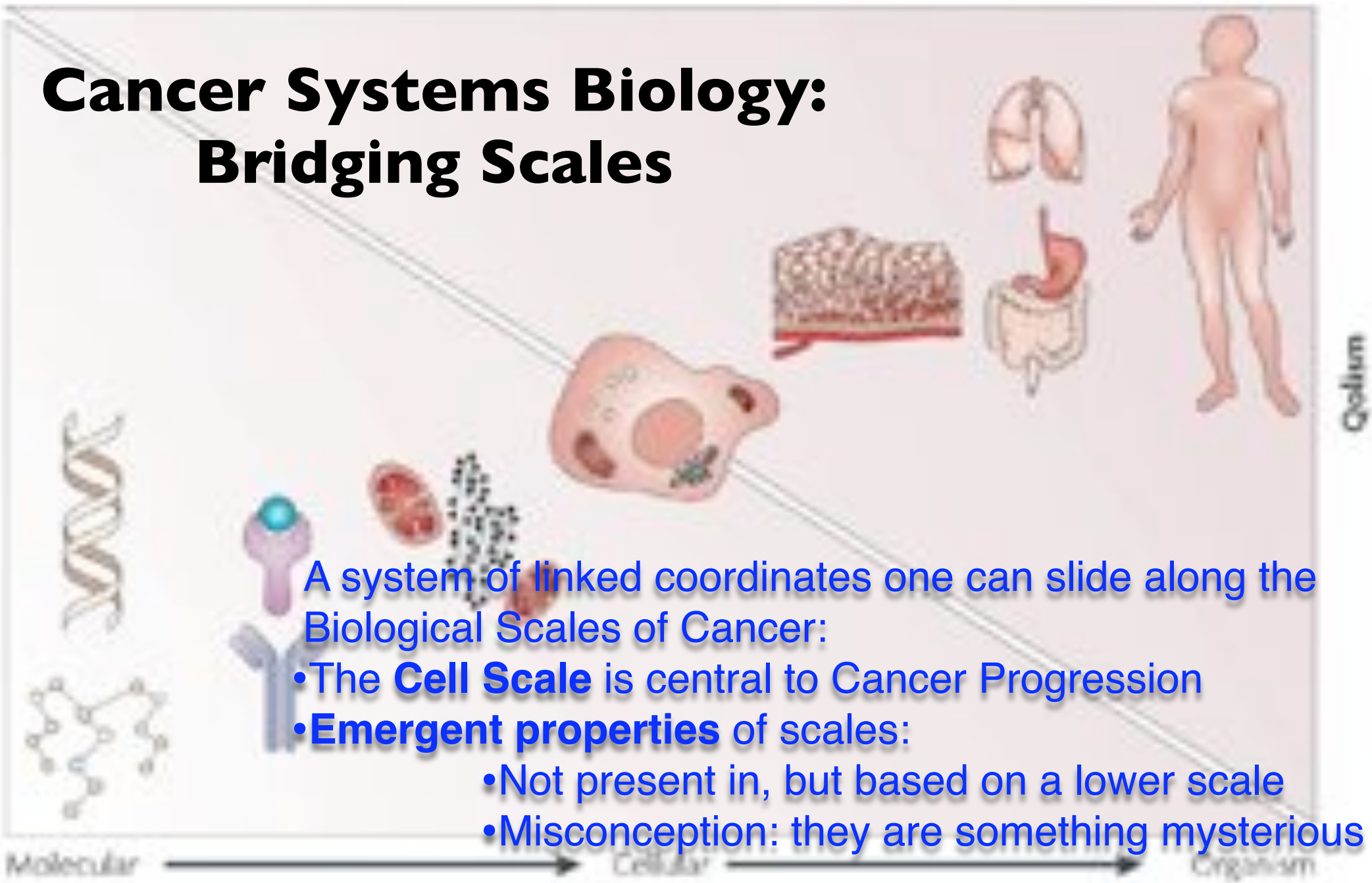


This is great! Molecular or Genetic Profiling is entering in the clinical practice in some instances. But, there is a complication.... Gene to Phenotype mapping is not one-to-one.

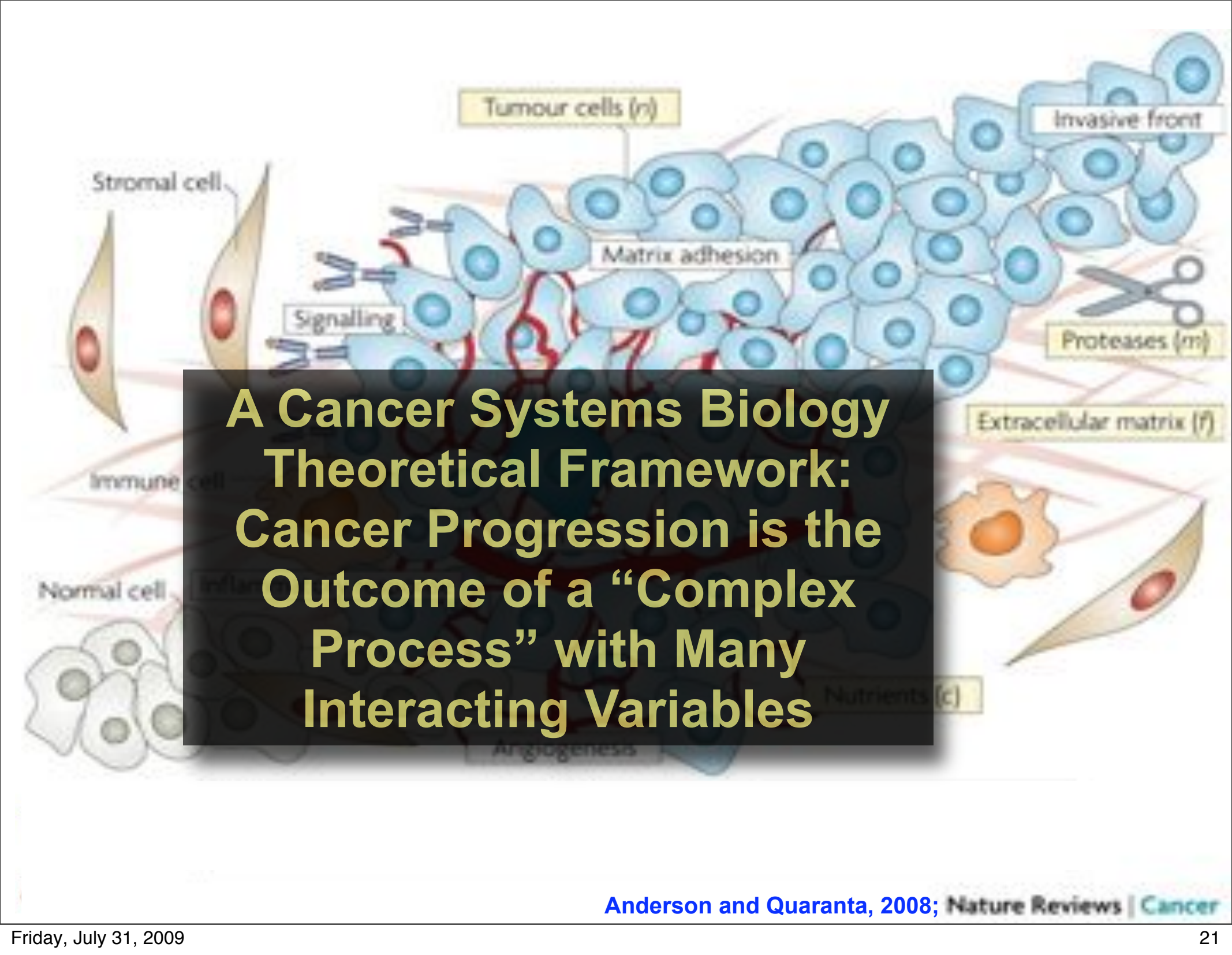
Molecular:



Cancer Systems Biology: Bridging Scales



Anderson and Quaranta, Nature Cancer Reviews, 2008



The diagram illustrates the complex biological processes of cancer progression. It features several key components: **Tumour cells (n)** shown as a cluster of blue cells; **Stromal cell** shown as a yellow elongated cell; **Immune cell** shown as a yellow cell with a red nucleus; **Normal cell** shown as a cluster of grey cells; **Signalling** represented by blue Y-shaped receptors; **Matrix adhesion** shown as red filaments connecting cells; **Invasive front** at the edge of the tumour; **Proteases (m)** represented by a pair of scissors; **Extracellular matrix (f)** shown as a network of fibers; and **Nutrients (c)** shown as a yellow cell with a red nucleus. The text is overlaid on a dark grey rectangular background.

**A Cancer Systems Biology
Theoretical Framework:
Cancer Progression is the
Outcome of a “Complex
Process” with Many
Interacting Variables**

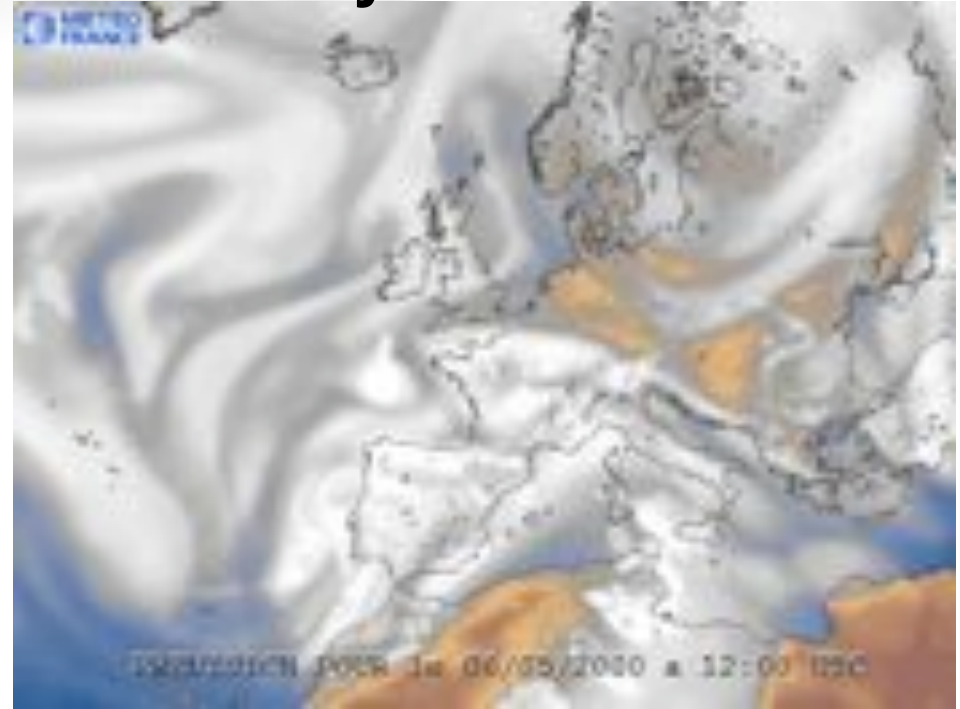
How does one do CSB?

- Collect large datasets
- Interpret them with mathematical models, from statistical to mathematical to computational.
- Validate the models

Modeling with Large Datasets Improves Prediction Accuracy



Satellite Pictures



Mathematical Prediction

- Input current weather information e.g. wind speed, pressure, temperature, humidity etc.
- Mathematical models are then solved numerically to predict how this information will change in time

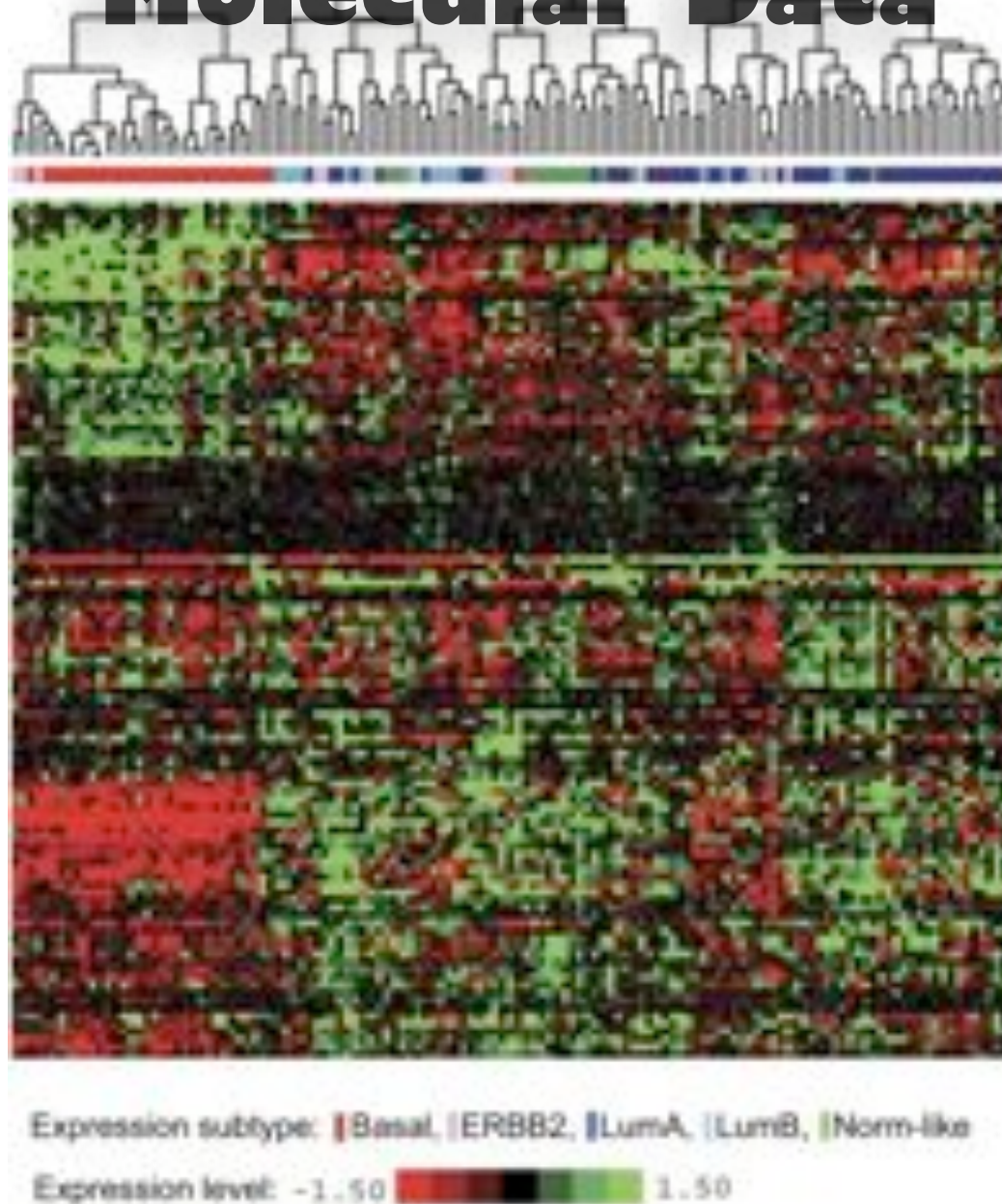
How one does CSB

- Does one need to collect large datasets?
 - Not to get going, but eventually yes, because accuracy of modeling improves with more data
 - Example from other sciences
 - Biological variability
- Why does one need models?
 - Large datasets cannot be easily grasped by human mind
 - Outcomes are often counterintuitive

CSB Examples: Data Collection, Production, Modeling

- The genetic scale
 - Microarrays
 - microRNAs
 - The molecular scale
 - Proteomics
 - Signaling networks
 - The cellular scale
 - Response to mE and drugs
 - Altschuler
 - Sorger
 - Our group
 - The tissue scale
 - The organism scale
 - The population scale
-
- Examples of modeling techniques
 - Statistical
 - Mathematical

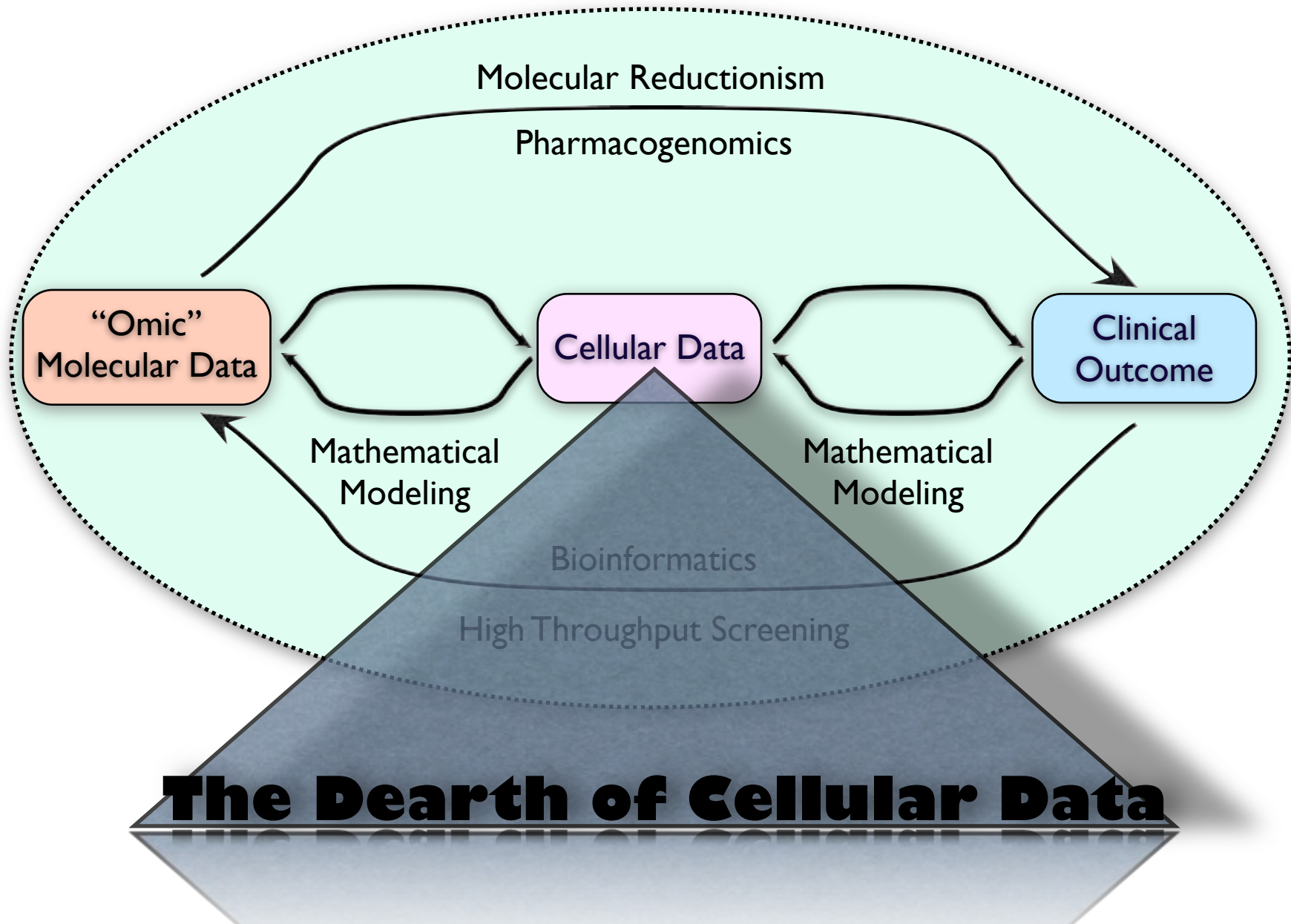
The Deluge of Genetic and Molecular Data



Chin et al. [Cancer Cell.](#)
10:529, 2006

Figure 4. Results of unsupervised hierarchical clustering of 130 breast tumors using intrinsically variable gene expression but excluding any transcripts whose levels were significantly associated with genome copy number. Red indicates increased expression, and green indicates reduced expression. An annotated version is provided as [Figure S3](#).

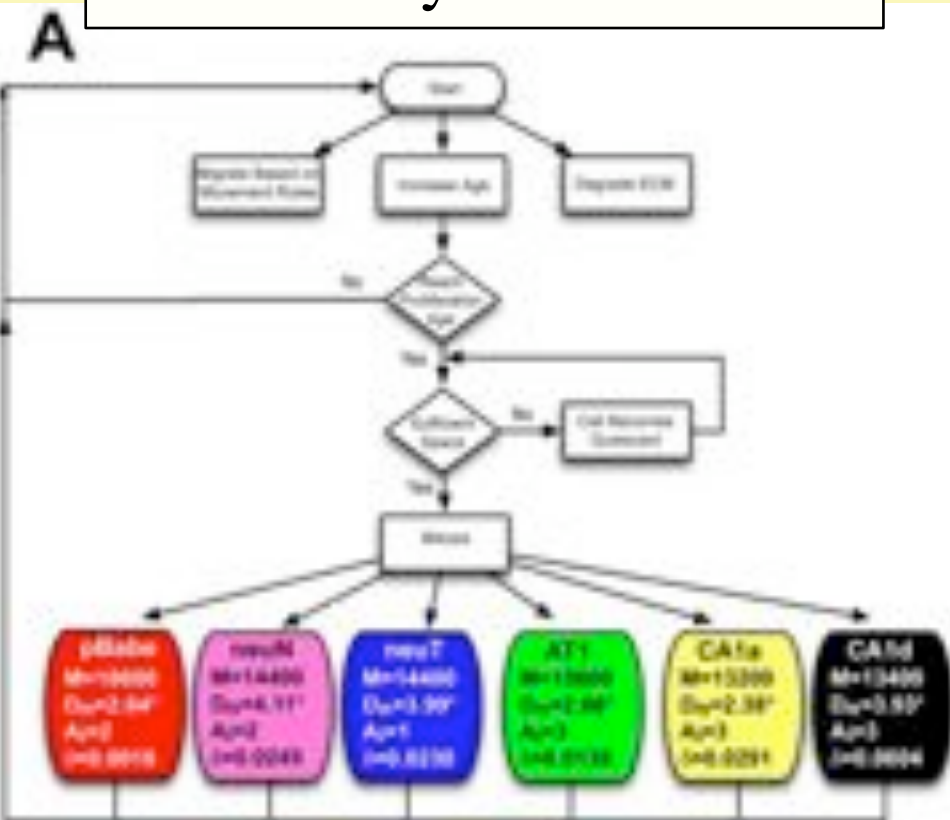
Cancer Systems Biology



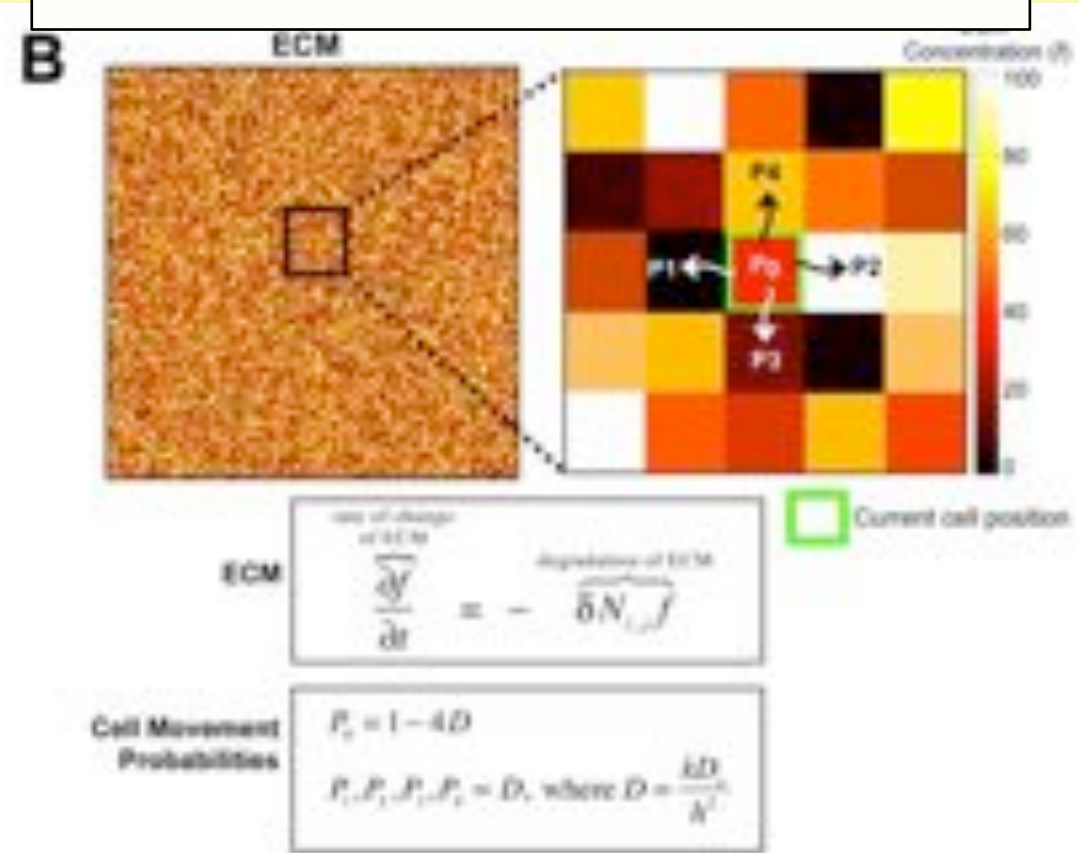
The Dearth of Cellular Data

Insufficient Cell Data is Particularly Acute in the Case of Cellular Automata Models

Cell Life Cycle Flow Chart



ECM Domain and Cell Movement



Tumor Heterogeneity and the Biology of Cancer Invasion and Metastasis¹

Isaiah J. Fidler

Cancer Biology Program, National Cancer Institute Frederick Cancer Research Center, Frederick, Maryland 21701

Abstract

The development of a metastasis is dependent on an interplay between host factors and intrinsic characteristics of malignant tumor cells. The process of metastasis is highly selective, and the metastatic lesion represents the end point of many destructive events that only a few cells can survive. Neoplasms, which are predominantly heterogeneous, contain a variety of subpopulations of cells with differing metastatic potential. Furthermore, metastatic cell variants have been shown to preexist in murine neoplasms of old and recent origin. The possible existence of highly metastatic variant cells within a primary tumor suggests that we no longer should consider a neoplasm to be a uniform entity. Efforts to design effective therapeutic agents and procedures against malignant tumors should be directed toward the few but fatal metastatic subpopulations of cells.

of the biology of the phenomenon and, therefore, allow the development of new approaches to the therapy of disseminated disease.

We have recently developed one such animal model for qualitative studies of metastasis. Mice are given i.d. injections, in the external ear, of 0.05 ml of tumor cell suspension. Three to 4 weeks later, when the tumors are established, the ear is amputated at its base and the mice are allowed to survive. Six to 8 weeks later, the mice are killed and examined for the presence of lymph node or visceral metastases. In the model shown in Fig. 1a, 25,000 viable cells of the B16 melanoma, syngeneic to the C57BL/6 mouse, were injected into the medial surface of the external ear. The ear and growing tumor were amputated 3 weeks after s.c. injection. If the tumor mass contained no metastatic cells, the amputation of the ear would be curative. Alternatively, if the growing tumor contained some metastatic cells, which invaded blood vessels and lymphatics



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cancer heterogeneity

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Results 1 - 10 of about 1,320,000 for [cancer heterogeneity](#). (0.22 seconds)

Heterogeneity

- What is it?
- How do we quantify it?

Wiktionary
 ['wɪkʃənəri] *n.*,
 a wiki-based Open
 Content dictionary
 Wiktionary [wɪkʃənəri]

search

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heterogeneity

English


Noun

heterogeneity (*countable and uncountable; plural heterogeneities*)

1. (*uncountable*) Diversity
2. (*countable*) A composition of diverse parts

Related terms

- [heterogeneous](#)

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Heterogeneity

From Wikipedia, the free encyclopedia
 (Redirected from [Heterogeneous](#))

Heterogeneous is an adjective used to describe an object or system consisting of multiple items having a large number of structural variations. It is the opposite of *homogeneous*, which means that an object or system consists of multiple identical items. [Matters of a quantum](#)

WIKIPEDIA
The Free Encyclopedia

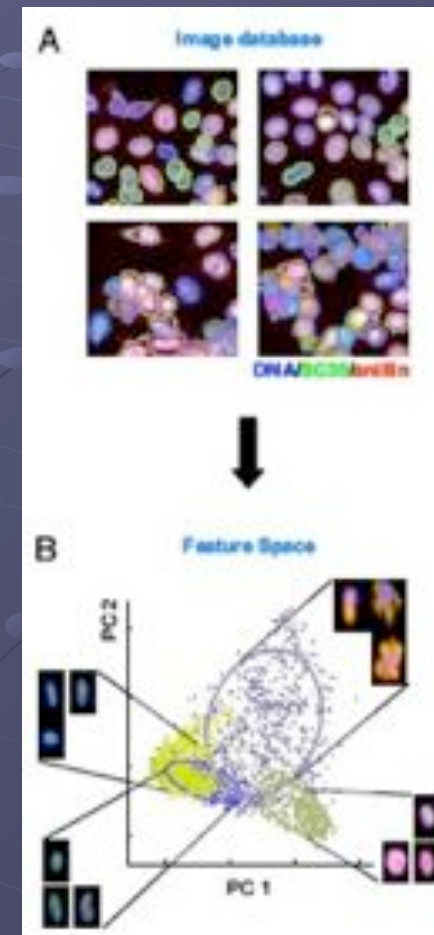


Cell Heterogeneity

- Genetic Heterogeneity
- Even genetically identical cells behave in different ways
- Non-Genetic Heterogeneity, sources:
 - protein expression
 - mRNA expression
 - Chromosomal abnormalities
 - Phenotypic response to stimuli

“the variation in cell behavior is far greater than previously recognized.”
(Gascoigne and Taylor, 2008)

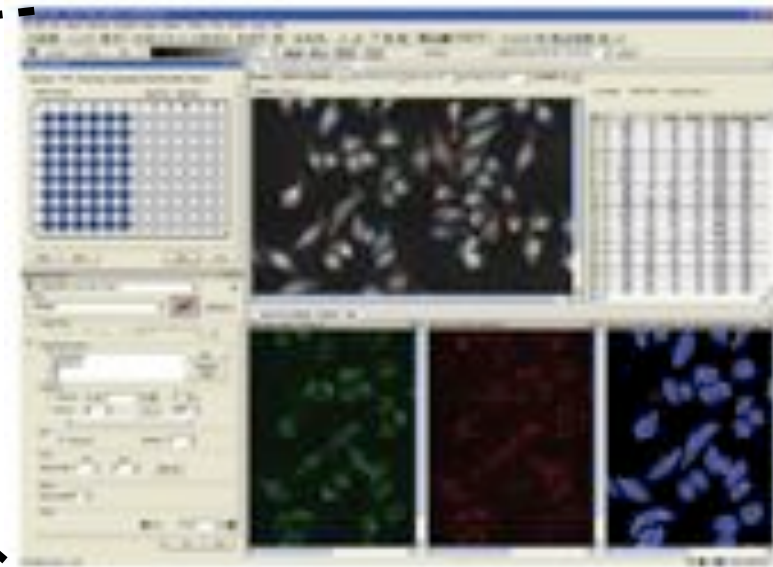
“*biology at the single-cell level sharply diverges from expectations*”
(Levsky and Singer, 2003)



Slack, et al., 2008

High-throughput Automated Microscopy Platform

Quantify cell population Adaptability from single-cell sampling



Cells - Breast Cancer Cell Panel (ICBP45)

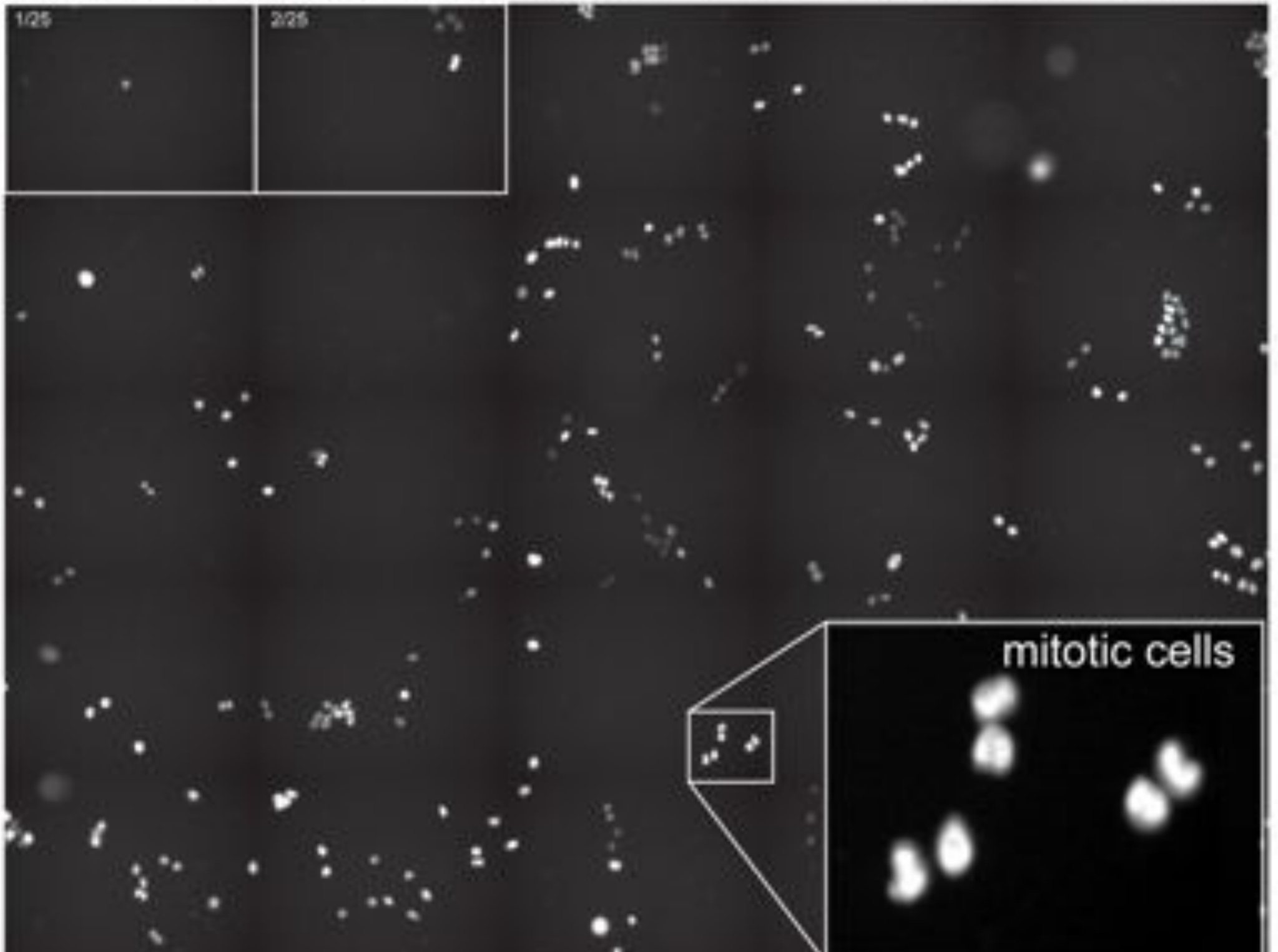
mEs stimulus

Mitogens (growth factors)
Nutrients (glucose, amino acids)
Other (insulin, oxygen)
Drug treatment

Phenotype traits

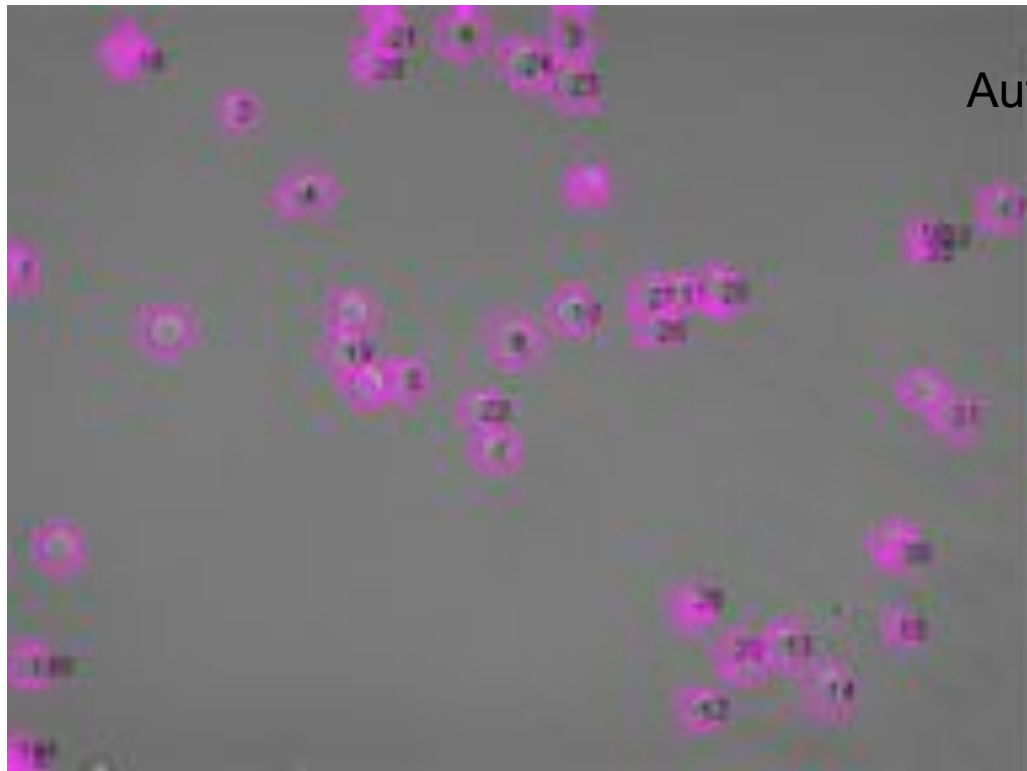
single cell distributions/spatial information
Proliferation (time to cell division)
Death (apoptosis)
Metabolism (glucose uptake)
Motility (velocity, angle distribution)

5X5 montage of adjacent images acquired using a 20X objective



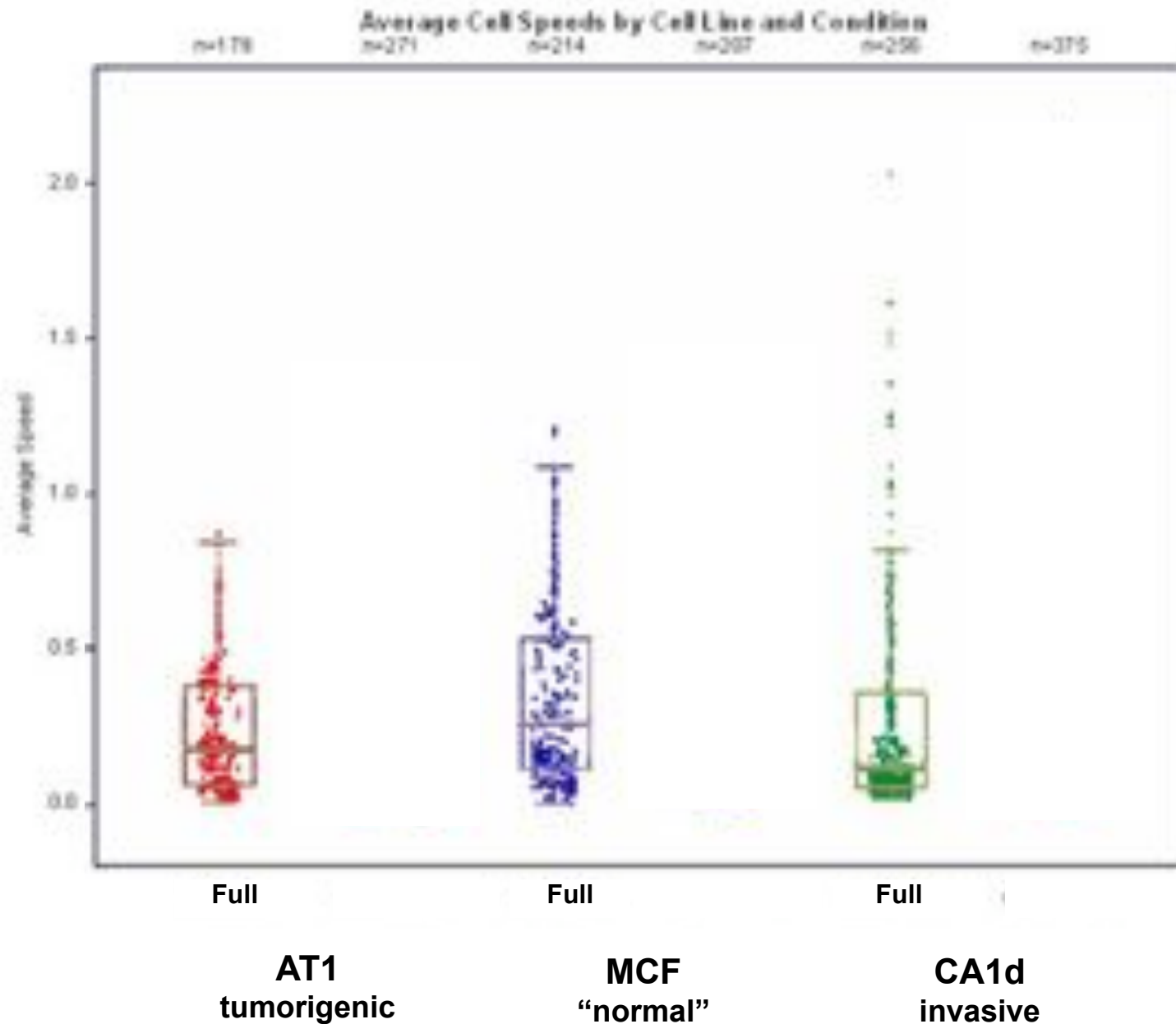
Automated Single Cell Tracking

Cell Lines	6	MCF, AT1, CA1d, HT-1080, A431, CAFTD
ECM	6	Ln-332, FN, Col, bLG4, LG3, Matrigel
Conditions	4	+/- serum, +/- Matrigel
# Movies	800	4,000 hrs
# Pictures	75,000	
Space Required	668 Gb	Raw images + stacks + tracks
# Cells tracked	7,300	
# x,y coordinates	454,000	

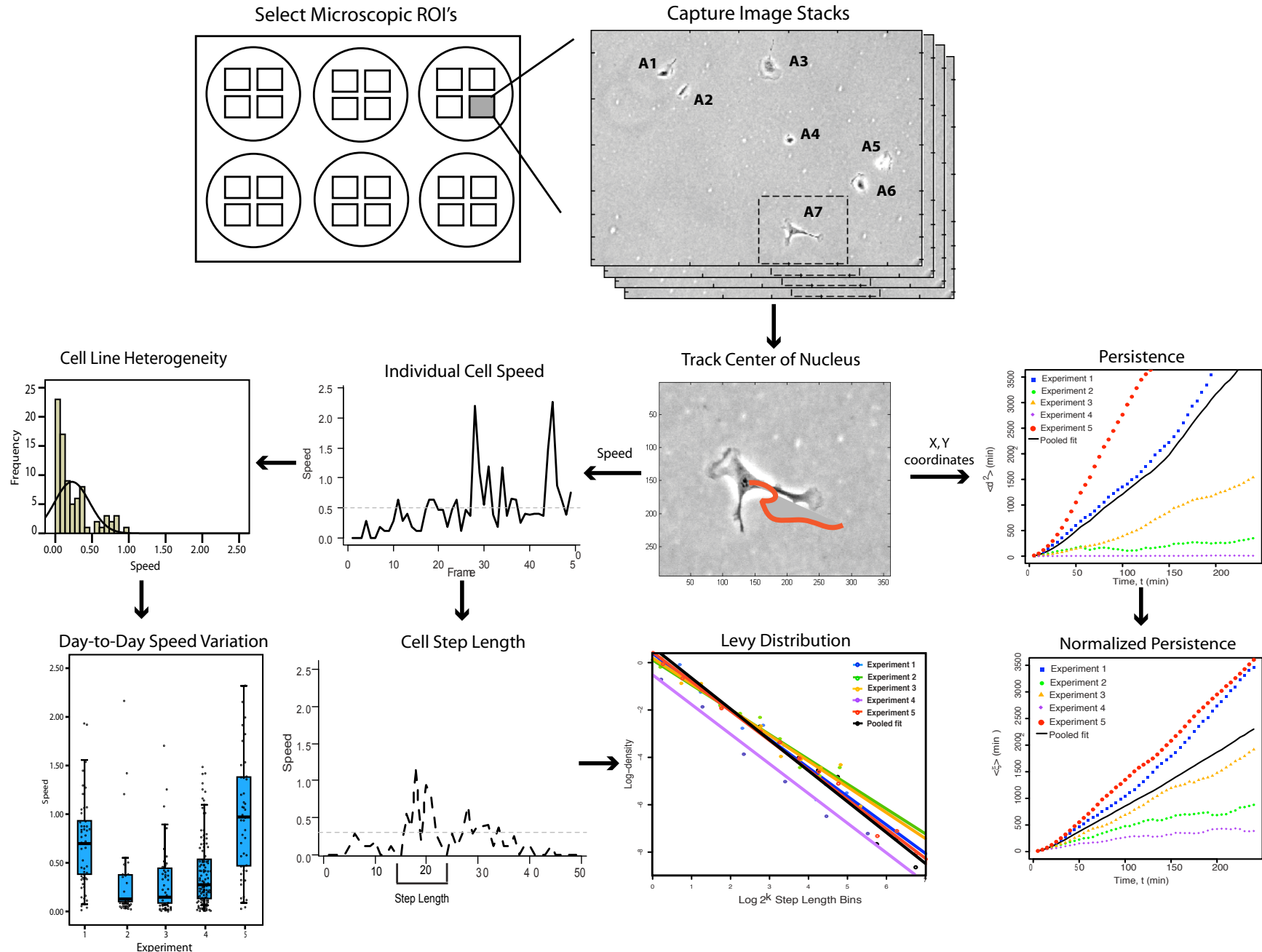


Automated Tracks

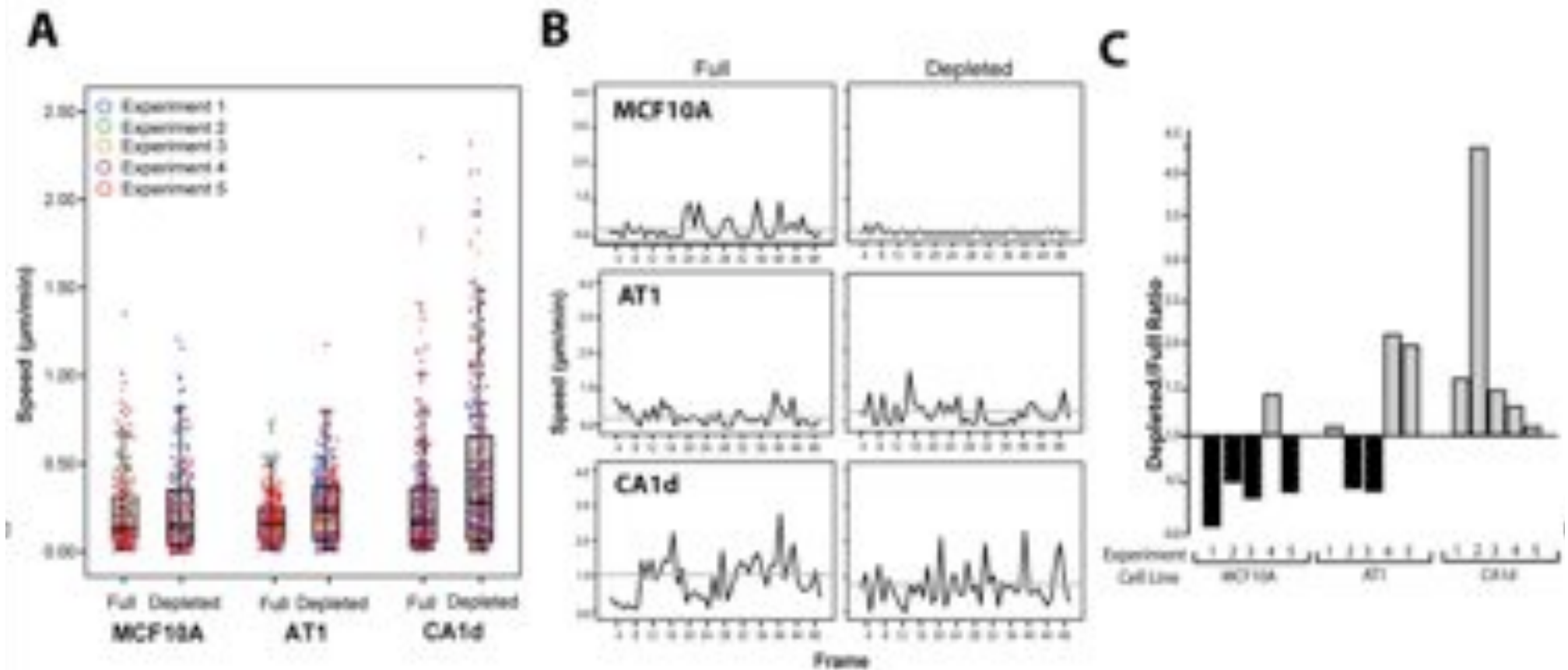
Evidence of Heterogeneity with Respect to Motility from Single-Cell Measurements



Quantifying Cell Heterogeneity with Respect to Motility



Heterogeneity of Motility within Cell Lines: Impact of mE Perturbations

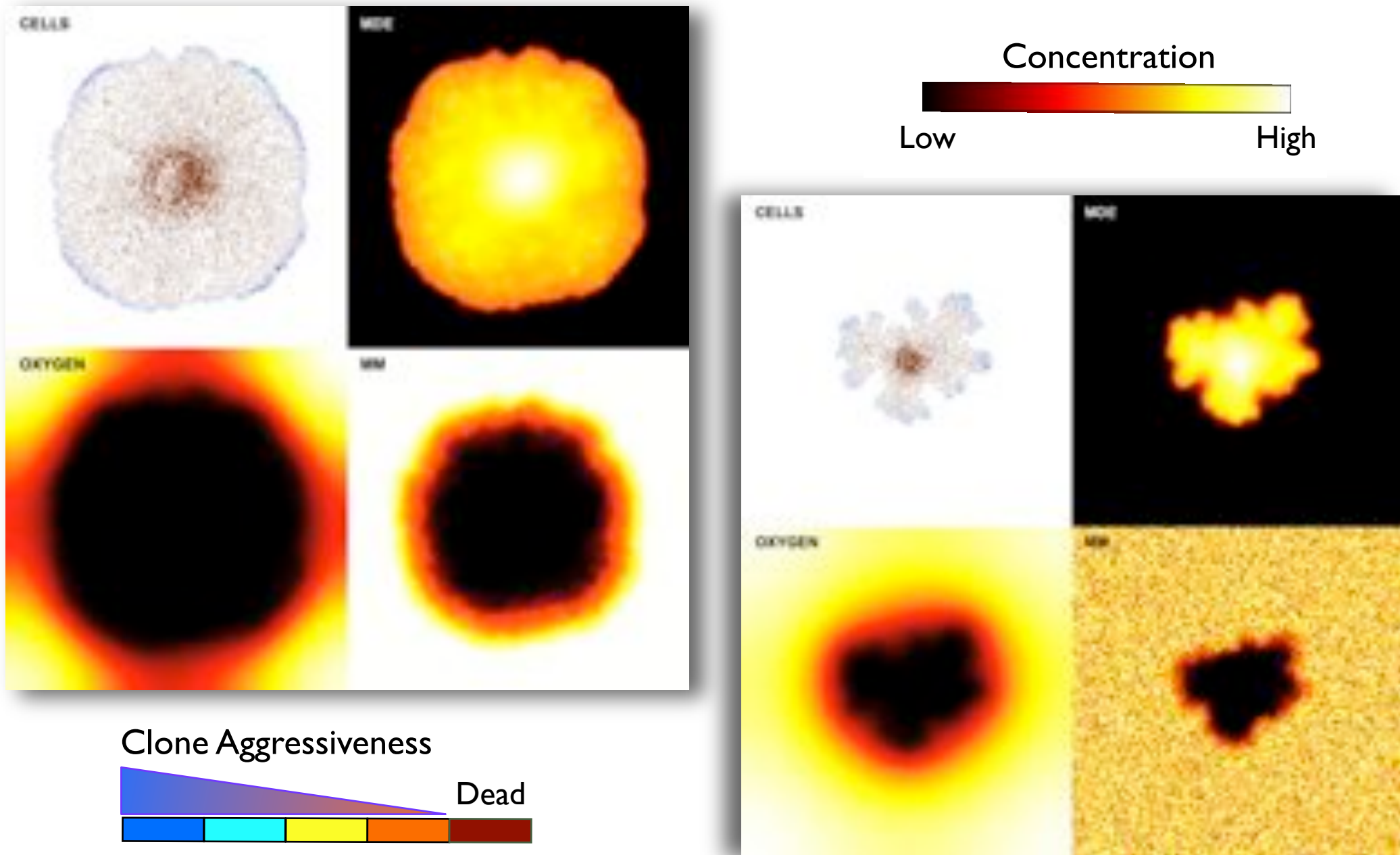


Trait Variability of Cancer Cells Quantified by High-Content Automated Microscopy of Single Cells

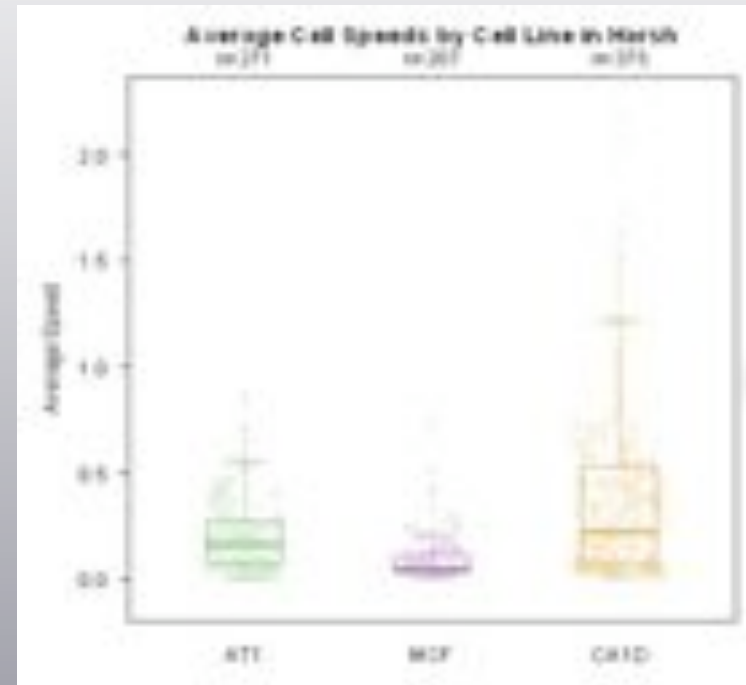
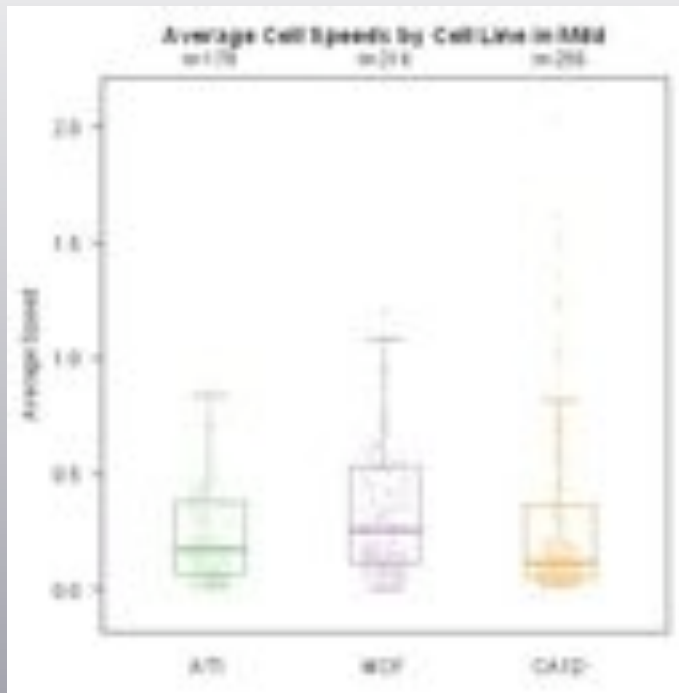
Vito Quaranta^{1,2,#}, Darren R. Tyson^{1,2}, Shawn P. Garbett²,
Brandy Weidow^{1,2}, Mark P. Harris¹, Walter Georgescu^{2,3}

Methods in Enzymology, vol.4xx, Computer Methods B, 2009 (or 2010)

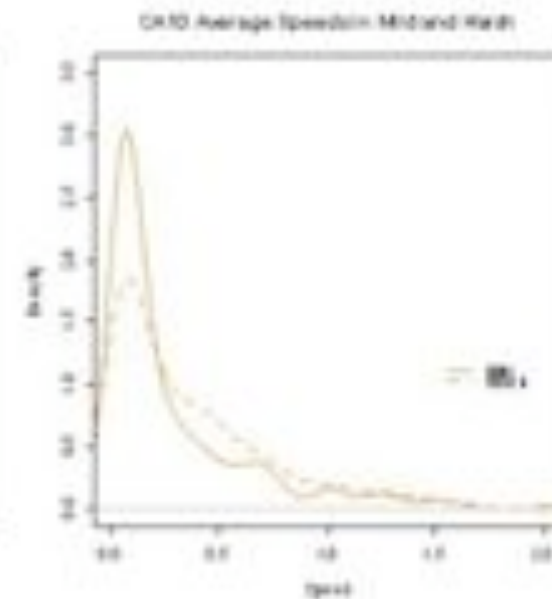
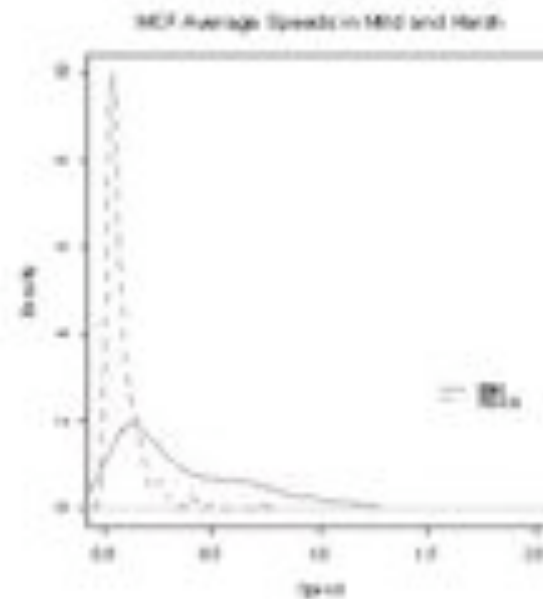
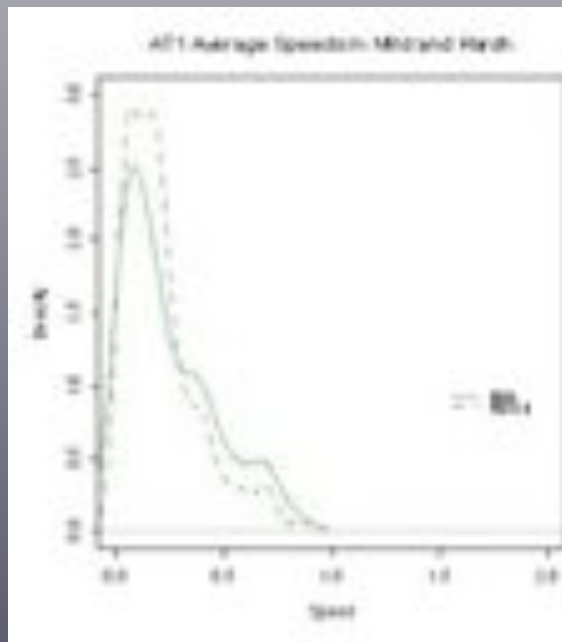
Theoretical Simulations of Tumor Progression: Impact of Matrix Composition on Morphology and Clonal Selection



Cell Motility Distribution Data



Response to
Harsh mE
Preliminary Data
by Mark Harris



Integration of Cancer Progression Variables in the Hybrid Discrete-Continuous Model

Continuous equations

<p>rate of change of matrix degrading enzyme</p> $\frac{\partial m}{\partial t}$	<p>diffusion of MDE</p> $D_m \nabla^2 m$	<p>decay of MDE</p> $- \lambda m$	<p>production of MDE by Cells</p> $+ \mu N_{i,j}$	<p>Matrix Degrading Enzymes</p>
<p>rate of change of Matrix Macromolecule</p> $\frac{\partial f}{\partial t}$	<p>degradation of MM by MDE</p> $= - \delta m f$			<p>Matrix Macromolecules</p>
<p>rate of change of oxygen</p> $\frac{\partial c}{\partial t}$	<p>diffusion of oxygen</p> $D_c \nabla^2 c$	<p>Consumption of oxygen by tumour cells</p> $- \gamma N_{i,j} c$	<p>production of oxygen by MM</p> $+ \beta f$	<p>Oxygen</p>

Discrete tumour cell equation

$$n_{i,j}^{q+1} = n_{i,j}^q P_0 + n_{i+1,j}^q P_1 + n_{i-1,j}^q P_2 + n_{i,j+1}^q P_3 + n_{i,j-1}^q P_4,$$

with $x=ih$, $y=jh$ and $t=qk$