

Is the Cell *Really* a Machine?

Daniel J. Nicholson



The Hallmarks of Cancer

Douglas Hanahan* and Robert A. Weinberg†

*Department of Biochemistry and Biophysics and
Hormone Research Institute

University of California at San Francisco
San Francisco, California 94143

†Whitehead Institute for Biomedical Research and
Department of Biology
Massachusetts Institute of Technology
Cambridge, Massachusetts 02142

After a quarter century of rapid advances, cancer research has generated a rich and complex body of knowledge, revealing cancer to be a disease involving dynamic changes in the genome. The foundation has been set in the discovery of mutations that produce oncogenes with dominant gain of function and tumor suppressor genes with recessive loss of function; both classes of cancer genes have been identified through their alteration in human and animal cancer cells and by their elicitation of cancer phenotypes in experimental models (Bishop and Weinberg, 1996).

Some would argue that the search for the origin and treatment of this disease will continue over the next quarter century in much the same manner as it has in the recent past, by adding further layers of complexity

Review

evolve progressively from normalcy via a series of pre-malignant states into invasive cancers (Foulds, 1954).

These observations have been rendered more concrete by a large body of work indicating that the genomes of tumor cells are invariably altered at multiple sites, having suffered disruption through lesions as subtle as point mutations and as obvious as changes in chromosome complement (e.g., Kinzler and Vogelstein, 1996). Transformation of cultured cells is itself a multistep process: rodent cells require at least two introduced genetic changes before they acquire tumorigenic competence, while their human counterparts are more difficult to transform (Hahn et al., 1999). Transgenic models of tumorigenesis have repeatedly supported the conclusion that tumorigenesis in mice involves multiple rate-limiting steps (Bergers et al., 1998; see *Oncogene*, 1999, R. DePinho and T. E. Jacks, volume 18[38], pp. 5248–5362). Taken together, observations of human cancers and animal models argue that tumor development proceeds via a process formally analogous to Darwinian evolution, in which a succession of genetic changes, each conferring one or another type of growth advantage, leads to the progressive conversion of normal human cells into cancer cells (Foulds, 1954; Nowell, 1976).

[HTML](#) The hallmarks of cancer

[D Hanahan, RA Weinberg - cell, 2000 - cell.com](#)

After a quarter century of rapid advances, **cancer** research has generated a rich and complex body of knowledge, revealing **cancer** to be a disease involving dynamic changes in the ...

☆ Save [Cite](#) Cited by 39272 [Related articles](#) [All 82 versions](#)

Hallmarks of Cancer: The Next Generation

Douglas Hanahan^{1,2,*} and Robert A. Weinberg^{3,*}

¹The Swiss Institute for Experimental Cancer Research (ISREC), School of Life Sciences, EPFL, Lausanne CH-1015, Switzerland

²The Department of Biochemistry & Biophysics, UCSF, San Francisco, CA 94158, USA

³Whitehead Institute for Biomedical Research, Ludwig/MIT Center for Molecular Oncology, and MIT Department of Biology, Cambridge, MA 02142, USA

*Correspondence: dh@epfl.ch (D.H.), weinberg@wi.mit.edu (R.A.W.)

DOI 10.1016/j.cell.2011.02.013

The hallmarks of cancer comprise six biological capabilities acquired during the multistep development of human tumors. The hallmarks constitute an organizing principle for rationalizing the complexities of neoplastic disease. They include sustaining proliferative signaling, evading growth suppressors, resisting cell death, enabling replicative immortality, inducing angiogenesis, and activating invasion and metastasis. Underlying these hallmarks are genome instability, which generates the genetic diversity that expedites their acquisition, and inflammation, which fosters multiple hallmark functions. Conceptual progress in the last decade has added two emerging hallmarks of potential generality to this list—reprogramming of energy metabolism and evading immune destruction. In addition to cancer cells, tumors exhibit another dimension of complexity: they contain a repertoire of recruited, ostensibly normal cells that contribute to the acquisition of hallmark traits by creating the “tumor microenvironment.” Recognition of the widespread applicability of these concepts will increasingly affect the development of new means to treat human cancer.

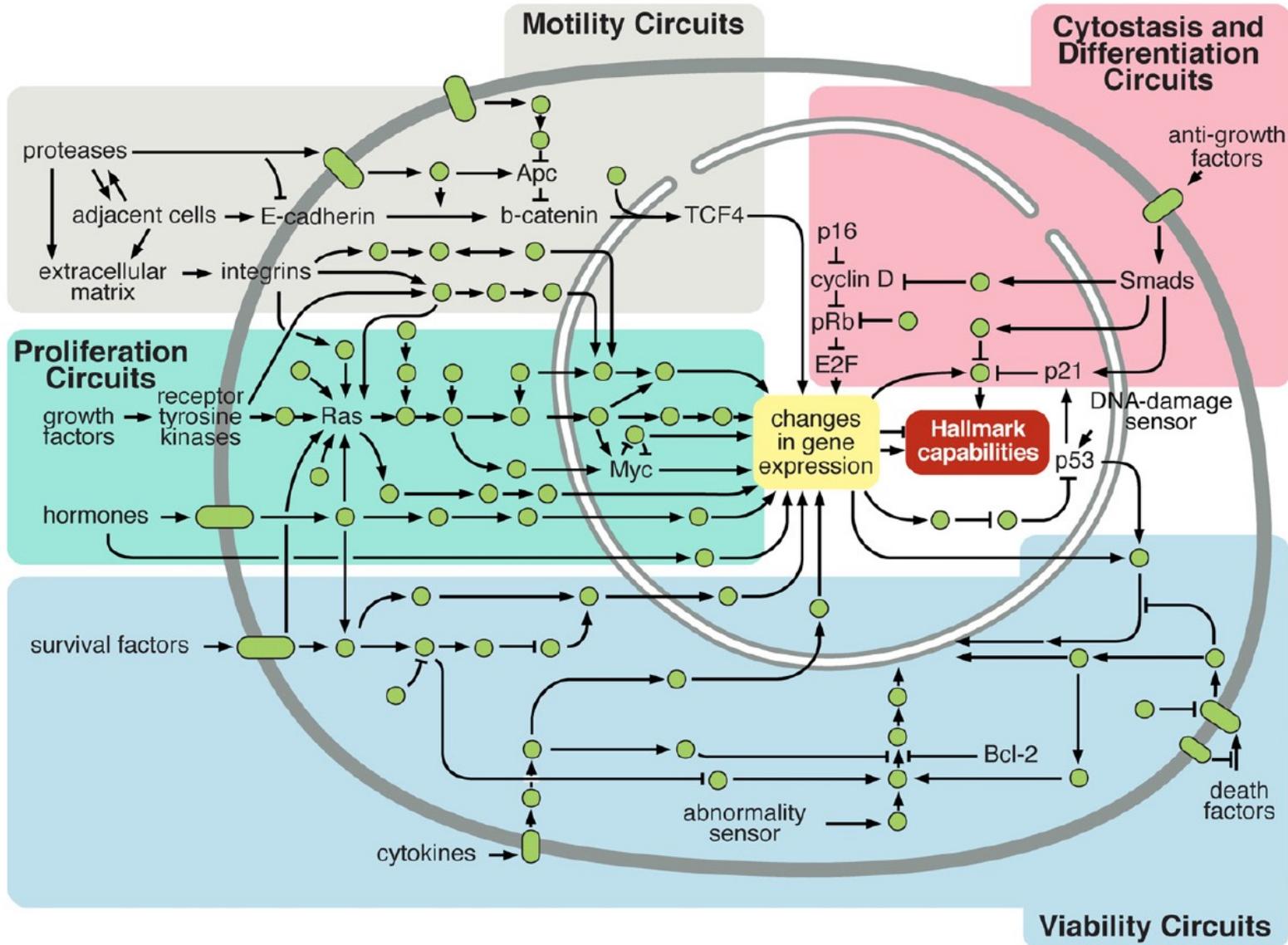
[HTML] [Hallmarks of cancer: the next generation](#)

D Hanahan, [RA Weinberg](#) - cell, 2011 - Elsevier

The **hallmarks** of **cancer** comprise six biological capabilities acquired during the multistep development of human tumors. The **hallmarks** constitute an organizing principle for ...

☆ Save [Cite](#) Cited by 63152 [Related articles](#) [All 107 versions](#)

Hallmarks of Cancer II (2011)



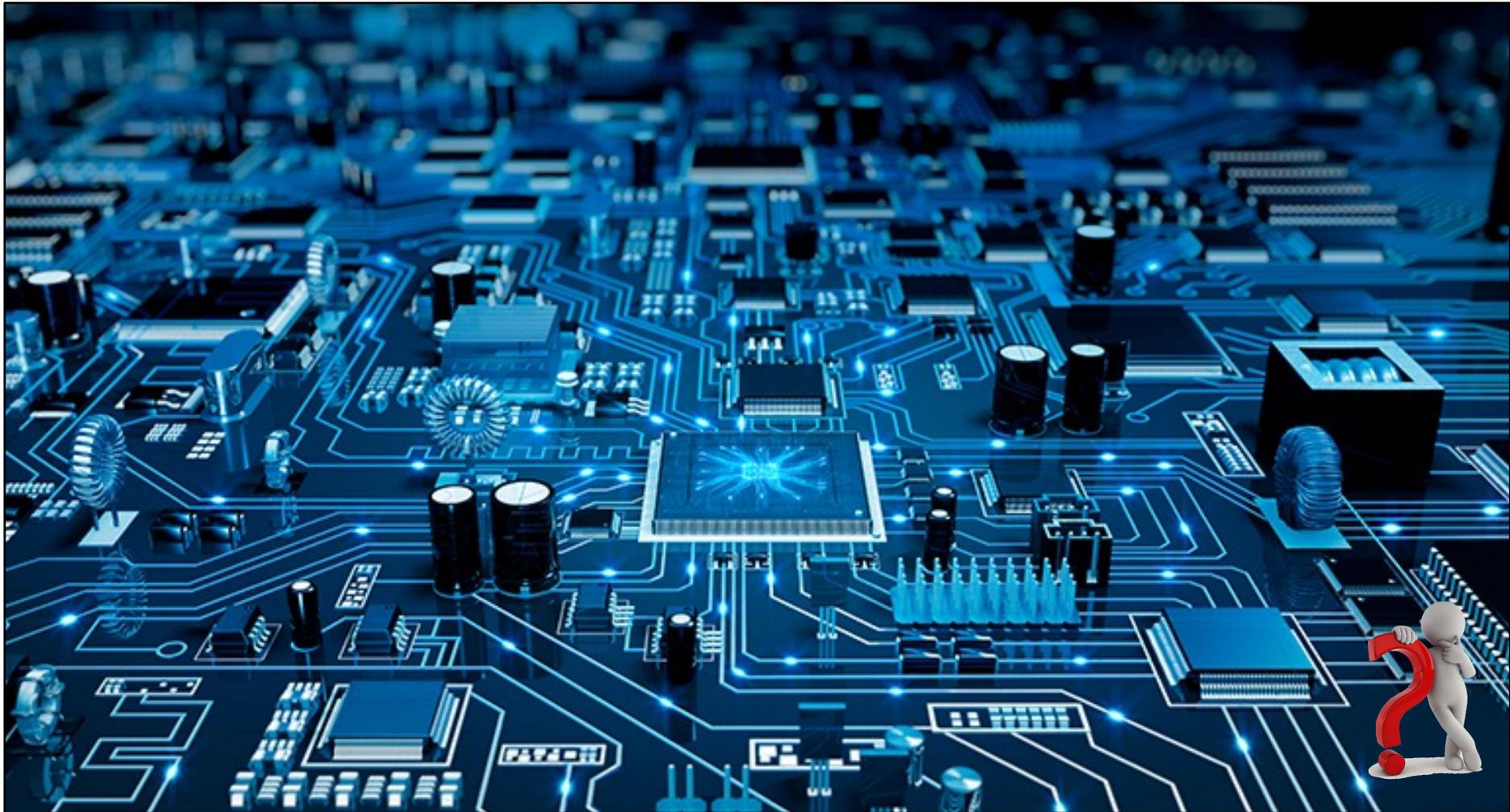
'The Integrated Circuit of the Cell'

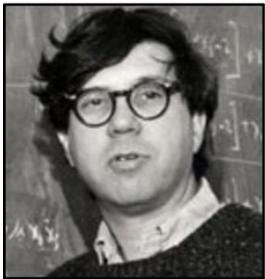
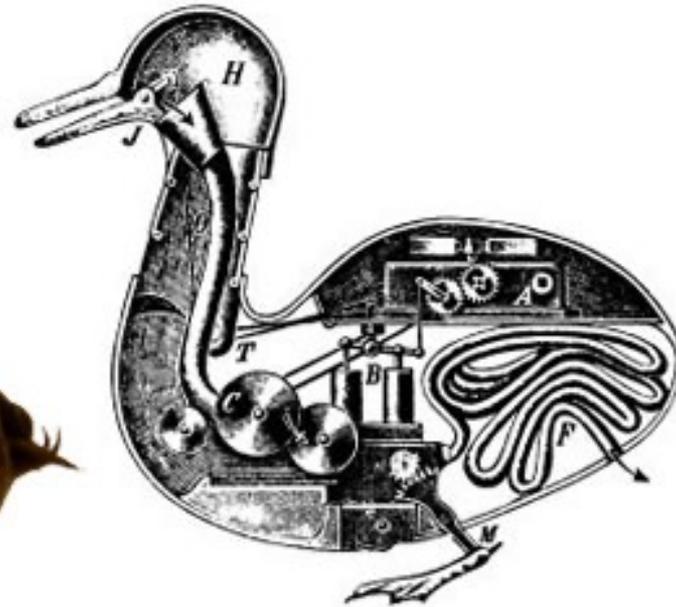
“Progress in dissecting signaling pathways has begun to lay out a circuitry that will likely mimic electronic integrated circuits in complexity and finesse, where transistors are replaced by proteins (e.g., kinases and phosphatases) and the electrons by phosphates and lipids. [...]

Two decades from now, having fully charted the wiring diagrams of every cellular signaling pathway, it will be possible to lay out the complete ‘integrated circuit of the cell’ upon its current outline.

We will then be able to apply the tools of mathematical modeling to explain how specific genetic lesions serve to reprogram this integrated circuit in each of the constituent cell types so as to manifest cancer.” (Hanahan & Weinberg 2000)

'The Integrated Circuit of the Cell'

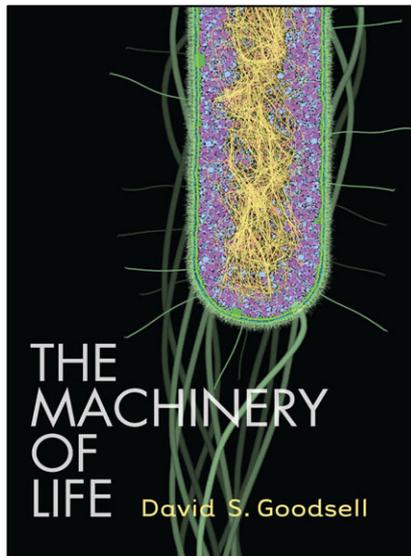




“Present day biology is the realization of the famous metaphor of the organism as a *bête-machine* elaborated by Descartes in Part V of the *Discours*” (Lewontin 2009)



“We animals are the most complicated and perfectly-designed pieces of machinery in the known universe” (**Dawkins** 1976)

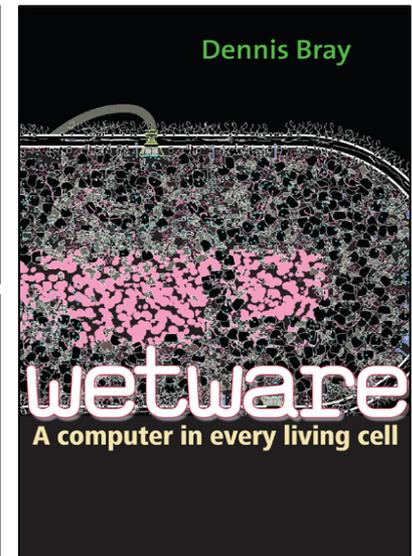


Cell, Vol. 92, 291–294, February 6, 1998, Copyright ©1998 by Cell Press

The Cell as a Collection of Protein Machines: Preparing the Next Generation of Molecular Biologists

Biological machines: from mills to molecules

Marco Piccolino



Cell, Vol. 68, 415–420, February 7, 1992, Copyright © 1992 by Cell Press

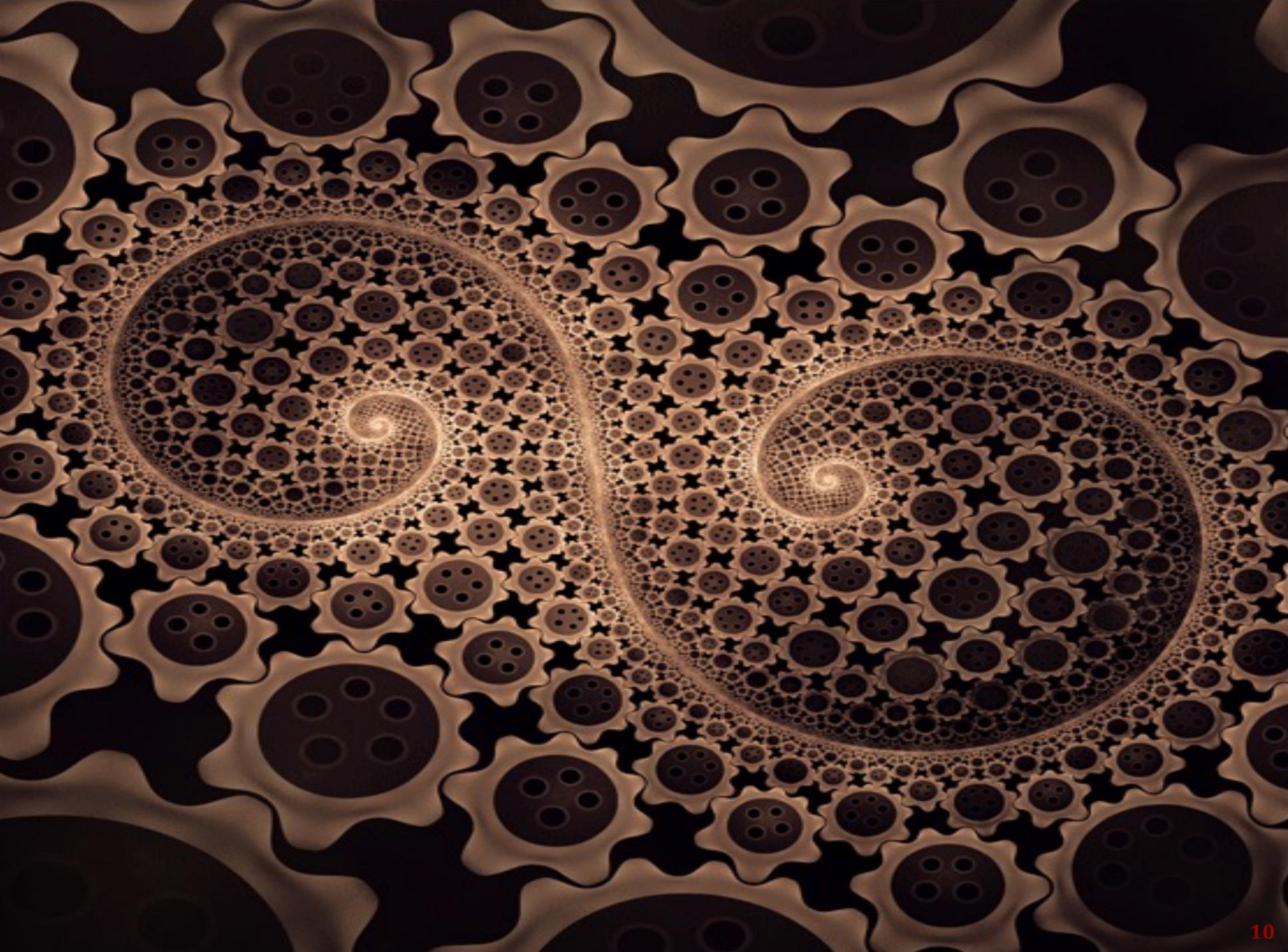
Unscrambling the Puzzle of Biological Machines: The Importance of the Details

Structural biology of cellular machines

Wah Chiu¹, Matthew L. Baker¹ and Steven C. Almo²

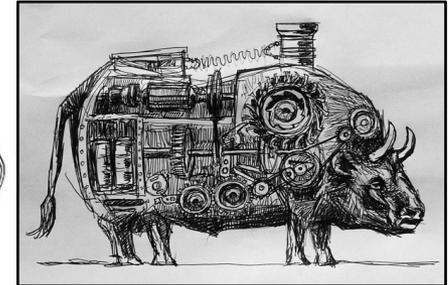
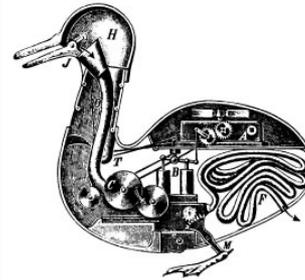
¹National Center for Macromolecular Imaging and Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, TX 77030, USA

²Department of Biochemistry, Albert Einstein College of Medicine, Bronx, NY 10461, USA

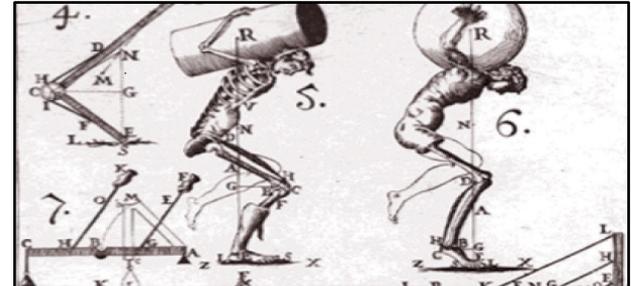


Mechanicism as a Philosophy of Nature

Machine Ontology



Reductionism



Determinism



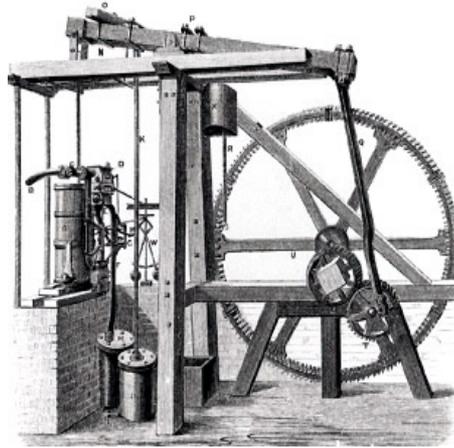
The Development of the Machine Conception of the Organism

17th Century



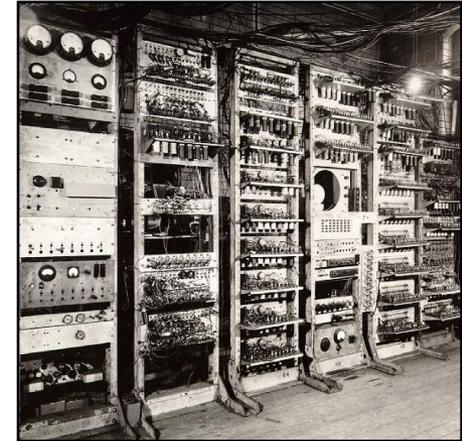
Descartes

18th Century



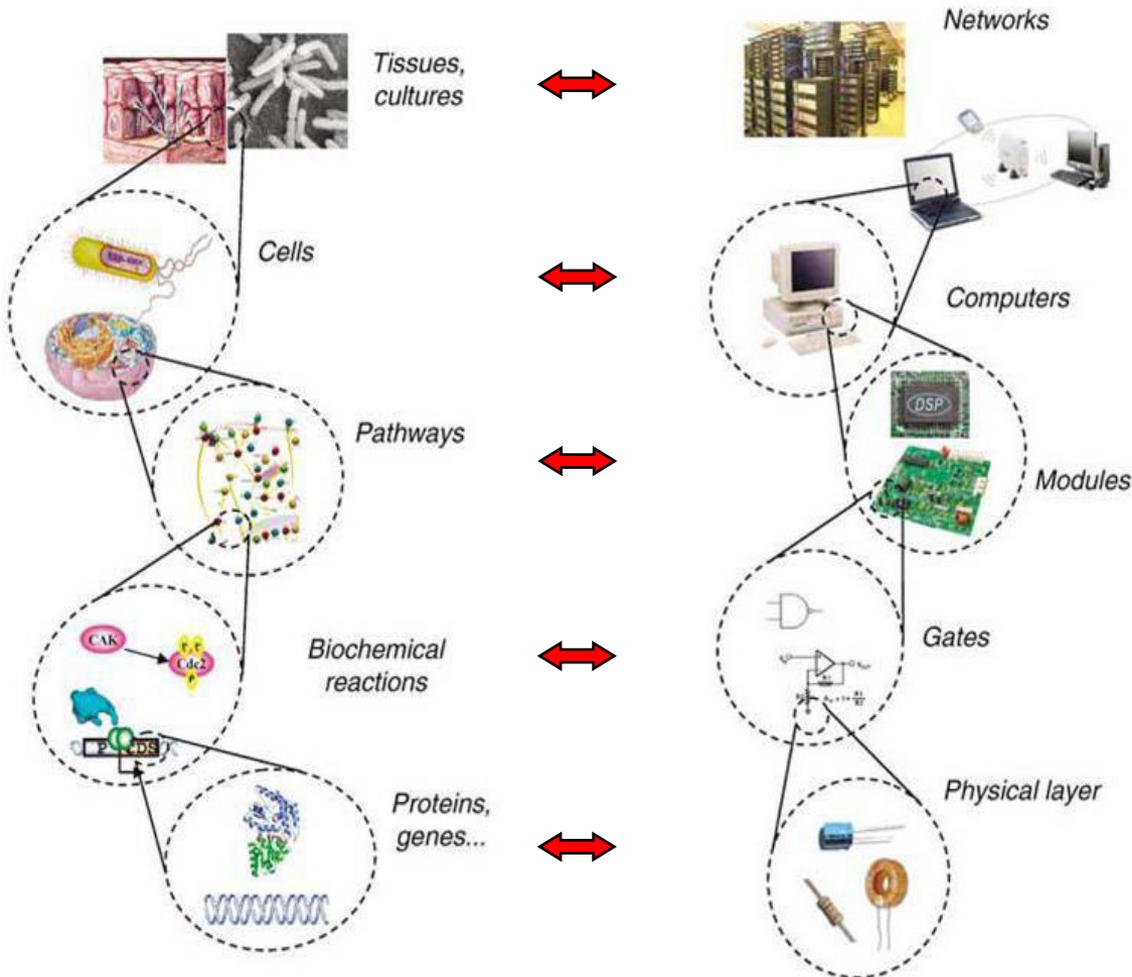
Lavoisier

20th Century



Jacob

“The analogy between an organism and a machine holds true to a remarkable extent at all levels at which it is investigated” (Changeux 1965)



© Friedrich A. Lohmüller, 2010



Mechanicism in Molecular Biology

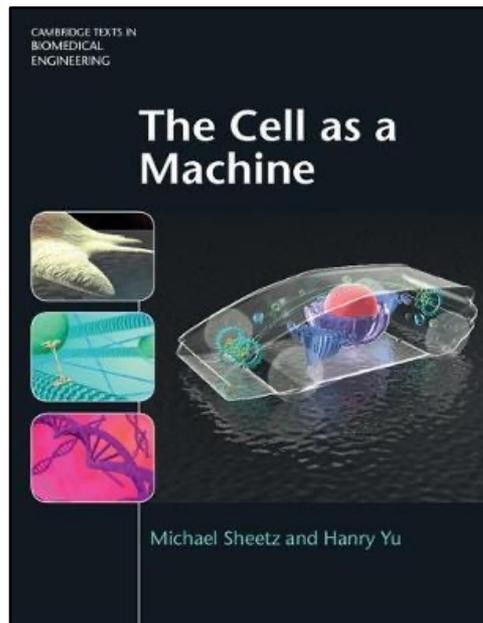
- Molecular biology is committed to the basic tenets of mechanicism:
 - Machine ontology

“By the microscopic clockwork function that establishes between DNA and protein, this system is thoroughly Cartesian: **the cell is indeed a machine**” (Monod 1972)
 - **Reductionism**

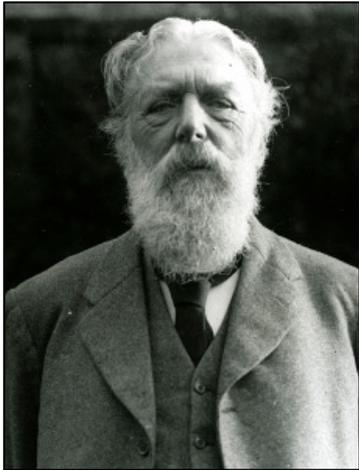
“The ultimate aim of the modern movement in biology is to explain all of biology in terms of physics and chemistry” (Crick 1966)
 - **Determinism**

“If I had the complete sequence of DNA of an organism and a large enough computer, I would be able to compute the organism” (Brenner, in Lewontin 2000)

So What is Wrong with Machine Conception of the Cell?

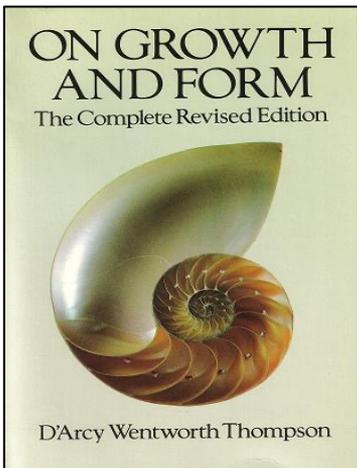


Cells \neq Machines: The Argument from Scale



“The **world** where bacillus lives, gravitation is forgotten, and the viscosity of the liquid, the resistance defined by Stokes’ law, the molecular shocks of the Brownian movement, also the electric charges of the ionized medium, make up the physical environment and have their potent and immediate influence on the organism.

The predominant factors are no longer those of our scale; we have come to the edge of a **world** of which we have no experience, and where all our preconceptions must be recast” (Thompson 1917)



Cells \neq Machines:

The Argument from Scale

- Differences of **size** and in the **physical scale** in which organisms live are of overwhelming importance in **determining their structure and behaviour**
- By virtue of **their microscopic size**, cells and their molecular components are subject to very different **physical forces** than macroscopic organisms
- Microscopic and macroscopic organisms inhabit different '**worlds**'. Whereas the **macroscopic world** is ruled by **gravity** and **inertia**, the **microscopic world** is dominated by **Brownian motion** and **diffusion**
- Our **intuition**, based as it is on our **experience** of the **macroscopic world**, **fails** when judging the **adaptive problems** that **cells** have to overcome

Cells ≠ Machines: The Argument from Scale

- Thus, we should be **extremely sceptical** of **analogies** that seek to explain **microscopic** entities by appealing to the properties of **macroscopic** ones
- Yet this is **precisely** what the **metaphorical** appeals to **machines** in the explanation of **cellular phenomena** attempt to do
- We draw on **machines** to explain features of **cells** because they are **familiar** and **intuitively intelligible** macroscopic objects of our **everyday experience**
- But if **machines** *were* the **size** of **cells** they would not be able to **function**, as their **physical environment** would be entirely different. We should avoid **distorting** the reality of cells by conceiving them as **machines**

The Rise of the (Molecular) Machines



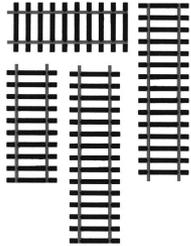
Cell, Vol. 92, 291–294, February 6, 1998, Copyright ©1998 by Cell Press

The Cell as a Collection of Protein Machines: Preparing the Next Generation of Molecular Biologists

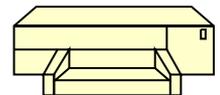
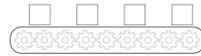
Bruce Alberts
President, National Academy of Sciences
2101 Constitution Avenue NW
Washington, D.C. 20418
Professor, Department of Biochemistry and Biophysics
University of California, San Francisco
San Francisco, California 94143

Subcellular assembly	Sample of 'molecular machine' language	Source reference
<i>Ribosome</i>	“probably the most sophisticated machine ever made”	Garrett 1999
<i>Proteasome</i>	“a molecular machine designed for controlled proteolysis”	Voges et al. 1999
<i>Bacteriorhodopsin</i>	“a deceptively simple molecular machine ”	Kühlbrandt 2000
<i>Apoptosome</i>	“a seven-spoked death machine ”	Salvesen et al. 2002
<i>Glideosome</i>	“a molecular machine powering motility”	Keeley et al. 2003
<i>Spliceosome</i>	“the most complex macromolecular machine known”	Nilsen 2003
<i>Blood clotting system</i>	“a typical example of a molecular machine ”	Spronk et al. 2003
<i>Condensin</i>	“the key molecular machine of chromosome condensation”	Strunnikov 2003
<i>Photosynthetic system</i>	“the most elaborate nanoscale biological machine in nature”	Imahori 2004
<i>Bacterial flagellum</i>	“an exquisitely engineered chemi-osmotic nanomachine ”	Pallen et al. 2005
<i>Myosin filament</i>	“a complicated machine of many moving parts”	Ohki et al. 2006
<i>RNA degradasome</i>	“a supramolecular machine dedicated to RNA processing”	Marcaida et al. 2006
<i>Cyclosome</i>	“a machine designed to destroy”	Peters 2006
<i>RNA Polymerase</i>	“a multifunctional molecular machine ”	Haag et al. 2007

The Diversity of Molecular Machines

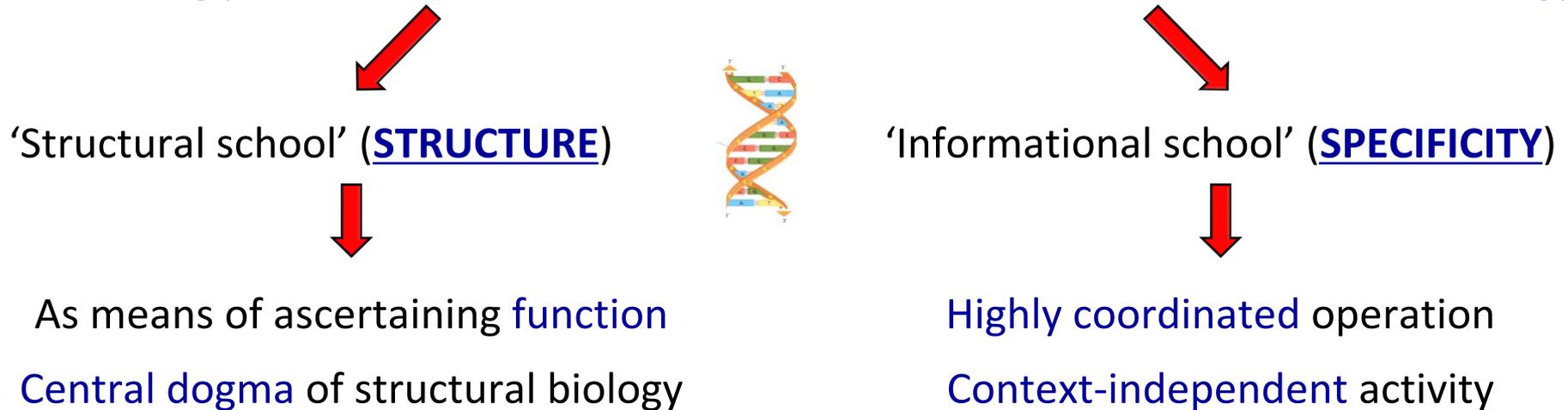


Maromolecular Assembly	Machine Analogy
<i>Cilium / Flagellum</i>	Propeller
<i>ATP synthase</i>	Generator
<i>Ribosome</i>	Factory assembly line
<i>Ion channel / Nuclear pore</i>	Gate / key / pass
<i>Actin filament network</i>	Train tracks
<i>Polymerase</i>	Copy machine
<i>Ligase</i>	Chain coupler
<i>Polymerase</i>	Copy machine
<i>Spliceosome</i>	Film editing machine
<i>Protein sorting mechanism</i>	Mail sorting machine
<i>Protease / proteasome</i>	Bulldozer / destroyer
<i>Magnetosome</i>	Compass



The Rationale of the Molecular Machine Concept

- Viewing proteins as molecular machines unifies two schools of molecular biology:



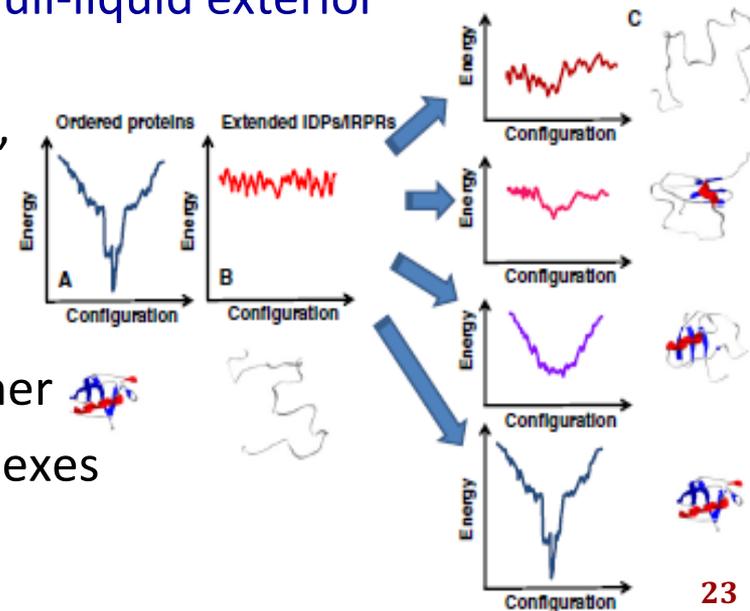
“Why do we call large protein assemblies underlying cell function protein *machines*? Precisely because, like the machines invented by humans to deal efficiently with the macroscopic world, these protein assemblies contain highly coordinated moving parts. Within each protein assembly, intermolecular collisions are not only restricted to a small set of possibilities, but reaction C depends on reaction B, which in turn depends on reaction A—just as it would in a machine” (Alberts 1998)

The Problem With the Molecular Machine Concept

- Due to their **tiny size**, macromolecular assemblies **cannot possibly** operate in the **orderly, reproducible manner** that is characteristic of machines
- In a **machine**, the **motions** of the various parts are **perfectly orchestrated**. For example, when a gear rotates, the shaft to which it is connected rotates in synchrony, a spring is compressed, a latch is released, etc.
- These movements are **purposeful, predictable**, and are always **precisely executed** in exactly the **same temporal sequence**
- In contrast, macromolecules are subject to **continuous Brownian motion**, which means that the **majority** of **conformational** changes they undergo are the result of 'random walks' that have **nothing to do** with their function

How the Molecular Machine Concept Overemphasizes Structural Rigidity

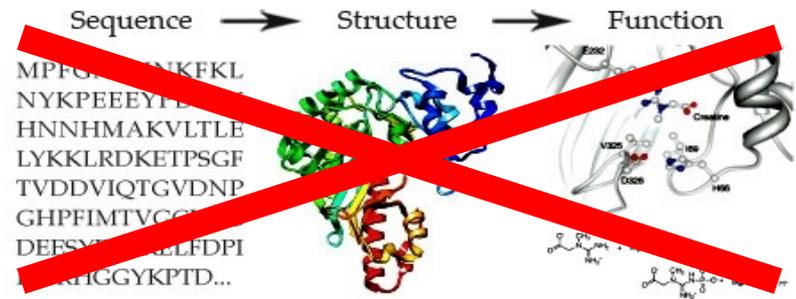
- By virtue of their **size**, proteins **cannot exhibit** the sort of **rigidity** and **specificity** that characterizes the **structure** and **operation** of **machines**
- In vivo, proteins behave more like **liquids** than solids; they are ‘**dense liquids**’ or ‘**melted solids**’ with a ‘**near-solid interior**’ and a ‘**full-liquid exterior**’
- Most proteins do not have a single conformation, but rather **stochastically sample** a suite of **possible configurations** depending on **context**
- Some proteins lack an ordered structure altogether (IDPs), forming **fluid, ever-flickering ‘fuzzy’** complexes



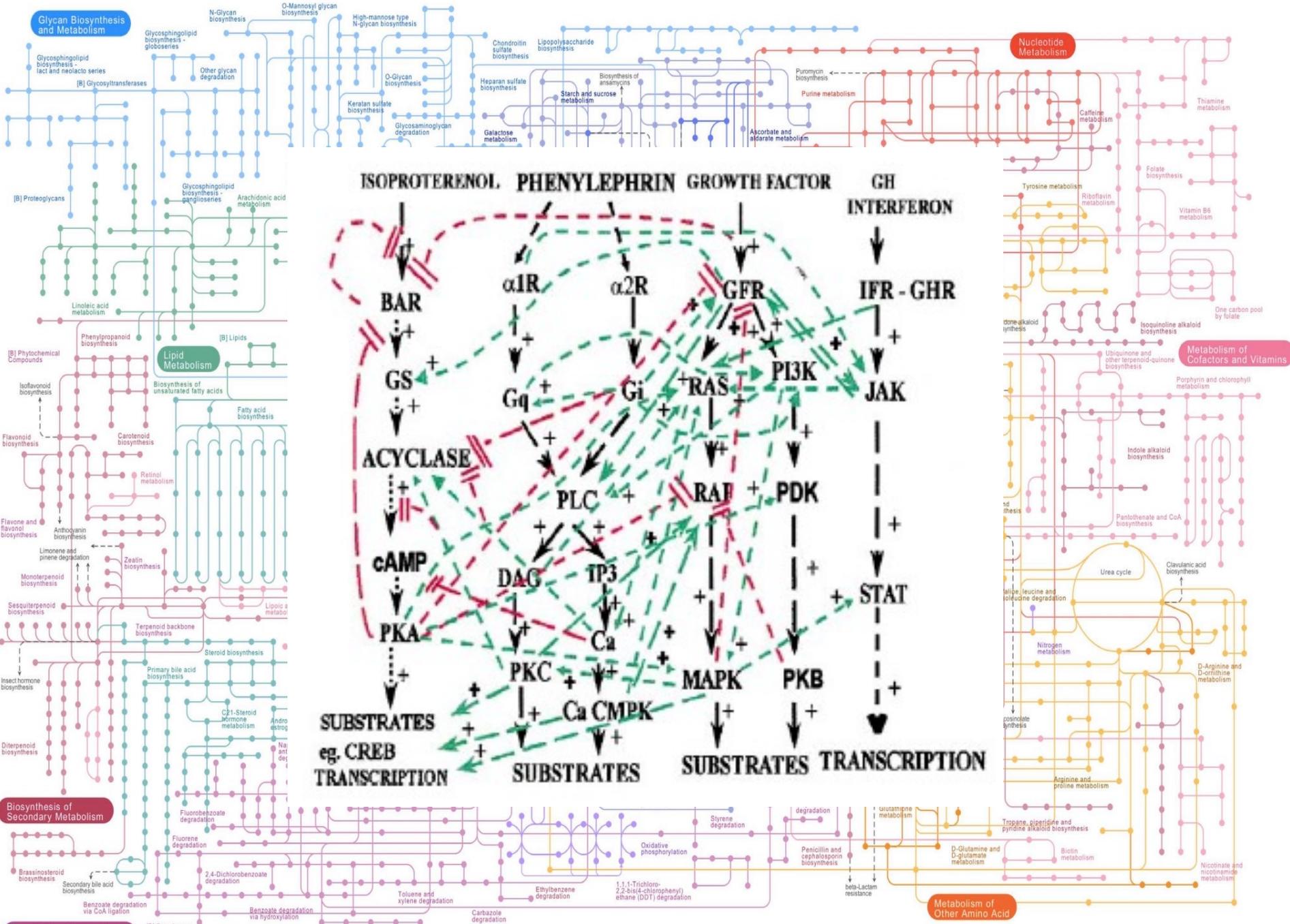
How the Molecular Machine Concept Overemphasizes Functional Specificity

- In proteins, structure does **not** unilaterally determine function. Proteins exhibit **behavioural repertoires**, ‘moonlighting’ according to the **needs** of the **cell**

- Most **protein-protein interactions** are **non-specific**. Interactions are **short** and caused by **stochastic** events. Associations are **transitory & contingent**



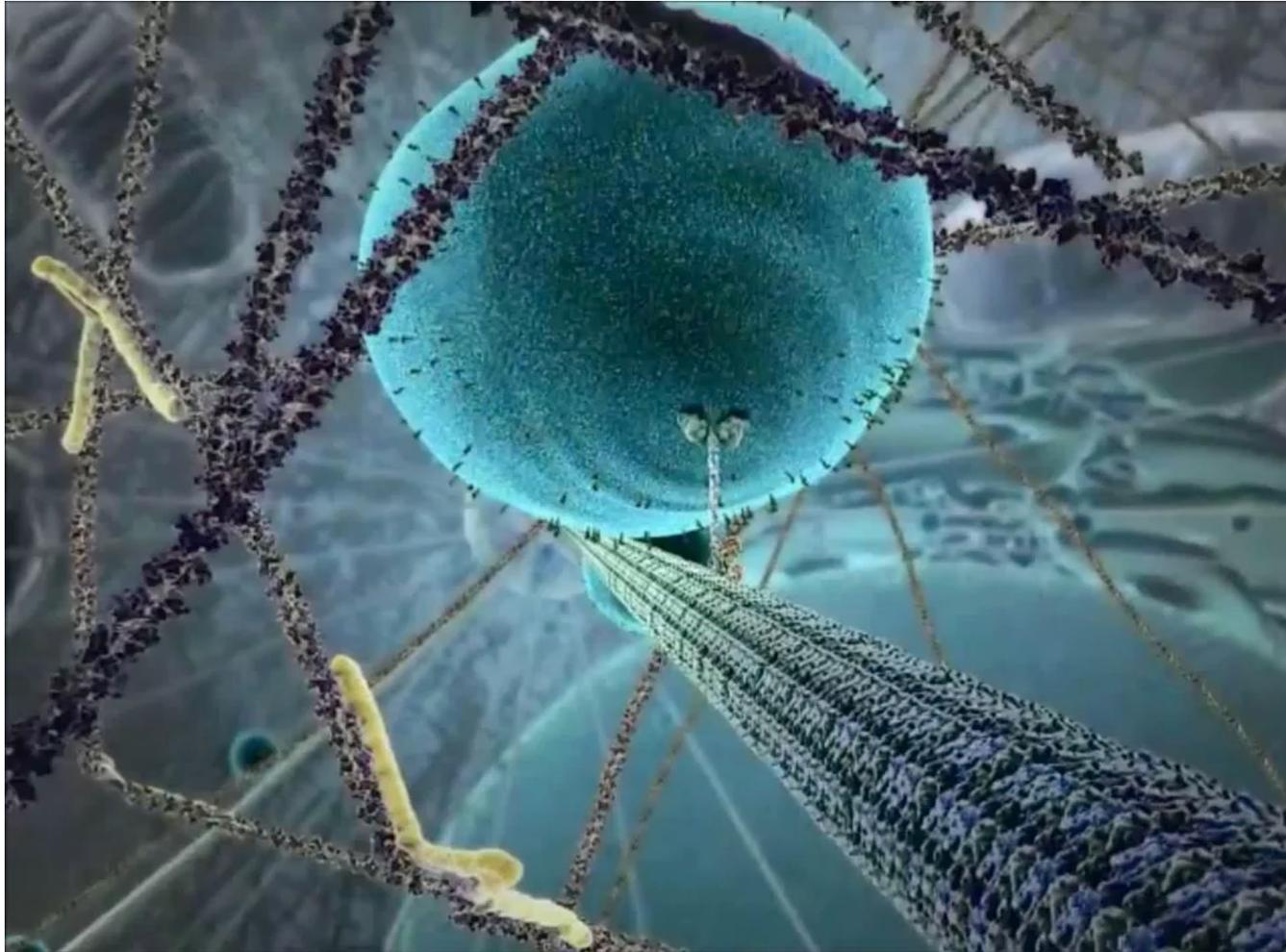
- Proteins exist in a **dynamic environment** and rely on **probabilistic collision** events with appropriate partners to **reliably perform** cellular functions
- This is all a consequence of the fact that, **by virtue of being so small**, most proteins are **constantly being knocked about** by stochastic forces



Molecular Motors: A Mechanicist Interpretation

- Molecular motors (e.g. kinesin, myosin) are viewed as ‘ingenious’ nano-machines, efficiently converting chemical energy into mechanical work
- It is argued that repetitive power strokes resulting from periodic conformational rearrangements driven by cycles of ATP hydrolysis move the protein forward
- Molecular motors move by ‘walking’ along the cytoskeleton. The ‘walking’ is enabled by the formation of dimers between motor domains (the ‘feet’) and microtubules or actin filaments (‘tracks’)

The Power-Stroke Model: A Well-Known Illustration



Problems with Power-Stroke Model: The Importance of Scale (Again)

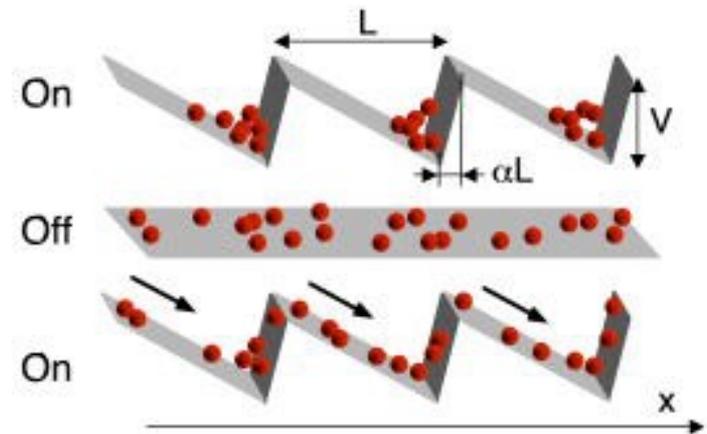
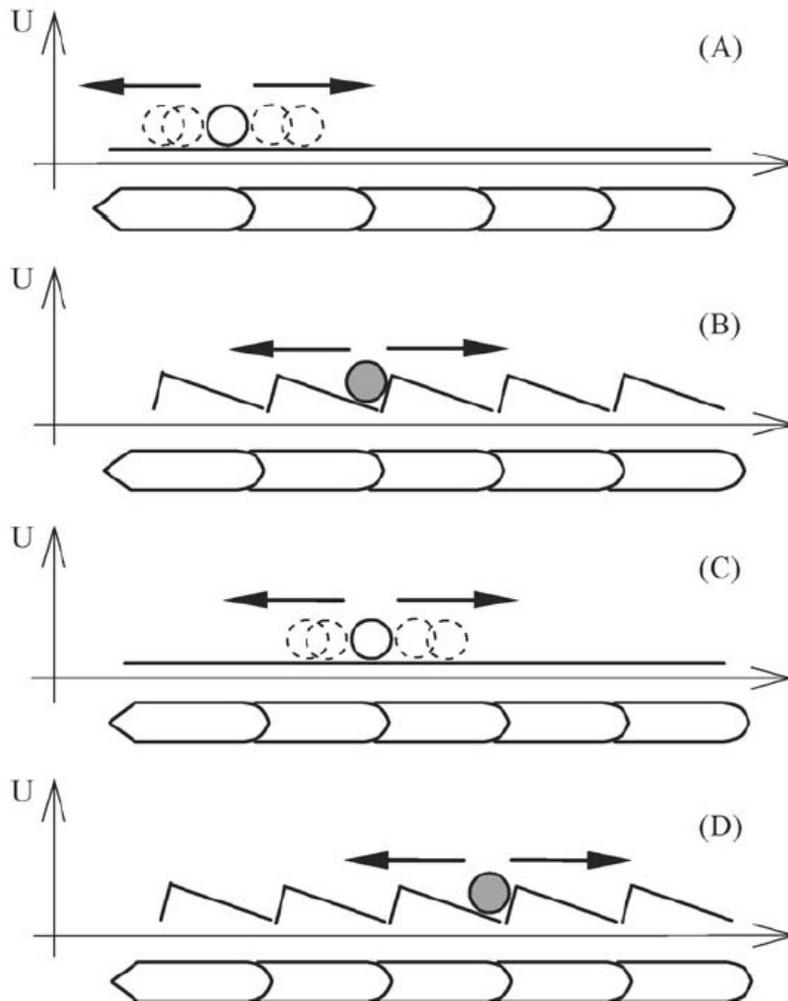
“For molecules, moving **deterministically** is like **trying to walk in a hurricane**: the **forces propelling** it along the desired path are **puny** compared to the **random forces** exerted by its environment”

“When considering the operation of a molecular motor, the forces that control the movement of **macroscopic** objects—in particular **gravity**—have little relevance. In the molecular world, **Brownian storms rage relentlessly**”

“Molecular motors are **tiny** and operate on a **physical scale** that makes them very different from the **man-made, macroscopic objects** we normally imagine when we hear the word ‘**machine**’”

“A macroscopic motor must either **work with Brownian motion or fight against it**, and the former seems far more preferable”

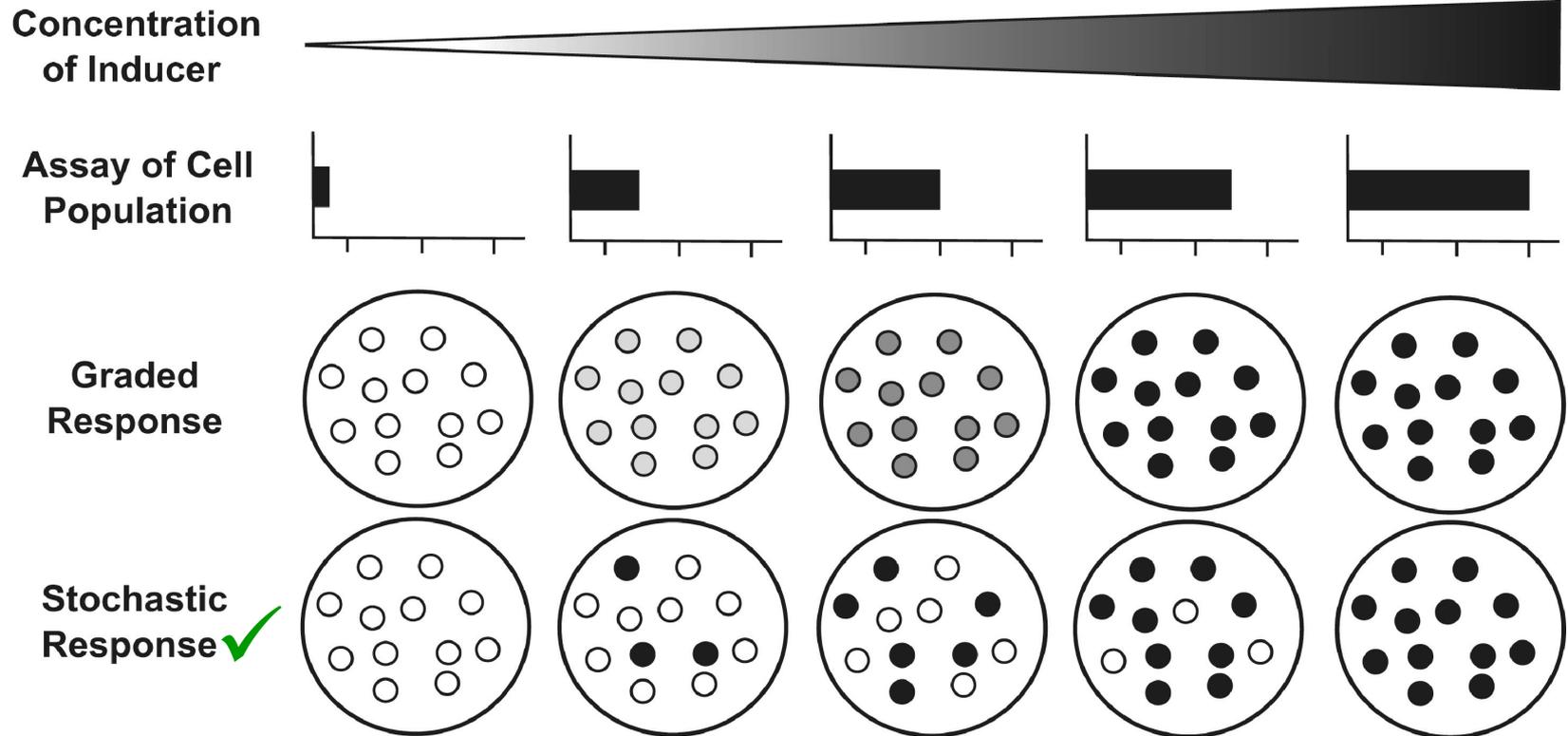
The Brownian Ratchet Model

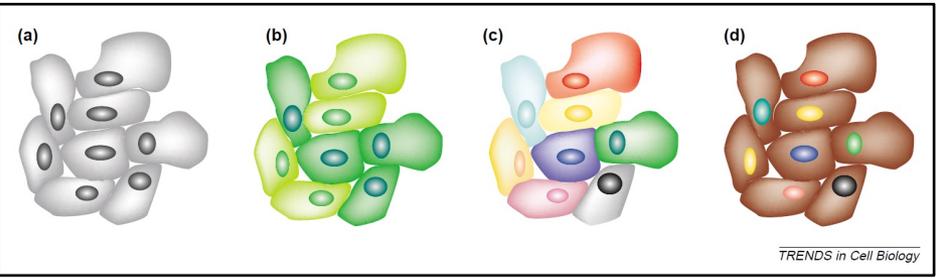


How Size Complicates the Predictability of Cellular Behaviour

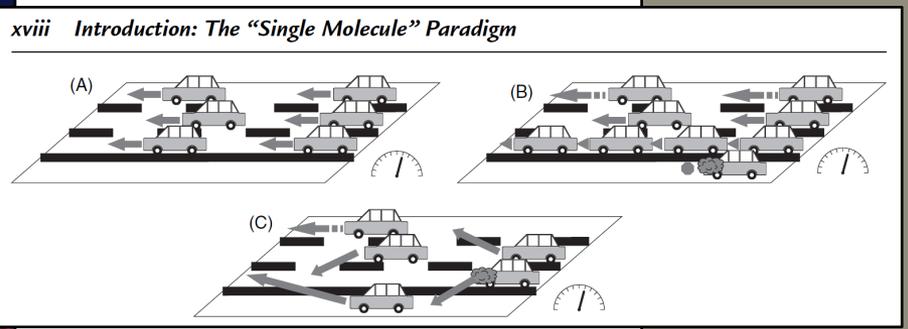
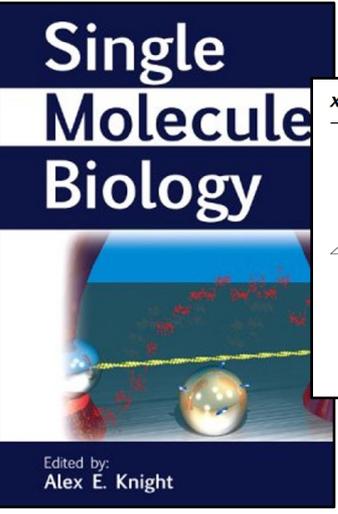
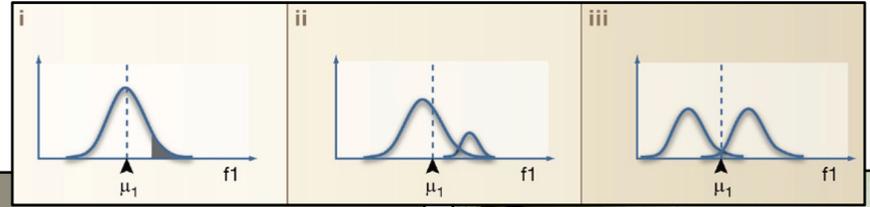
- The machine conception of the cell has led to the view that its behavioural patterns are predictable because they result from the execution of set programs of gene expression or signal transduction, in which a precise sequence of steps is followed and a pre-determined response is produced
- In fact, most response patterns of individual cells are unpredictable. The variation in cellular responses results from random fluctuations in the probability of occurrence of a critical, all-or-nothing step in the cell that requires the action of individual molecules subject to stochasticity
- The predictability of the overall process of development overall arises because millions of molecules have an extremely low probability of all "misbehaving" together. But the smaller the number of molecules involved in a process, the harder it becomes to predict its behaviour

Non-Genetic Cell Heterogeneity: The Case of Gene Expression





No two cells are the same, even if genetically identical. Our reliance on ensemble methods has resulted in the 'myth of the average cell': a statistical contrivance for representing our knowledge beyond the limits of detection

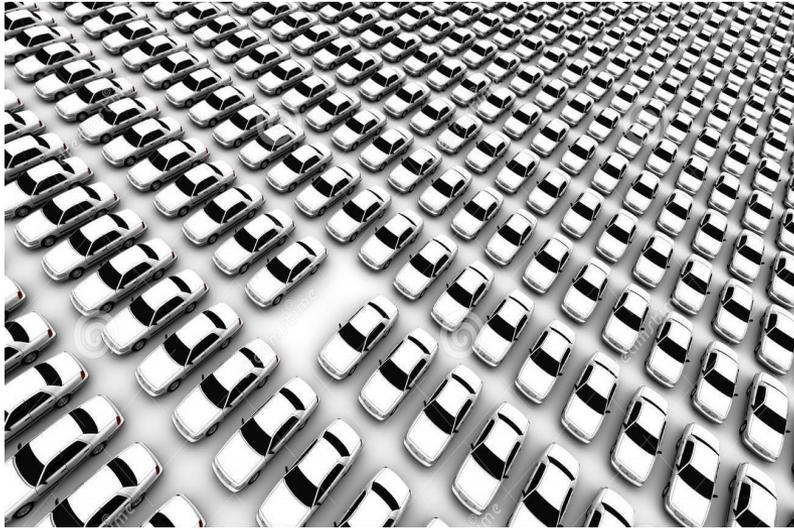




EVERY CELL IS UNIQUE

Tell its story with single-cell biology

Every Cell is Unique



Hallmarks of Cancer: New Dimensions

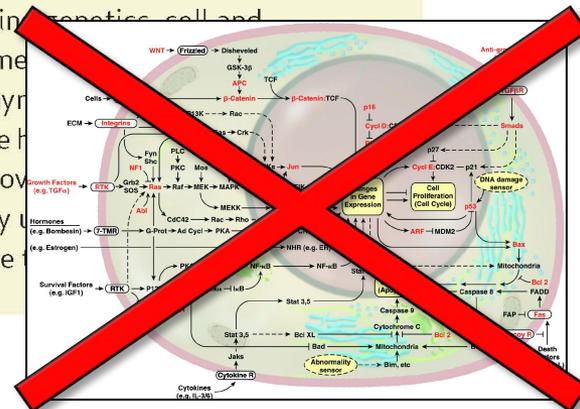


Douglas Hanahan

ABSTRACT

The hallmarks of cancer conceptualization is a heuristic tool for distilling the vast complexity of cancer phenotypes and genotypes into a provisional set of underlying principles. As knowledge of cancer mechanisms has progressed, other facets of the disease have emerged as potential refinements. Herein, the prospect is raised that phenotypic plasticity and disrupted differentiation is a discrete hallmark capability, and that nonmutational epigenetic reprogramming and polymorphic microbiomes both constitute distinctive enabling characteristics that facilitate the acquisition of hallmark capabilities. Additionally, senescent cells, of varying origins, may be added to the roster of functionally important cell types in the tumor microenvironment.

Significance: Cancer is daunting in the breadth and scope of its diversity, spanning tissue biology, pathology, and response to therapy. Ever more powerful experimental tools and technologies are providing an avalanche of “big data” about the myriad of the diseases that cancer encompasses. The integrative concept embodied in the hallmarks of cancer is helping to distill this complexity into an increasingly logical science, and the provisions presented in this perspective may add value to that endeavor, to more fully understand the mechanisms of cancer development and malignant progression, and apply that knowledge



Number of Times 'Circuit' Is Used

- Hallmarks of Cancer I (2000) → 28
- Hallmarks of Cancer II (2011) → 34
- Hallmarks of Cancer III (2022) → 4

General Conclusions: Why Does This Matter?

- The **acceptance** of the machine conception of the cell is what **justifies** in the mind of biologists their appeal to **reductionistic, gene-centric, and deterministic** approaches in dealing with a wide range of problems, including **cancer**
- If we want to **convince** our experimental colleagues of the **shortcomings** of their approaches, it can be helpful to show them: (a) **where** these approaches **come from**; (b) what conceptions **justify them**; and (c) what **alternatives** might be available to them