

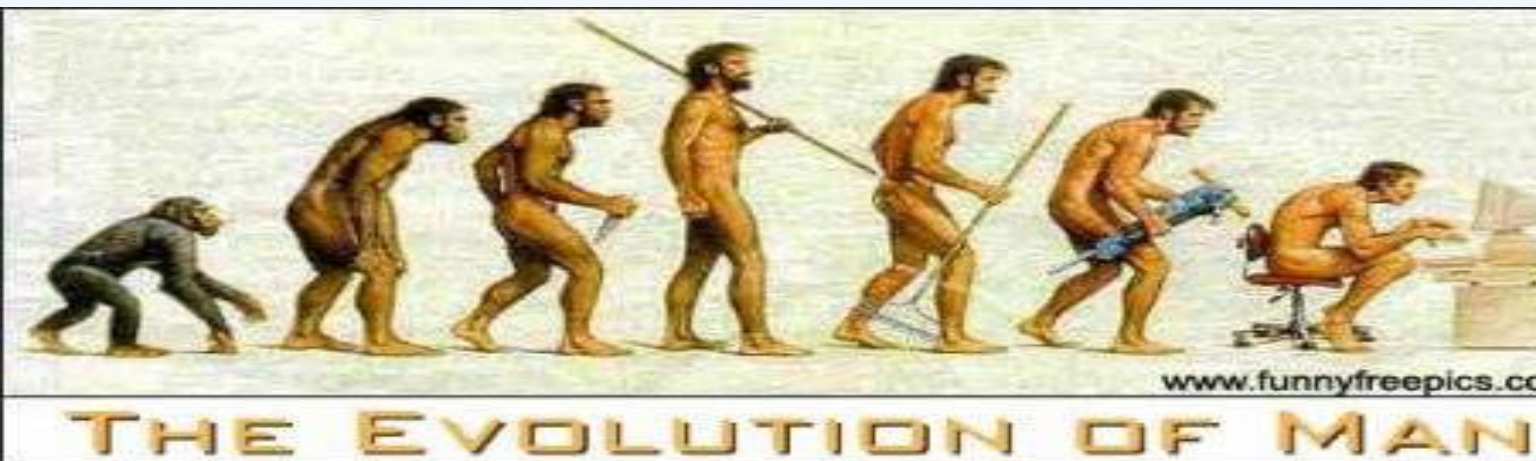


The Evolution of Automation for Pharmaceutical Lead Discovery

Andy Pope, Platform Technology & Science,
GlaxoSmithKline

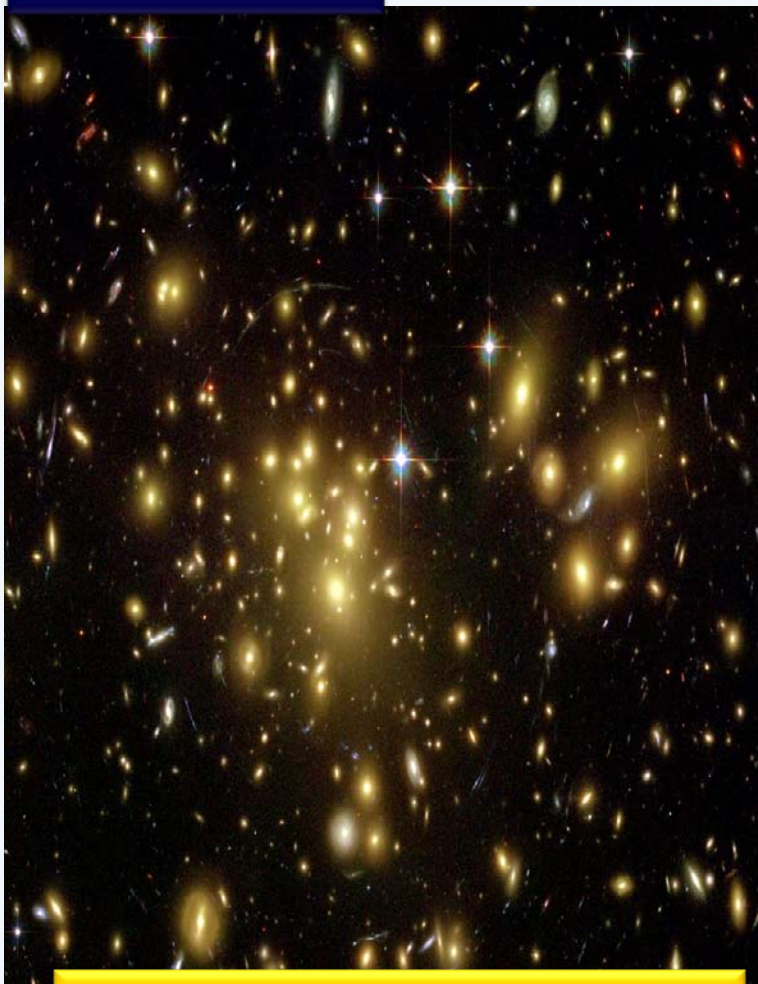
Some themes

- The role of Hit identification/cpd profiling in Pharma R&D
- The physical tasks required
- How automation is used to perform those tasks
- Process/technology evolution in the last decade
- How have our thinking, emphasis and capabilities evolved?
- Prospects for the future



Screening: a central component of drug discovery

Potential drugs



Curated chemical Collection
- *Sampling drug-like space*

New medicine

Safety and efficacy

Drug candidate

Medicinal chemistry

Validated drug target &
lead molecule

Medicinal chemistry

Selectivity, specificity,
MoA assays
- *validation of disease
intervention concept*

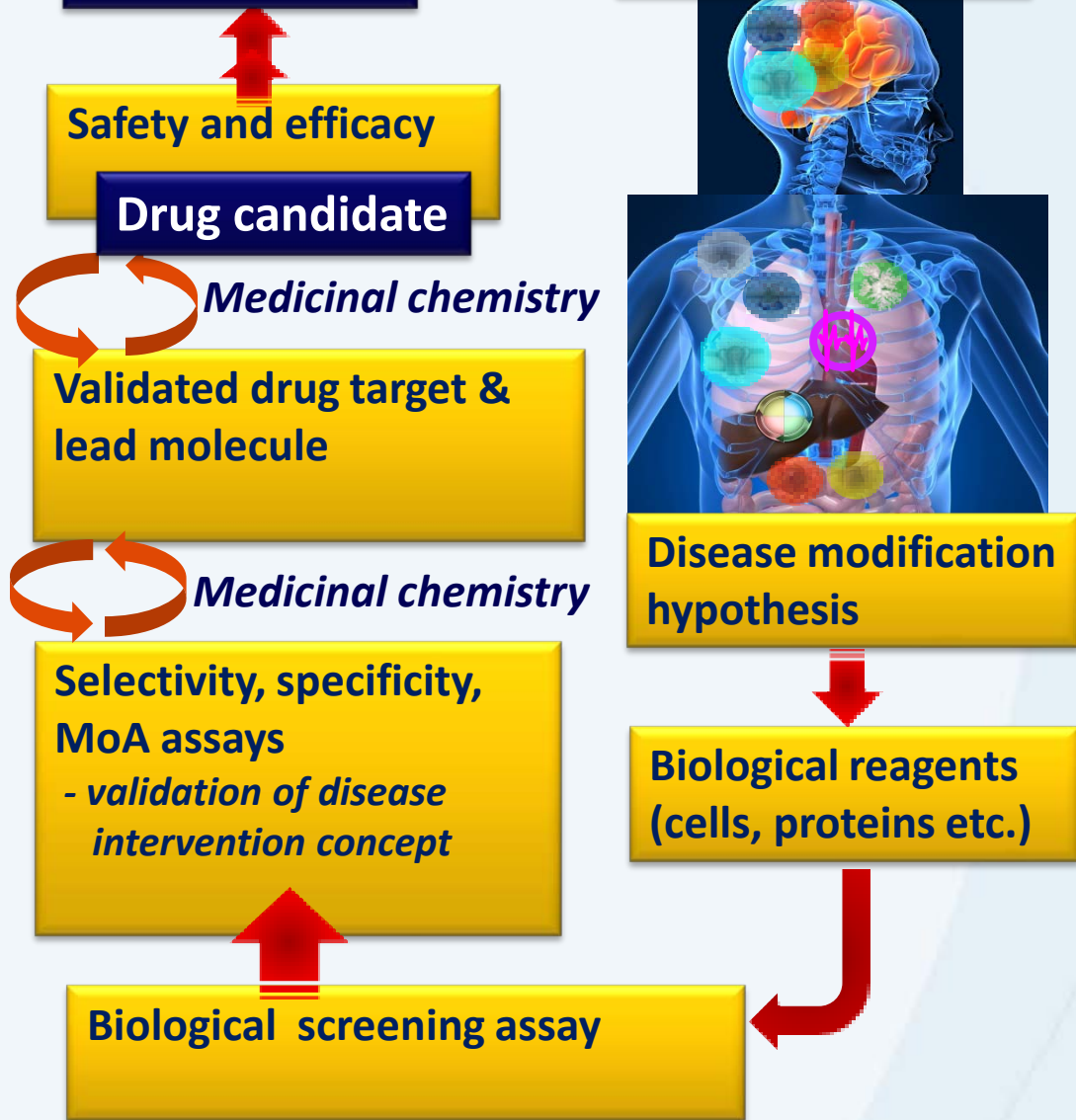
Biological screening assay

Potential targets

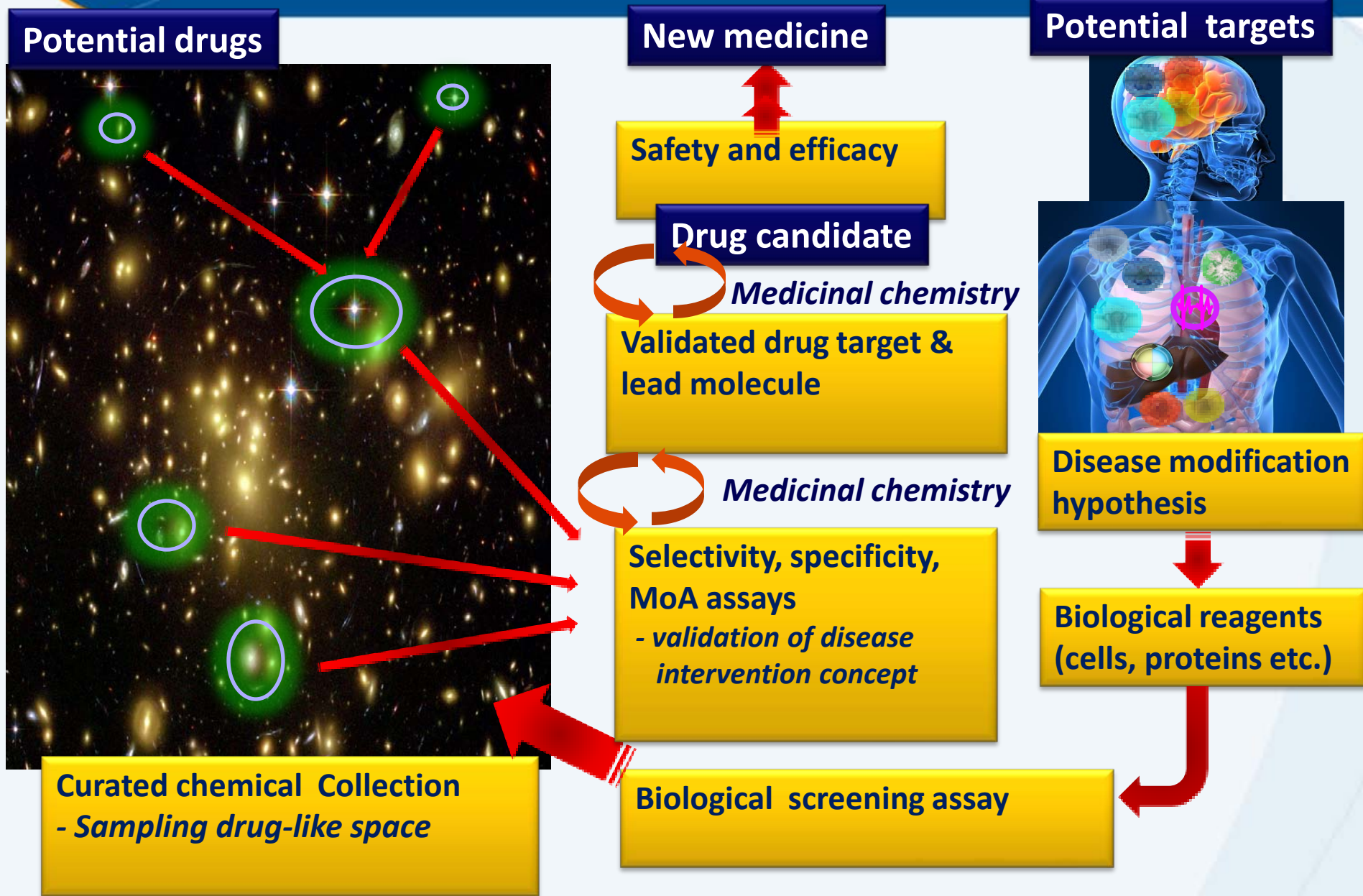


Disease modification
hypothesis

Biological reagents
(cells, proteins etc.)



Compound Screening: a central component of drug discovery



Compound Screening in The Drug Discovery Process

Test compounds

~10⁶

~10⁶

~1000's

~30

10's

few

Drug targets

1000's

100's

~100

~30

10's

few



Chemical Probe discovery

Hit identification

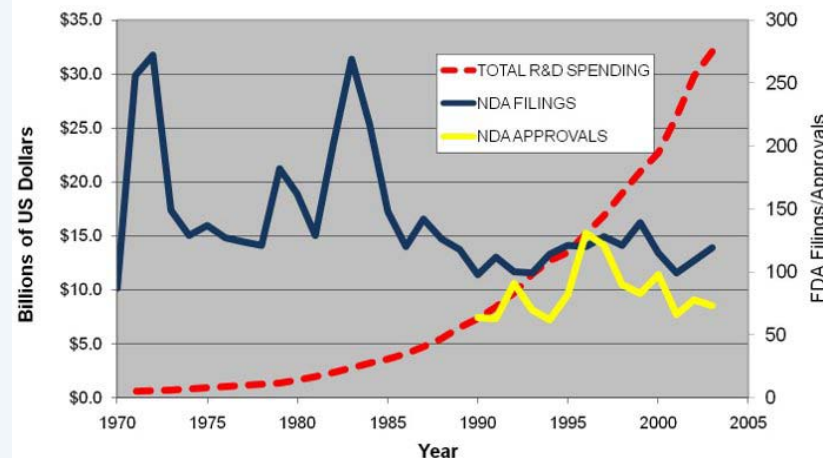
Compound optimization profiling

Safety & attrition profiling

Compound Mechanism of action

Compound Characterization profiling

PhRMA Member Company R&D Costs Per Year and FDA Supplied NDA Data



Overall ~15 years, ~1.5B dollars/NCE

~1 yr

~ 3 yrs

Compound Screening: The Physical process

- Liquid dispense

~1/100th final vol.

~1/3rd final vol.

~1/3rd final vol.

~1/3rd final vol.



- Mix
- Incubate
- Centrifuge
- (not!) Separate

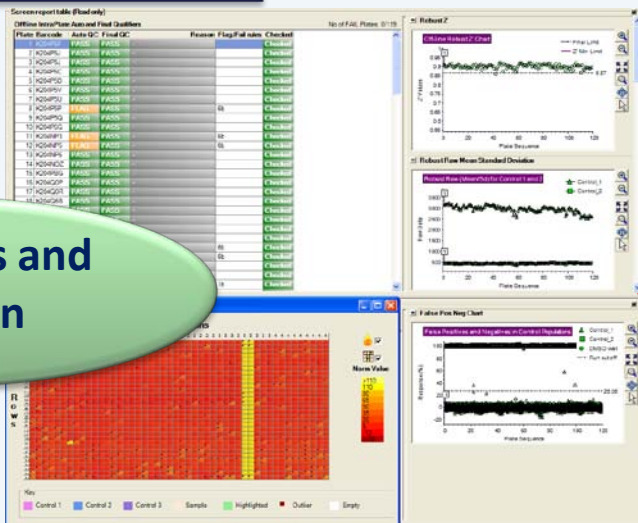
Cpd Stock Solution
(e.g. 1 mM DMSO)

Biological reagent
(e.g. purified enzyme)

Biological co-factor
(e.g. enzyme substrates)

Detection reagents
(e.g. fluorescent)

Data analysis and interpretation



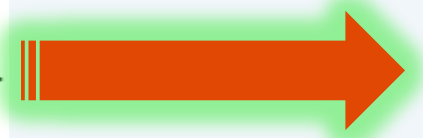
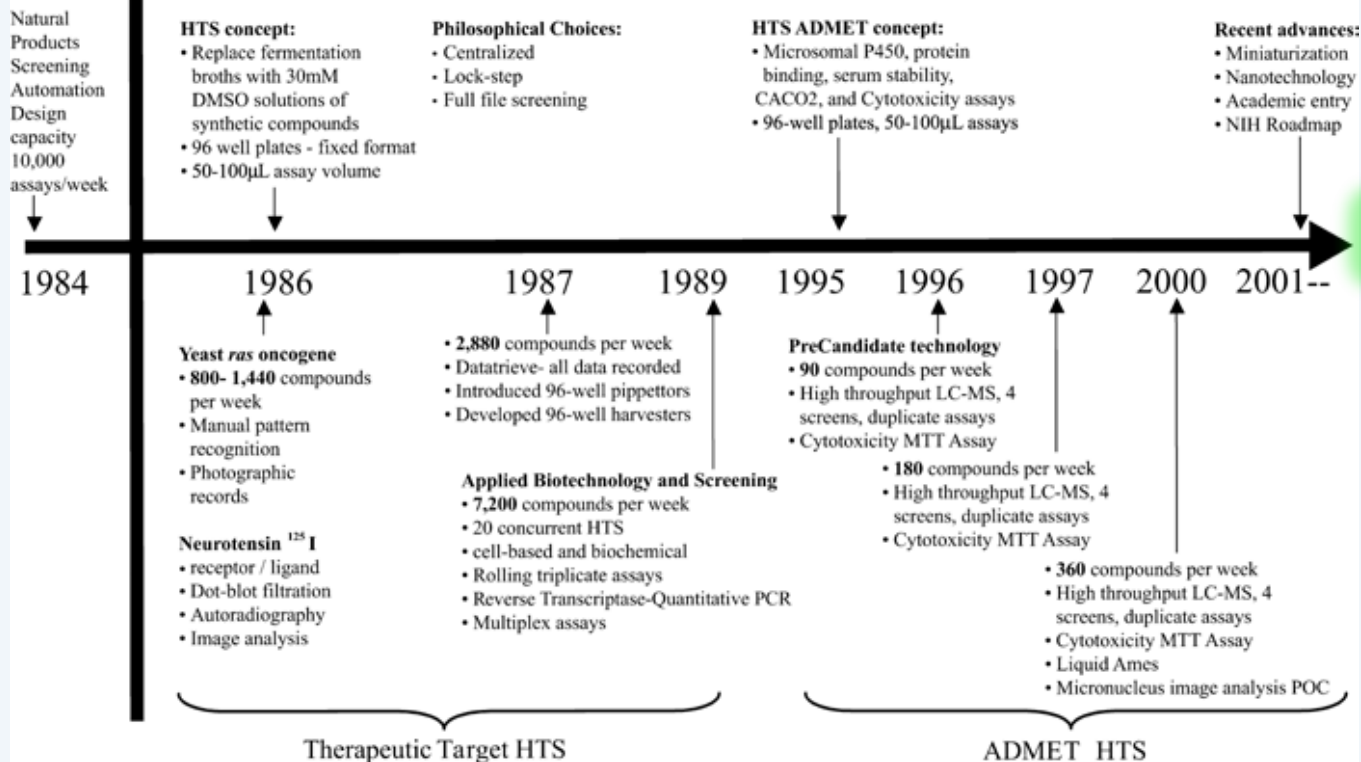
Signal detection
- Photon-based



The Origins of Compound Screening

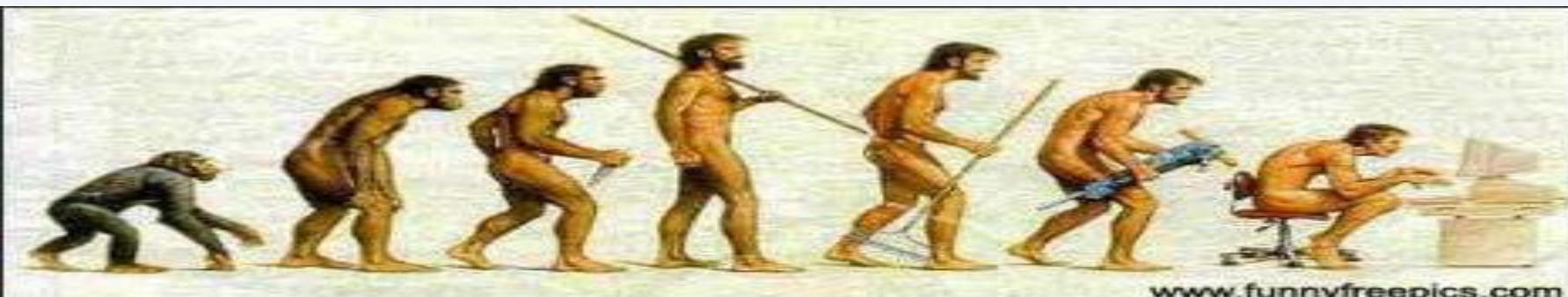
HTS Origin & Evolution

from Pereira & Williams (2007) *Brit. J. Pharmacol.* 152, 53

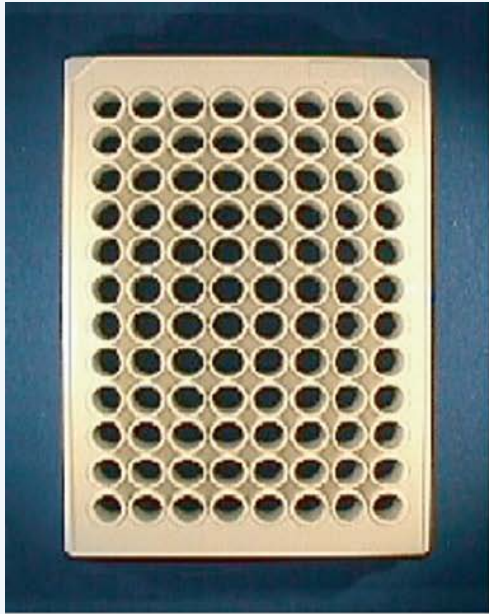


Today's focus

The "modern" era 2001-2010

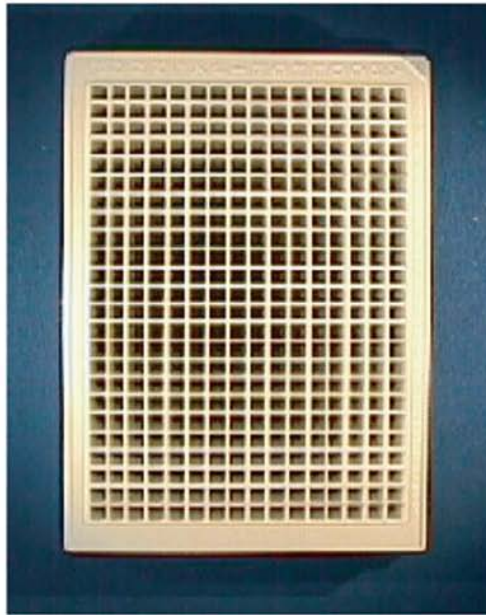


Another view – the microplate



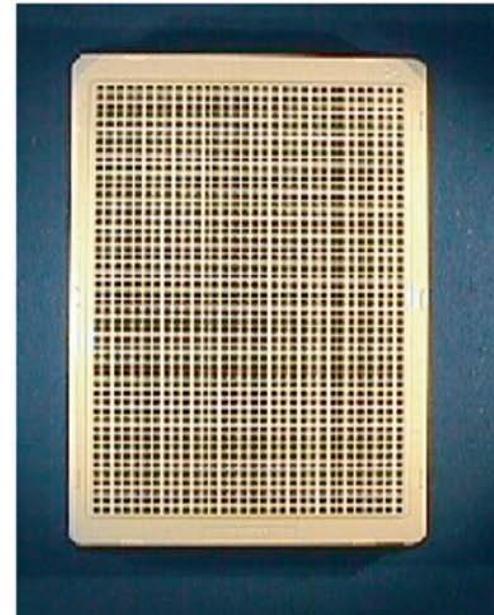
1980's

**- 96-well plate
~100 uL volume**



1990's

**384-well plate
~ 50 uL volume**



2000's

**1536-well plate
2-5 uL volume**

Looking back on the last 20 years..

- 1990 – Screening (as opposed to design) becomes the method of choice to discover drug starting points.**
- 1995 – Excitement builds around genome sequencing and combi-chem**
- 2000 - Major investments to “industrialize” drug discovery**
- 2005 - Major focus on time, cost, efficiency, quality (i.e. real data manufacturing)**
- 2008 - Focus on “re-personalizing” drug discovery, solving drug attrition, maximizing success on difficult targets, “new” biology**
- 2010 - Integration, flexibility and return on investment in a cost-constrained environment**

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Pre-2000 flavor – “How do I get this to work?”

- Techniques for performing miniaturized homogeneous biological assays in microplates nascent
- Hardware for detection just emerging
- Reagent dispense in the sub uL volume emerging
- Compound dispense hardware for nL not commercially available – limiting assay miniaturization
- Automation systems relatively rudimentary, unreliable and limited by v. slow single motion devices
- corporate deals aimed yield unique capability and competitive advantage via large bespoke integration (e.g. Evotec, Aurora)
- IT (and statistics) for handling large data volumes emerging

Homogeneous fluorescence readouts for miniaturized high-throughput screening: theory and practice

Andrew J. Pope, Ulrich M. Haupts and Keith J. Moore

Single-Molecule Detection Technologies in Miniaturized High-Throughput Screening: Fluorescence Intensity Distribution Analysis

KEITH HAUPPTS*, MARTIN RÜDIGER*, STEPHEN ANTMAN*, SANDRA TURBINO*, RYAN BRIDGMAN*, CHARLOTTE WARDON*, JONATHAN BURT BRIDGMAN*, CHARLOTTE CARY*, KEITH J. MOORE, ANDREW J. POPE*

Microfluidic technologies are becoming a powerful readout format to support ultra-high-throughput screening (uHTS) based on the analysis of fluorescence intensity fluctuations detected from a small confocal volume containing single or a few molecules. This review discusses the theory and practice of fluorescence intensity distribution analysis (FIDA), which decomposes multiplexed fluorescence signals into individual components. FIDA also provides a powerful method to extract relevant biological data in the presence of compound fluorescence background.

ABSTRACT
This paper describes, for the first time, a new ultra-high-throughput screen (uHTS) based upon fluorescence anisotropy and performed entirely in 1536-well assay plates. The assay is based upon binding and displacement of a BODIPY-F1 labeled substrate to a specific binding site on the chromosome from *Escherichia coli* (E. coli). The screen was performed at uHTS rates (i.e., >100,000 assays well⁻¹ day⁻¹) using entirely commercially available equipment. In order to examine the reproducibility of detection of test compound effects, assays were performed in duplicate. Both overall assay statistics and reproducibility for individual compound results were excellent, at least equivalent to conventional 96-well assays. Furthermore, artifacts observed in assays as a result of autofluorescence from test compounds. Well-level quality control procedures were developed to detect, eliminate, or even correct for such effects. Moreover, development of a brighter, longer wavelength probe bound upon CDR3 markedly reduced such interferences. Overall, the data demonstrate that fluorescence anisotropy-based uHTS is now a practical reality.

INTRODUCTION
High throughput screening (HTS) is well established.¹⁻³ The term HTS is generally accepted to refer to HTS assays that use 96-well microplates with assay volumes of 100 µl performed at high density (i.e., 1536 wells plate⁻¹) with the dominant screening modality in focus. Moreover, recent advances in liquid handling and detection technologies mean that uHTS is now a practical proposition.⁴⁻⁶ In particular, the development of homogeneous fluorescence assays has allowed uHTS to be implemented in a wide range of assay formats.⁷⁻¹¹ Fluorescence assays are particularly well suited to the format of high-throughput screening (i.e., plate reader based) and microplate (i.e., bead based) assays in fluorescence detection systems. These assays are well suited to the format of high-throughput screening (i.e., plate reader based) and microplate (i.e., bead based) assays in fluorescence detection systems. These assays are well suited to the format of high-throughput screening (i.e., plate reader based) and microplate (i.e., bead based) assays in fluorescence detection systems.



Macroscopic versus microscopic fluorescence techniques in (ultra)-high-throughput screening

Ulrich Haupts, Martin Rüdiger and Andrew J. Pope

The pharmaceutical industry currently faces a major challenge in implementing the tools necessary for ultra-high-throughput screening (uHTS). The rational choice of appropriate readout technologies is crucial for the success, and fluorescence-based approaches will play a major role. Here, advanced fluorescence techniques and their applicability to uHTS will be discussed.

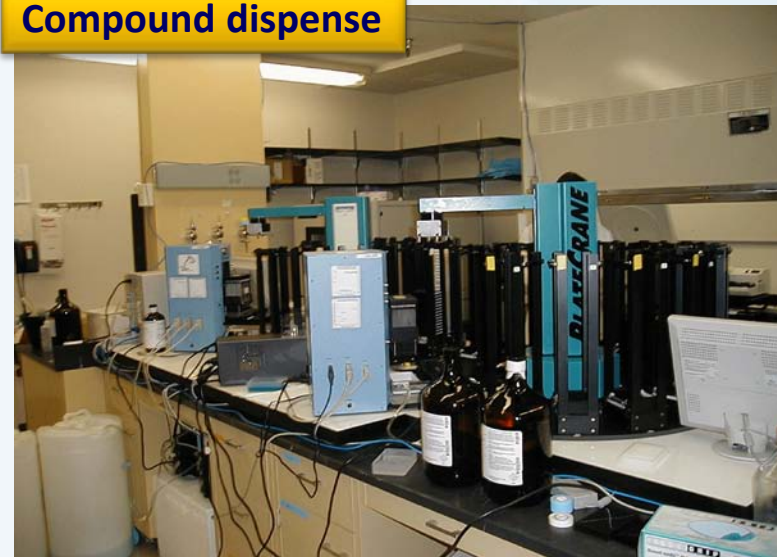
In the past few years, there has been intense changes in the scope and importance of uHTS. When drug discovery was a slow, sequential process, the major driving force was the identification of novel compounds. However, the major driving force today is the identification of novel compounds that can be used in combination with existing drugs to improve the efficacy of existing drugs. This has led to a rapid expansion of the number of assays performed in uHTS. The number of assays performed in uHTS is now in the range of 100,000 to 1,000,000 assays per day. This has led to a rapid expansion of the number of assays performed in uHTS. The number of assays performed in uHTS is now in the range of 100,000 to 1,000,000 assays per day. This has led to a rapid expansion of the number of assays performed in uHTS.

Typical Pre-2000 HTS Screening Lab

Compound store



Compound dispense



Screening robot



- 100-250K cpds, screened as mixtures
- the only way to manage cost and throughput
- 96/384-well plates only
- <1M assay data points per year

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Year 2000 flavor - “industrialization of drug discovery”

Inspired by Human Genome and promise of combinatorial chemistry, vision was to solve R&D productivity via increases in scale and automation of drug discovery activities

- *Specialized facilities with large flexible lab spaces*
- *Infrastructure and manpower to manage compound logistics*
- *Large (impressive, expensive) Integrated Screening Robots*
- *Big budgets*

The coffee mug said;

“we will marry genes & chemistry to create a small molecule ligand for every potential drug target”



Typical High Throughput Screen Process

Primary Screen
(10 uM – singlicate)

*Statistical separation
from null effect
population*



*Chemical
clustering if hit
rate >1%*

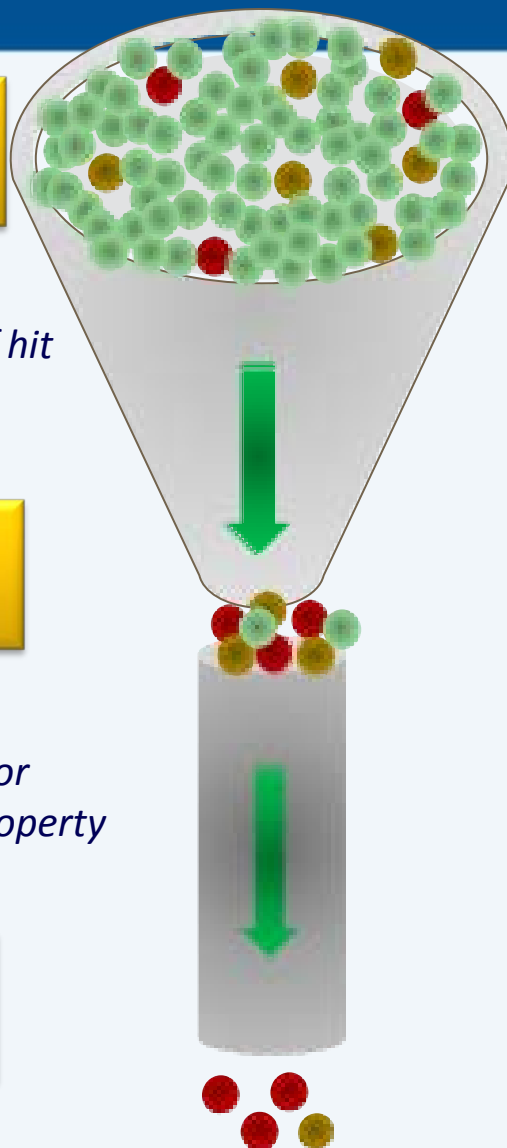
Confirmation
(10 uM – duplicate)

*Eliminate false
positives from
primary*



*Chemical
clustering for
diversity property
sampling*

Dose response
(11 pt 3-fold dilution)

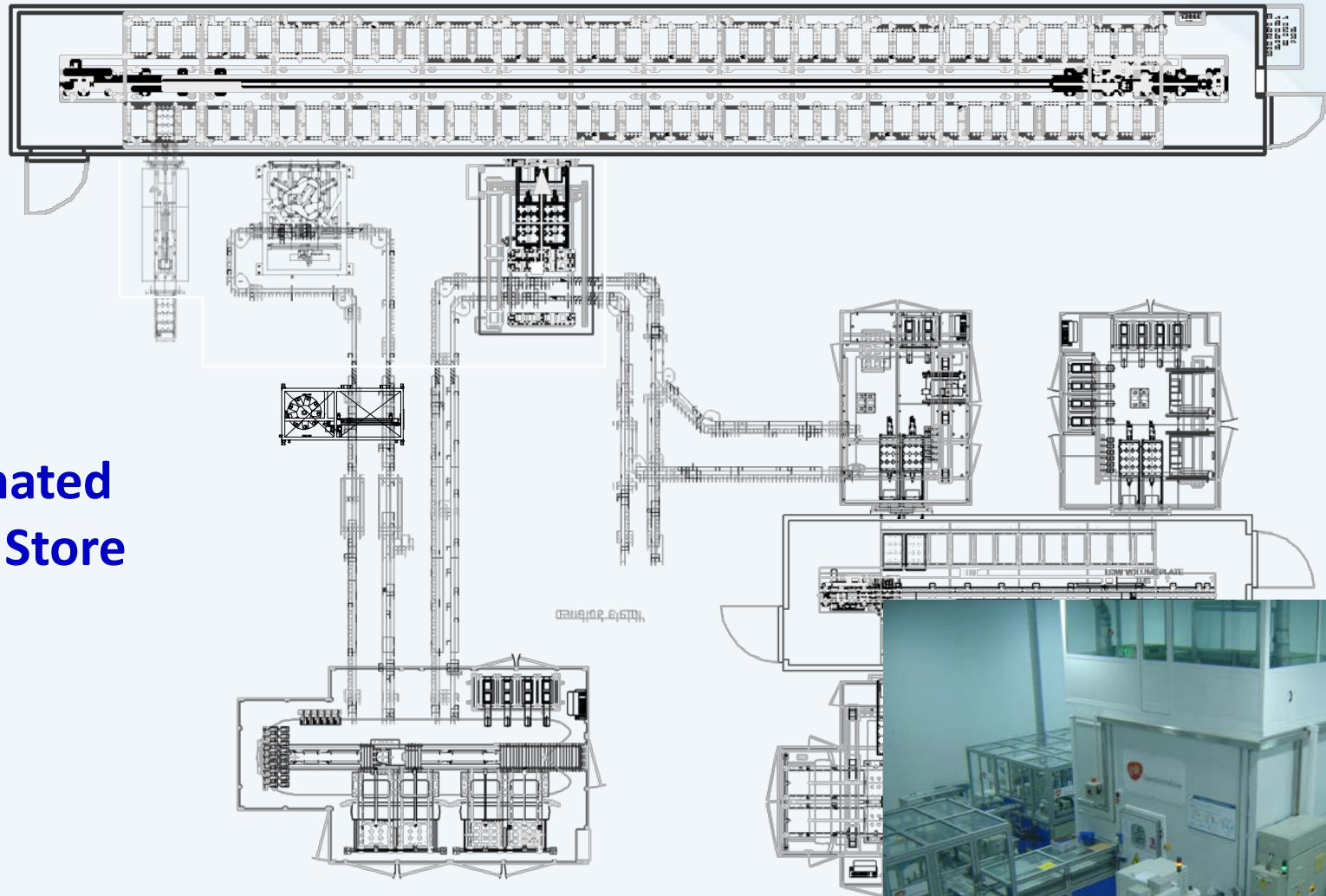


Entire collection (100%)

Potential actives (<1%)

Real hits (<0.1%)

Compound management and supply



**Automated
Liquid Store**



Compound management and supply – large Scale automation

~50 feet

Archive tubes
10 mM (~3M)

Random
tube
access

Test
plate
creation

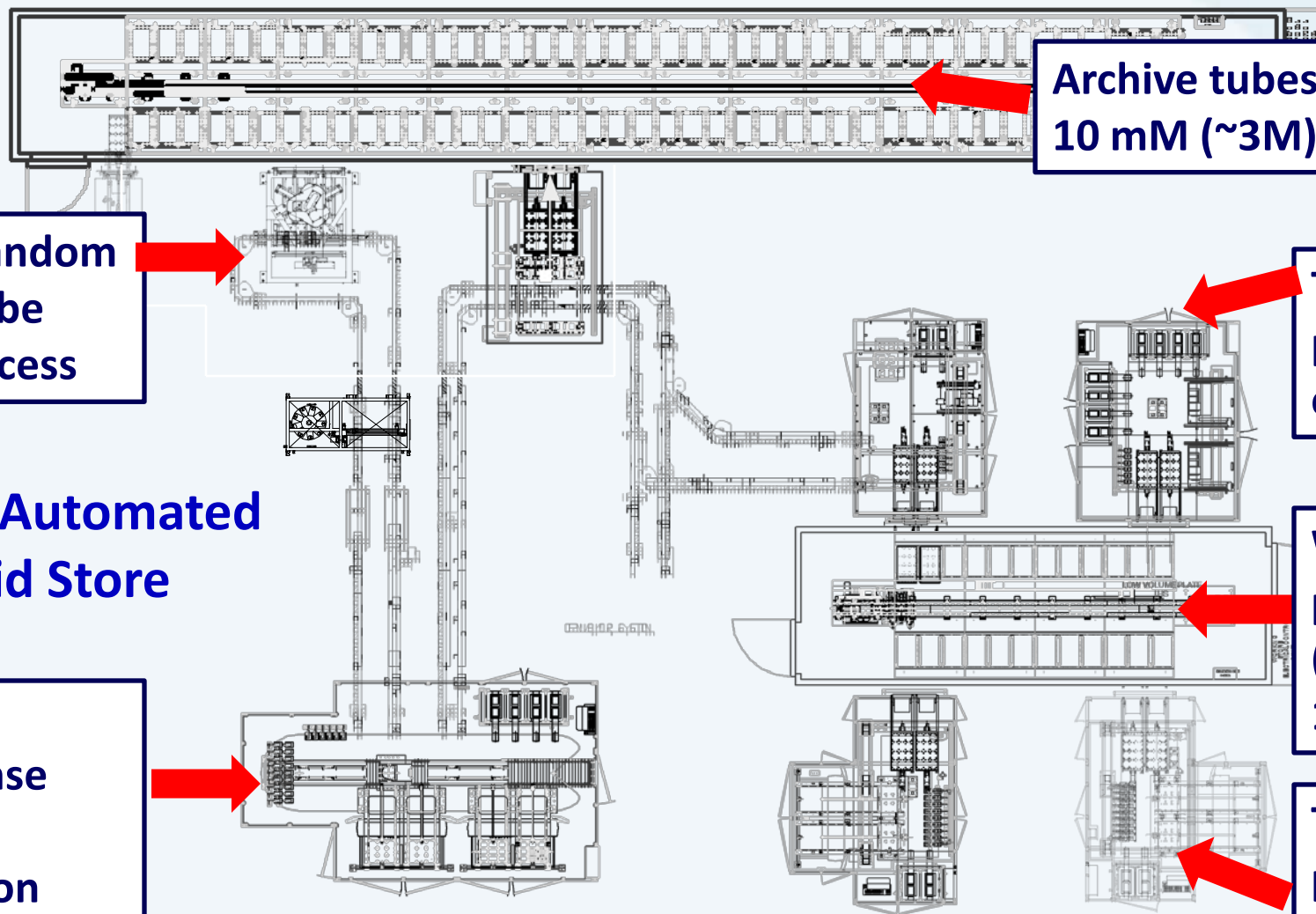
GSK Automated
Liquid Store

Dose
Reponse
plate
creation

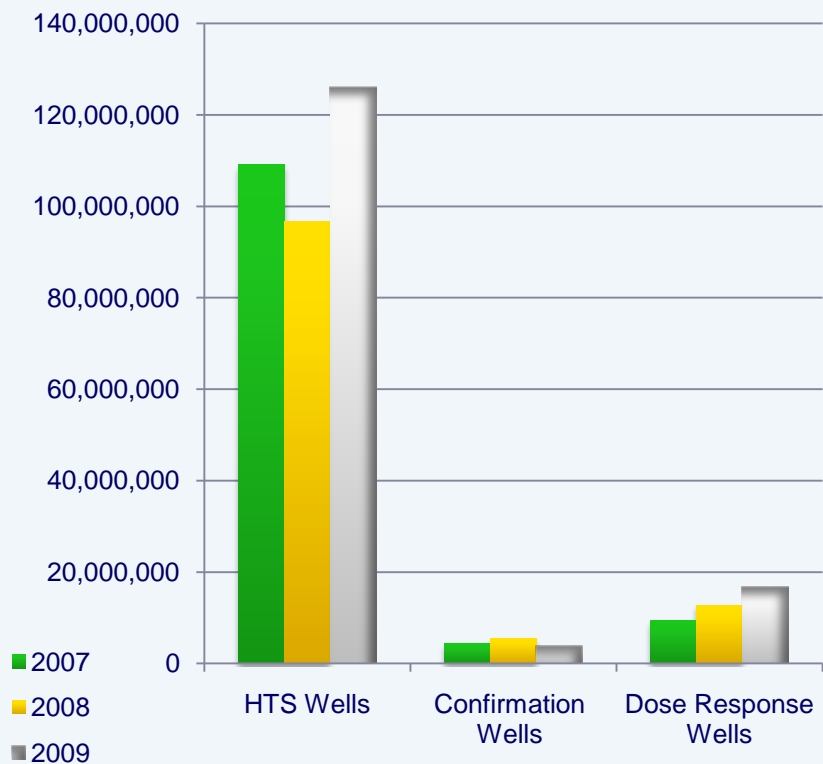
Working
plates
(10,000)
1 mM

Test
plate
creation

~90 feet



Large robotics, large output...



Compound Screening: The Physical process

- Liquid dispense

$\sim 1/100^{\text{th}}$ final vol.

$\sim 1/3^{\text{rd}}$ final vol.

$\sim 1/3^{\text{rd}}$ final vol.

$\sim 1/3^{\text{rd}}$ final vol.



- Mix
- Incubate
- Centrifuge
- (not!) Separate

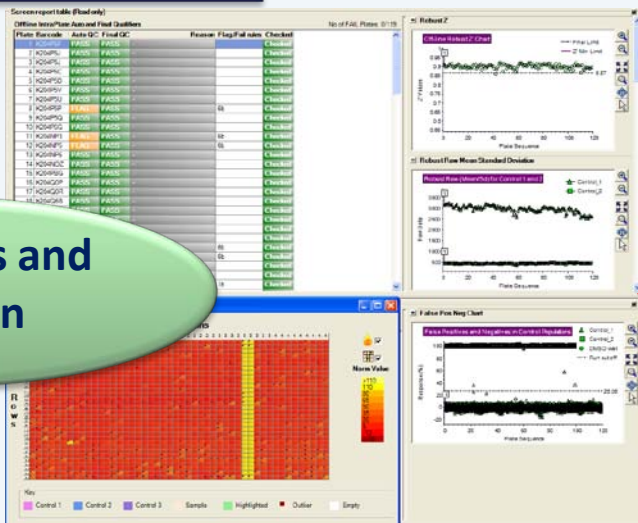
Cpd Stock Solution
(e.g. 1 mM DMSO)

Biological reagent
(e.g. purified enzyme)

Biological co-factor
(e.g. enzyme substrates)

Detection reagents
(e.g. fluorescent)

Data analysis and interpretation



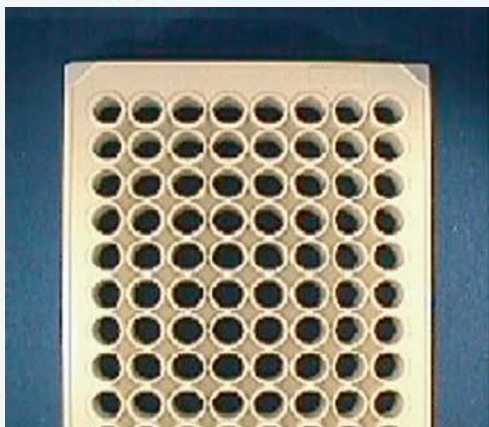
Signal detection
- Photon-based



Automating compound handling versus biological assays

	Compounds	Biological assays
No. of operations per test	few (1-2)	More (4-8)
Typical liquid handling range - liquids dispensed	50 nL – 500 nL DMSO, H2O	1- 5 uL Buffers, proteins, detergents, cells
Process variability	None	As biology demands - incubations etc.
Batch size	Optimal for system	Determined by system and signal stability
Instrumentation used	Constant – liquid handlers bar code readers, transport, holding devices, lid/de-lid	Variable – liquid handlers, incubators, centrifuges, multiple readers, lid/de-lid,

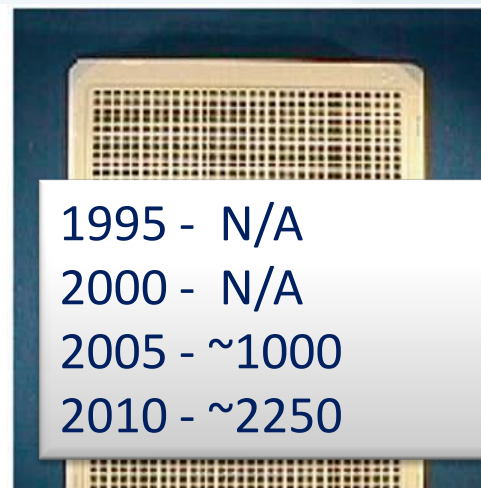
A lot of plates to handle!



1995 - ~500
2010 - N/A (40,000!)



1995 - ~150
2000 - ~2000
2005 - ~4000
2010 - ~9000



1995 - N/A
2000 - N/A
2005 - ~1000
2010 - ~2250

Number of microplates required for a single HTS campaign

1995 - 200K cpds (mixtures of 10/well)
2000 - 500K cpds (discretetes)
2005 - 1M cpds (discretetes)
2010 - 2.5M cpds (discretetes)



Integrated High Throughput Screening Assay Systems

Integration of existing stand-alone lab instruments

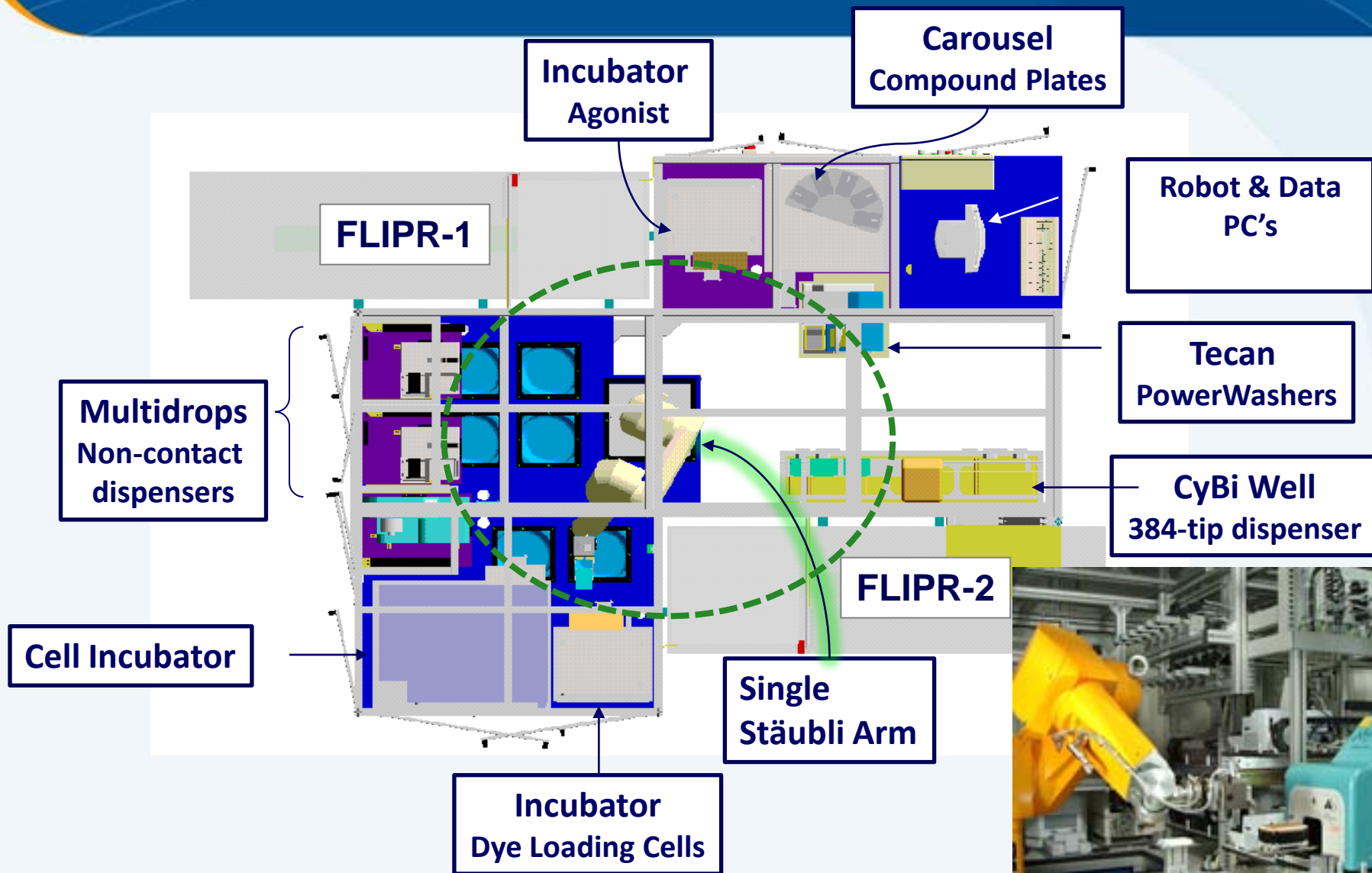
- anthropomorphic arm used to transport microplates between third party components
plate readers, dispensers, incubators etc.
e.g. Thermo CRS, RTS etc.



Total solutions

- “Soup to nuts” including specialized devices from vendor
- Variety of motion types
e.g. Evotec, TAP, Proteodyne

RTS Cellular Assay Platform (~year 2000)



RTS Cellular Assay Platform (~year 2000)

~ 189 x384 well plates/run
~ 20 hr (if perfect!)
~ 72,500 tests per day
~ 220,000 tests/week/system
~ 1-3 systems

Incubator
Agonist

Carousel
Compound Plates

Robot & Data
PC's

Tecan
PowerWashers

CyBi Well
384-tip dispenser

Multidrops
Non-contact
dispensers

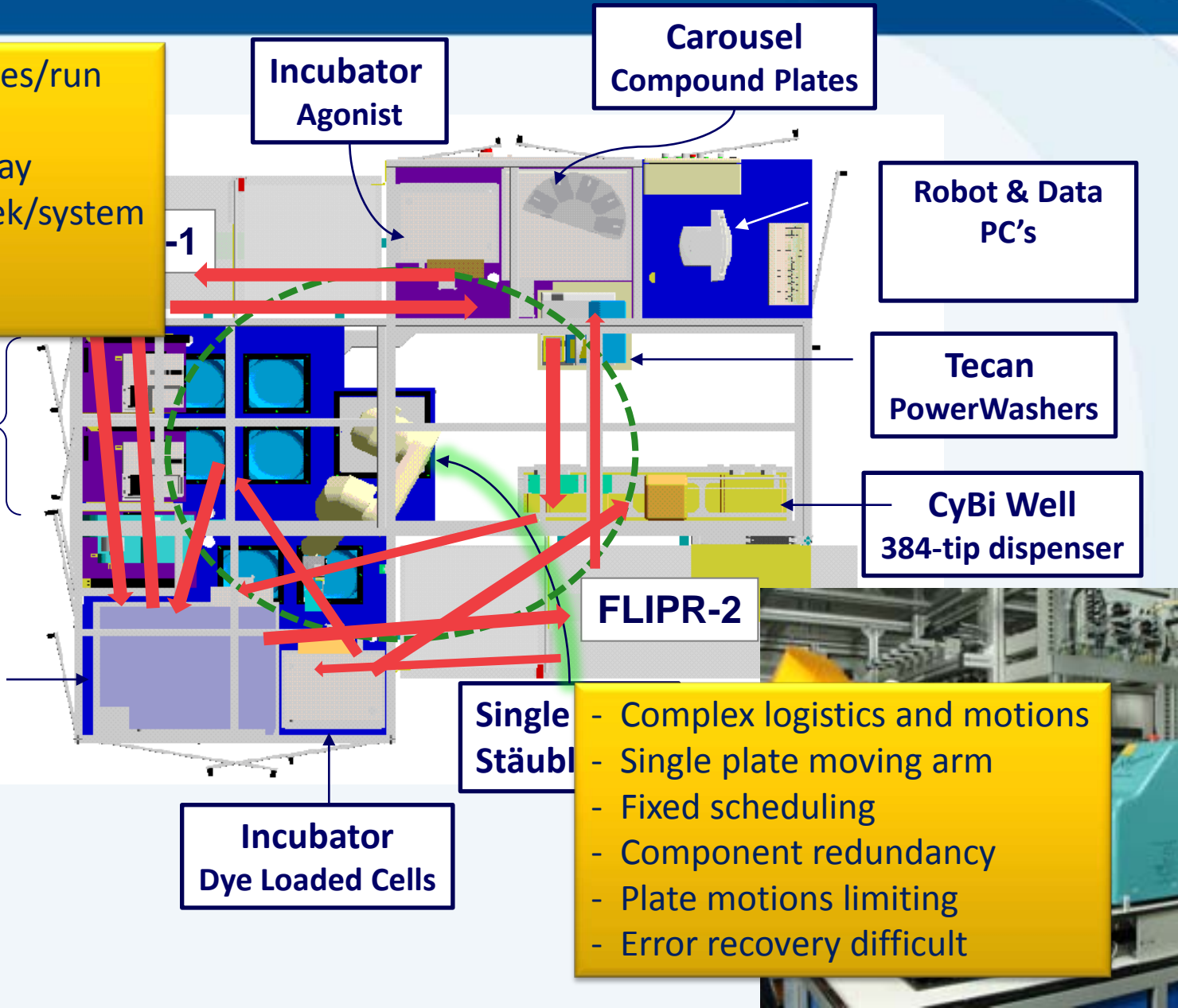
Cell Incubator

FLIPR-2

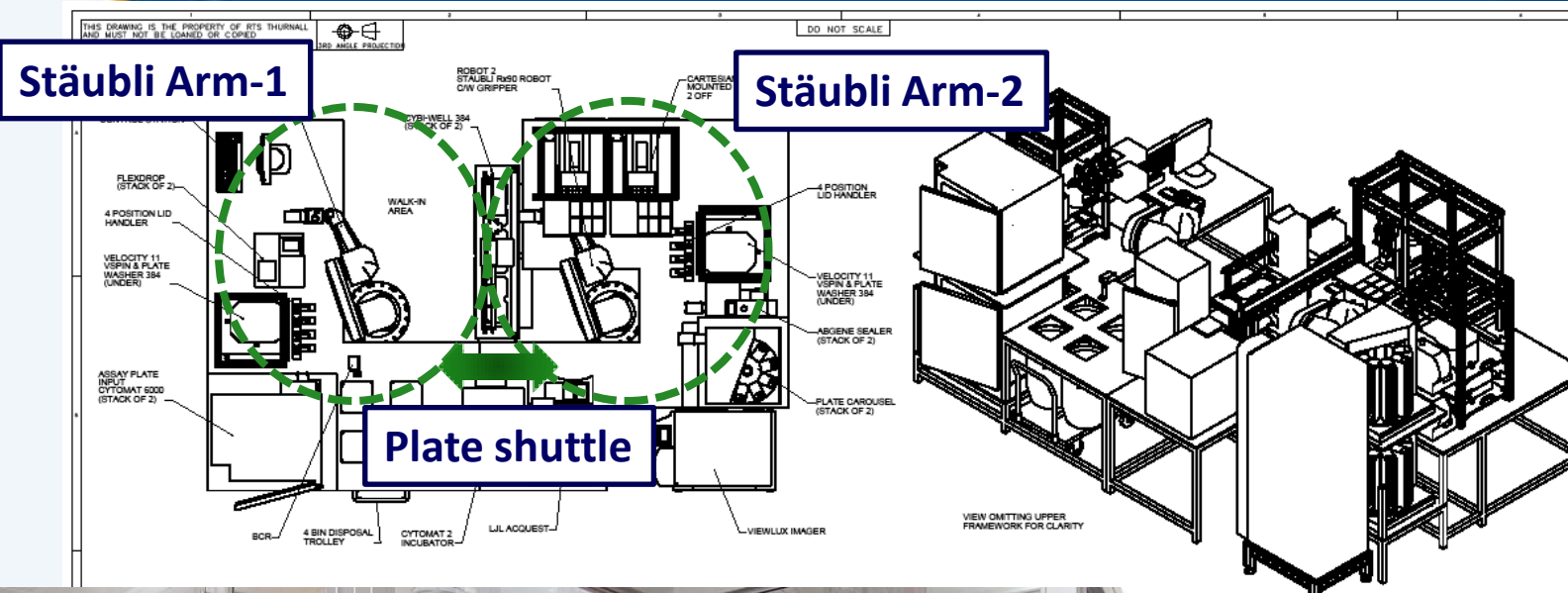
Single
Stäubli

Incubator
Dye Loaded Cells

- Complex logistics and motions
- Single plate moving arm
- Fixed scheduling
- Component redundancy
- Plate motions limiting
- Error recovery difficult



RTS Biochemical Assay Platform (~year 2003)

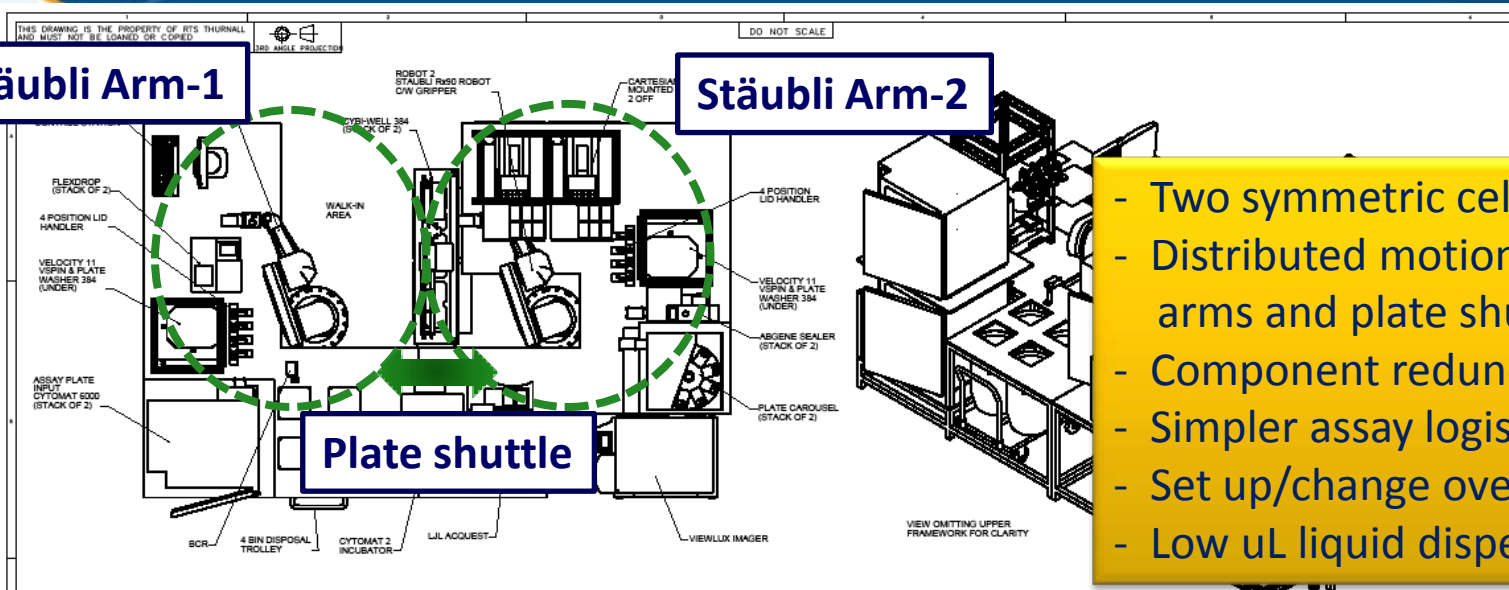


RTS Biochemical Assay Platform (~year 2003)

Stäubli Arm-1

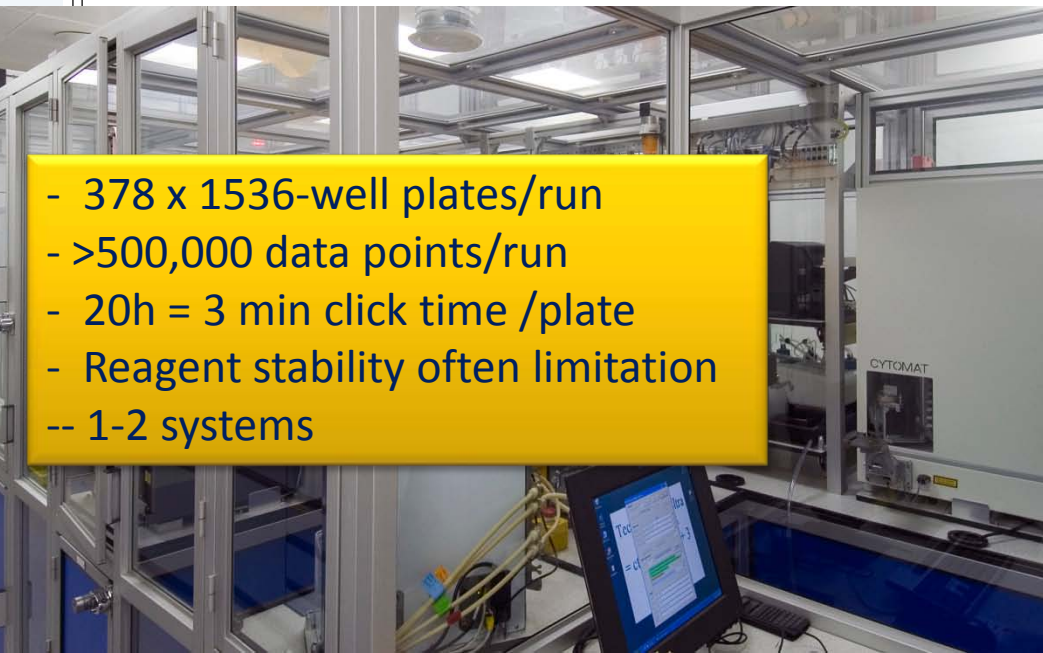
Stäubli Arm-2

Plate shuttle



- Two symmetric cells (1 or 2 robots)
- Distributed motion to two arms and plate shuttle
- Component redundancy
- Simpler assay logistics
- Set up/change over time
- Low uL liquid dispense critical

- 378 x 1536-well plates/run
- >500,000 data points/run
- 20h = 3 min click time /plate
- Reagent stability often limitation
- 1-2 systems



Integrated High Throughput Screening Assay Systems – Issues/learning's

- Third party devices often not robust enough (product refresh cycles)
- Locked out of product cycles/technology advances by monolithic integrations
- Large systems (and redundancy) tie up devices even when not used
- True process bottlenecks were not foreseen; particularly around motion and plate holding
- Biology is unique each time – transfer/adaptation to automation can take as long as screening
- Change over time relatively slow
- When screening lab output = Output of a few big robot(s); long lead times and uncertainty from scheduling limited automation resource result

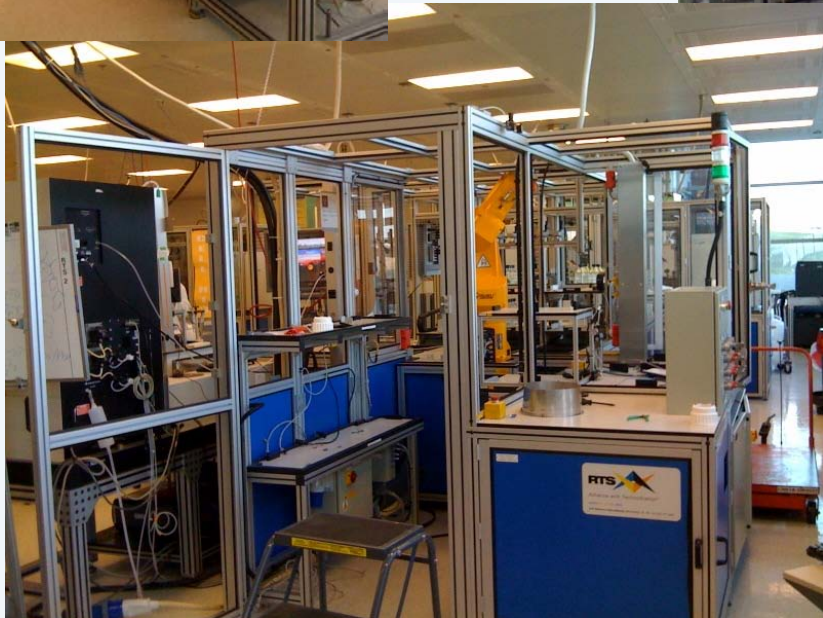
AndBiology does not arrive in a predictable fashion or matched to hardware resource!

Looking back on the “Screening Factory” era

- Many investments were essential and pivotal to success; others didn't stand the test of time
- Throughput and volume of work increased greatly, but so initially did lead times and duration
- Quality
- The extent to which senior management or investors were impressed just by the scale of the operation (as opposed to value created) decreased over time
- Initial thinking the industrialization would lead to de-skilling (robot operators) was naïve – **more data needs more interpretation and higher scientific skills**

Quote from 1999 management presentation “We will miniaturize, homogenize, de-humanize”

If there is a better way...don't be a slave to the machine



2008-10

- Outdated (and/or unreliable) peripherals
- Slow change-over's, lead in times
- Logistics can't keep up with process
- People find a better way

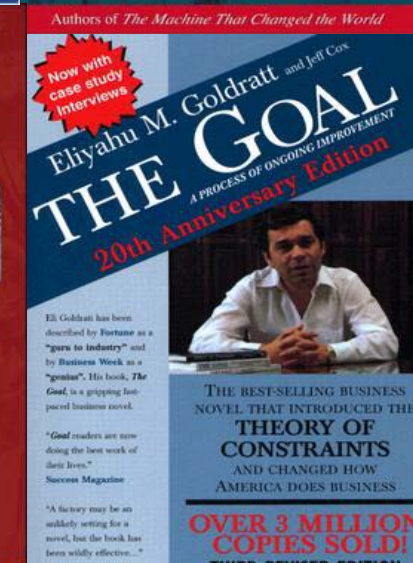
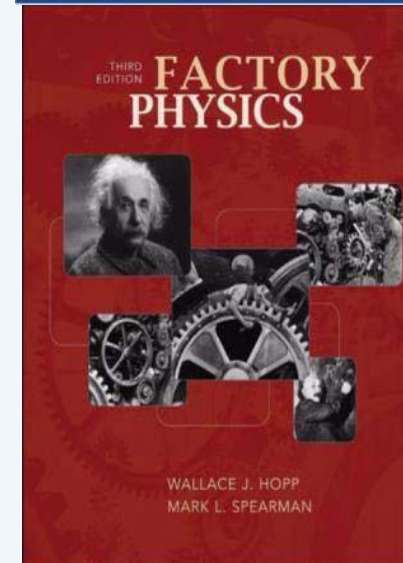
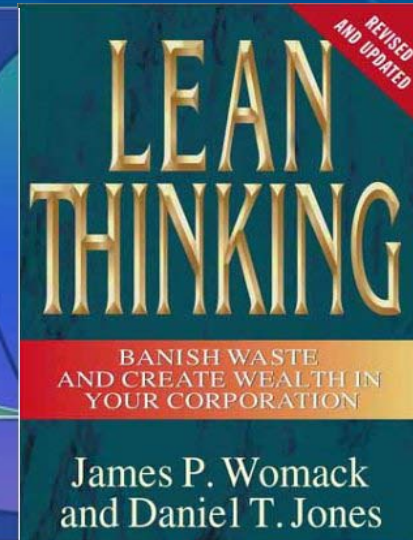
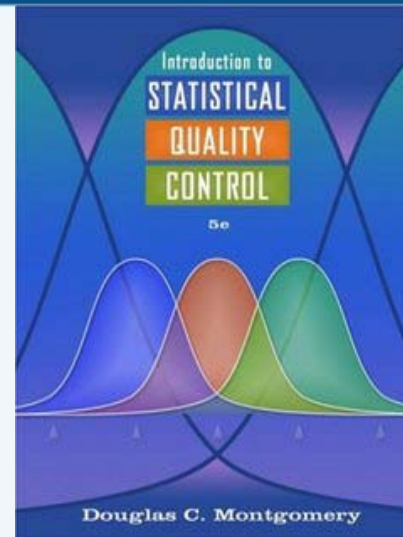
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Learning to see (2005)

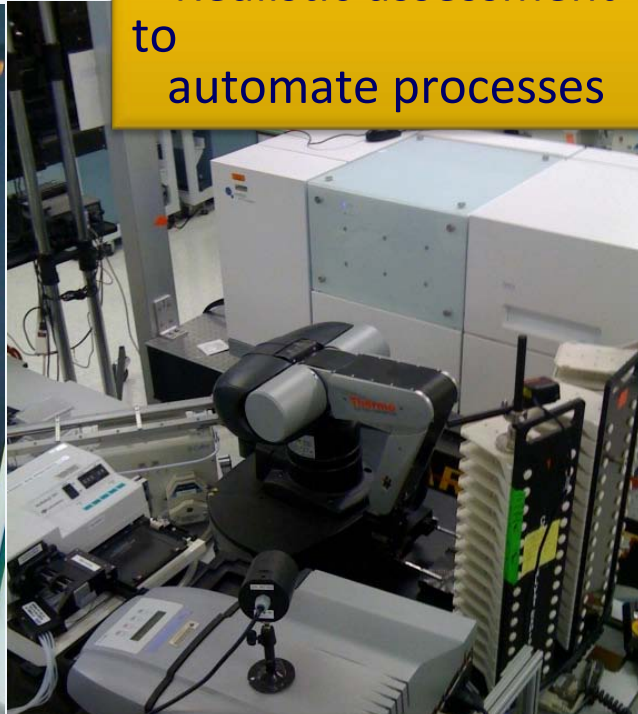
“If we’re calling it a Screening Factory, maybe we should learn something about manufacturing!”

- *Discovery teams as customers of a product*
- *Importance of delivery speed*
- *Customer demand/satisfaction*
- *Work in progress*
- *Quality*
- *Policy deployment*
- *Identification of bottleneck*
- *Waste elimination/workspace organization*
- *Human and machine resource deployment*



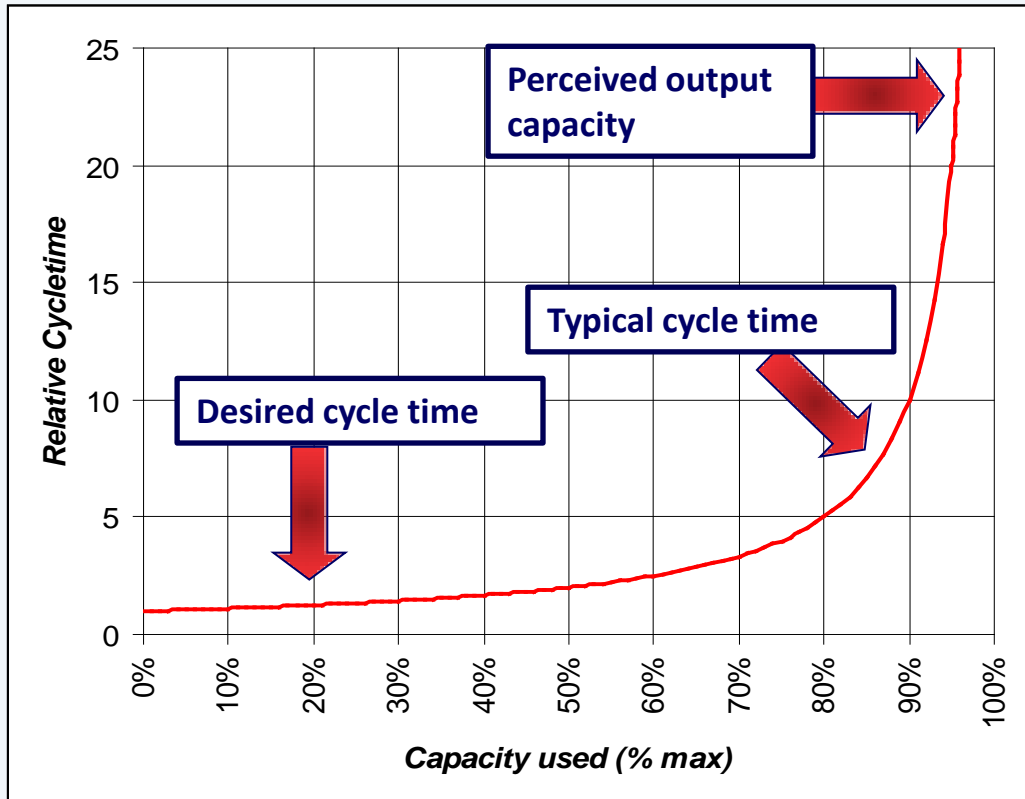
“Right sizing” automation of lab processes

- Timeliness and Quality critical
- Constraining work in progress is critical to cycle time (which helps lead time)
- Realistic assessment of how, whether and when to automate processes



- Light, flexible integrations of parts of a process
- Rapid changeovers
- Low costs = high useable redundancy (low utilization)

Cycle-time versus capacity



Limited number of “monument” resources resulted in long scheduled lead times

Total integrations tied up devices and fixed stoichiometry

Large uncontrolled fluctuations in number of screens resulted in extended cycle time

Perception that increasing speed decreased quality was false
- the opposite was true

Policy deployment examples

CONWIP (Constrained Work in Progress)

Max one primary screen at a time per group of ~10 scientists

- between 0-4 running (median 2), previously 0-11!

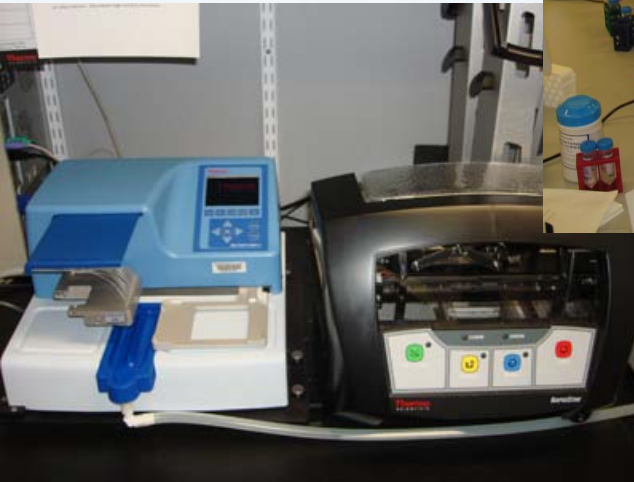
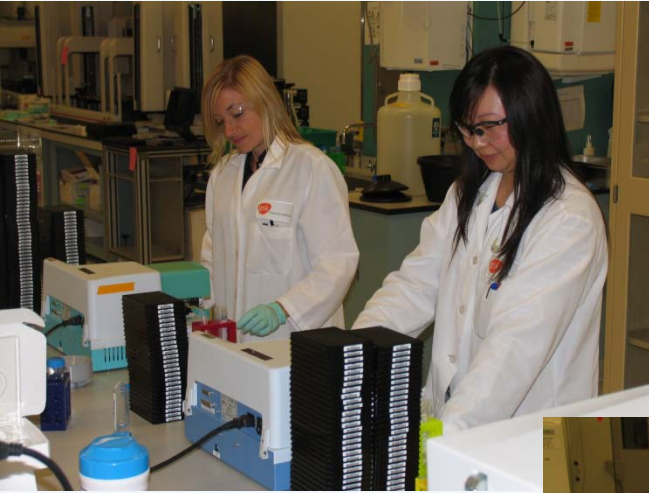
ACP (Absolute Completion Priority)

Priority always given to effort at latest stage in the overall process
(i.e. Dose response screen X >> Confirm screen Y >>> Primary screen Z)

....fit of previous automation paradigms?

Bucket brigade plus light automation

- For simple logistics, perhaps the fastest method (~750K data points/day)
- People move individual plates for rapid steps – stacks for extended steps (e.g. signal read)
- No inherent fixed device stoichiometry
- Quality equivalent or higher



Implications of “Learning to see”

- **Hardware redundancy as opposed to utilization**
- **Policy deployment for speed, lead time, quality, productivity**
- **“Right-size” the automation process, including de-coupling tasks**
- **Recognize and respect bottlenecks/monuments (e.g. carefully manage order priority and Utilization of large cpd supply robots)**
- **Get quality and process right at the start – the fun part is before and after the (boring uneventful) screen**
- **Organizational structure**
 - **Team based working, hands (and brains) to solve problems if needed**

Screening history through beverage containers

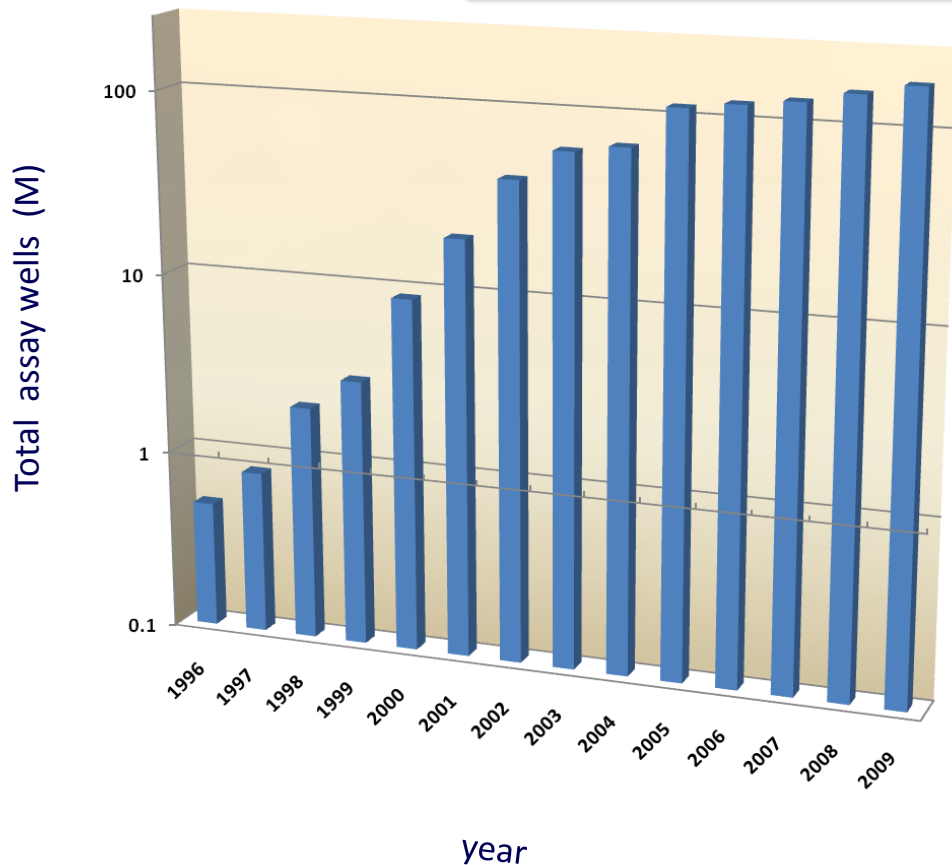
2000: We can do anything, lets do *everything*

2007: Do the right things *fast*

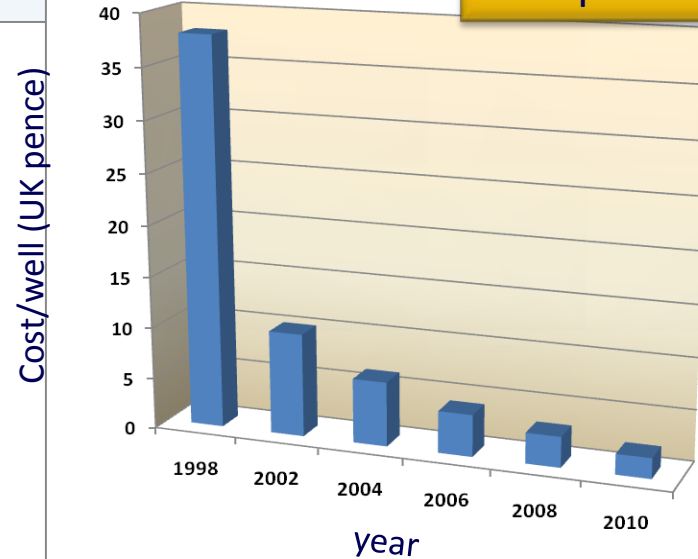


Cost and volume

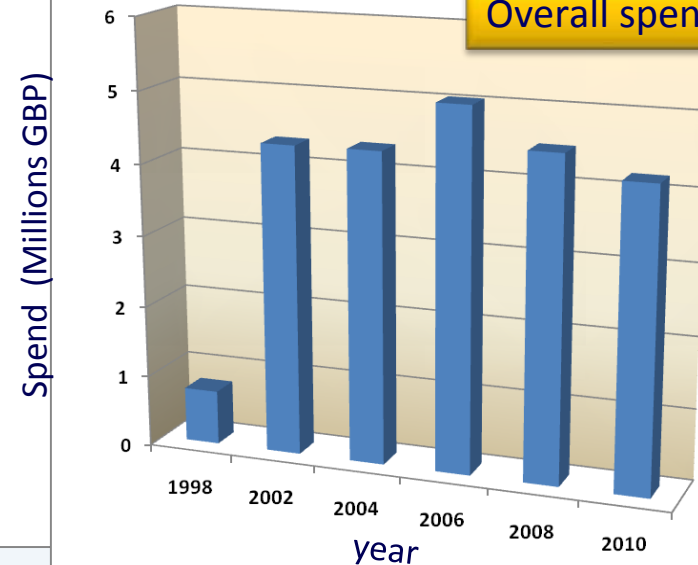
Total HTS wells



Cost per well

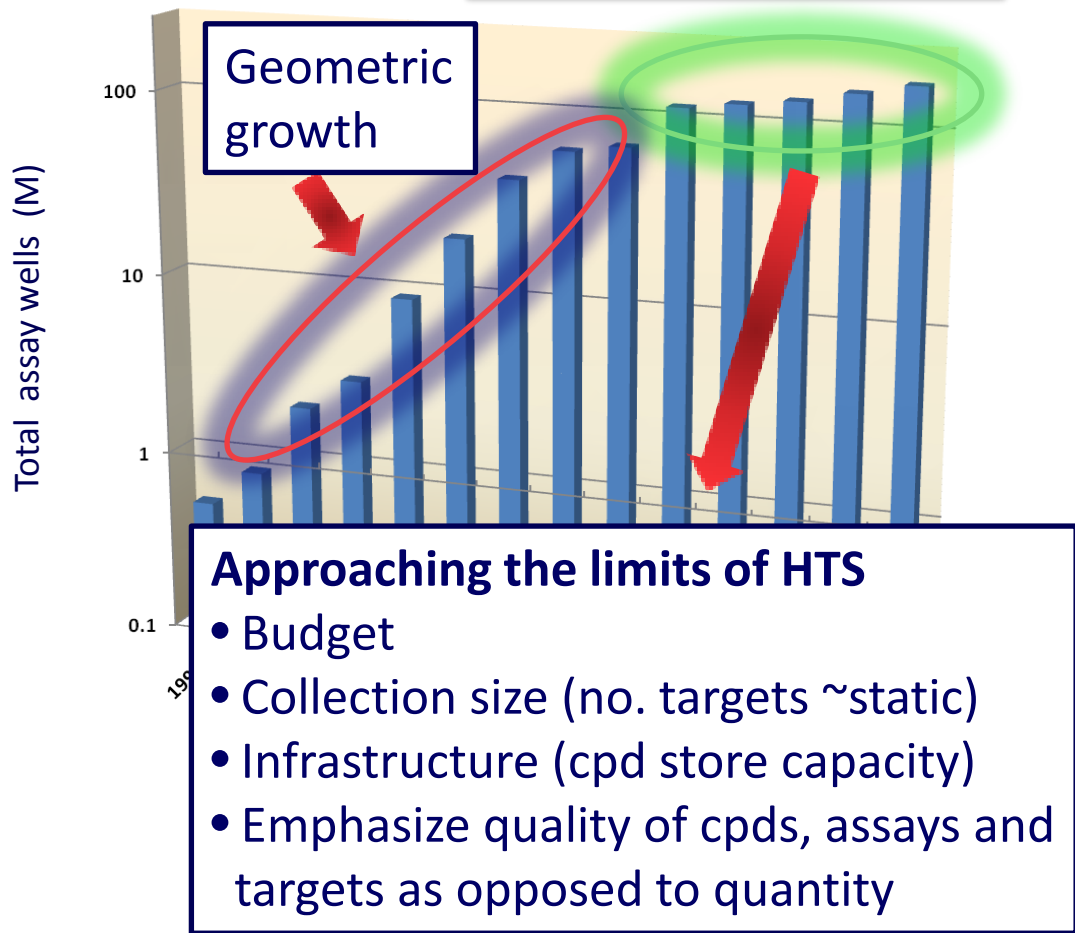


Overall spend

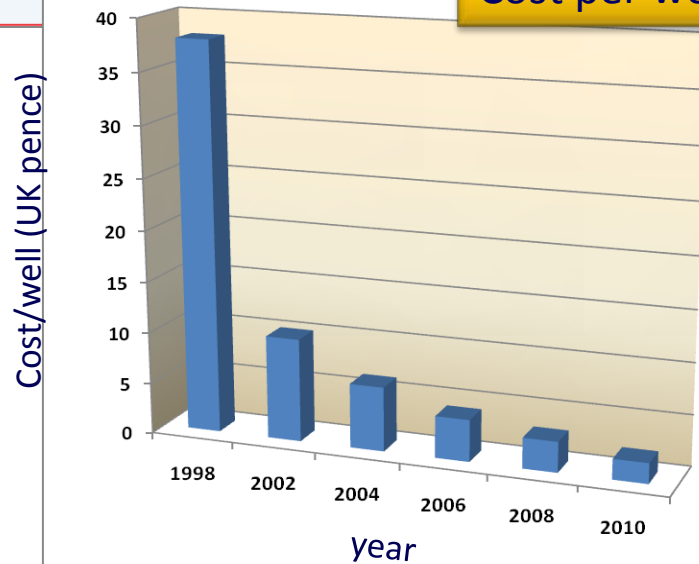


Cost and volume

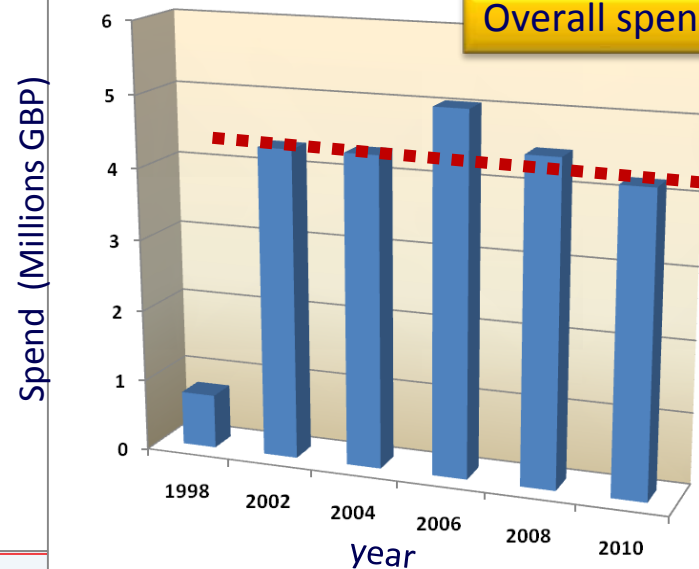
Total HTS wells



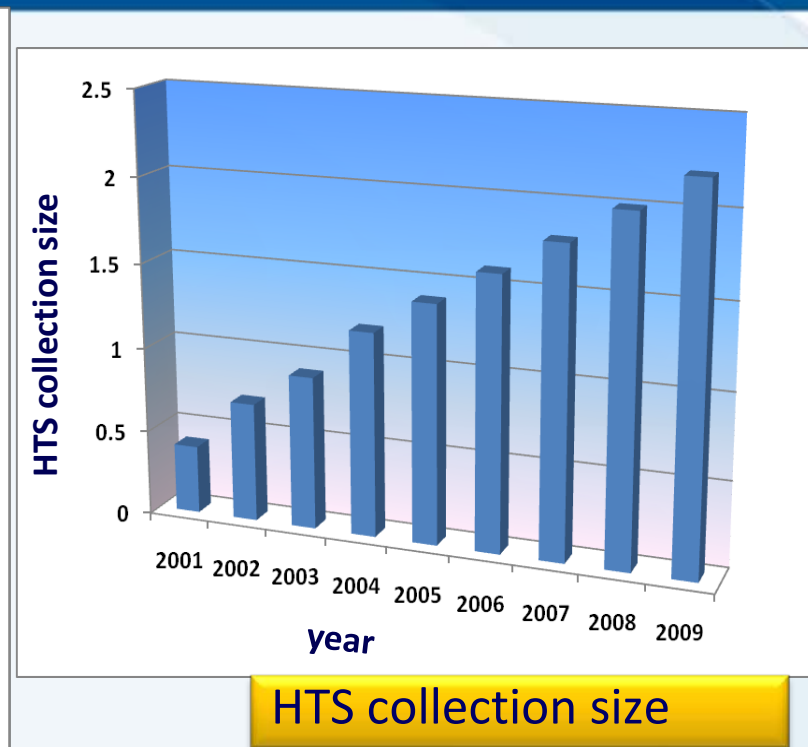
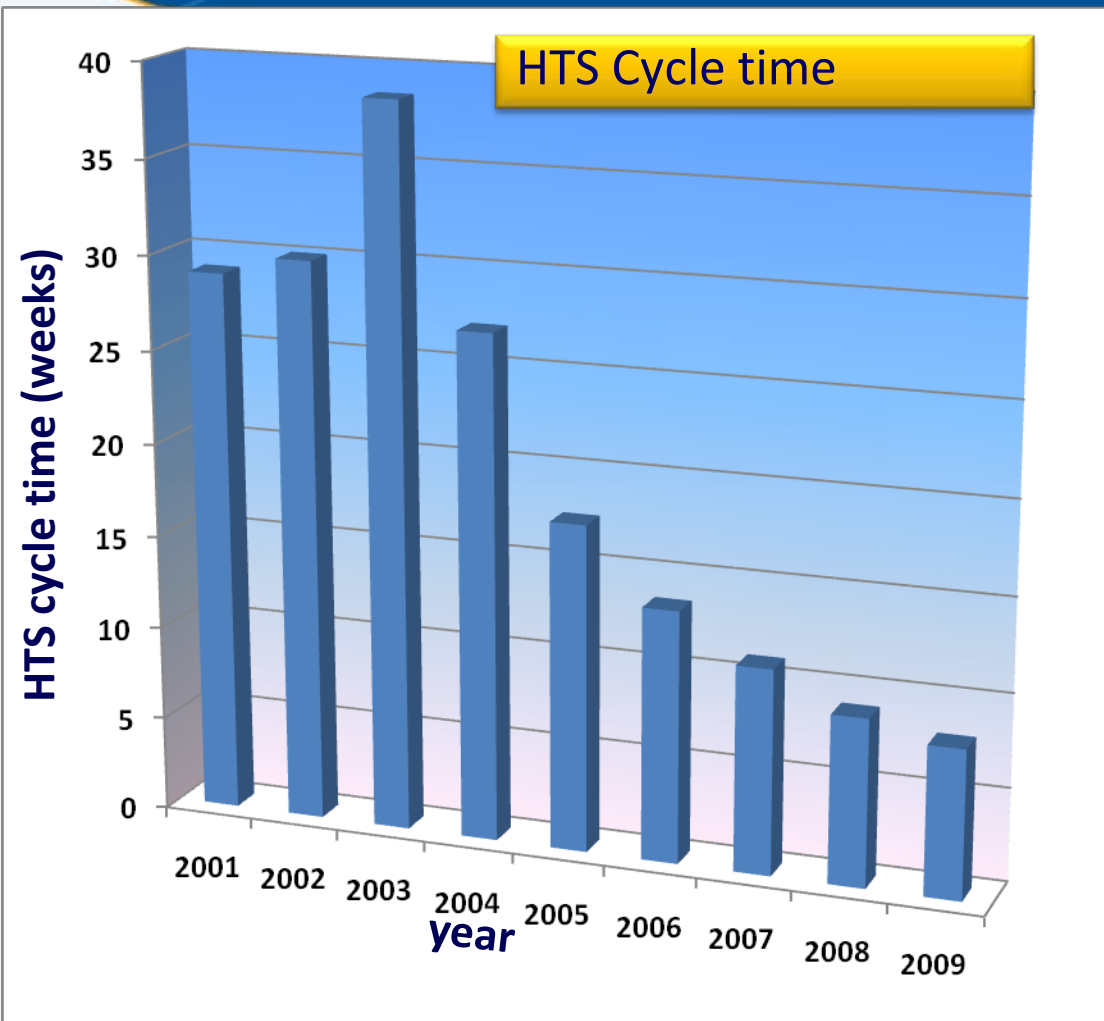
Cost per well



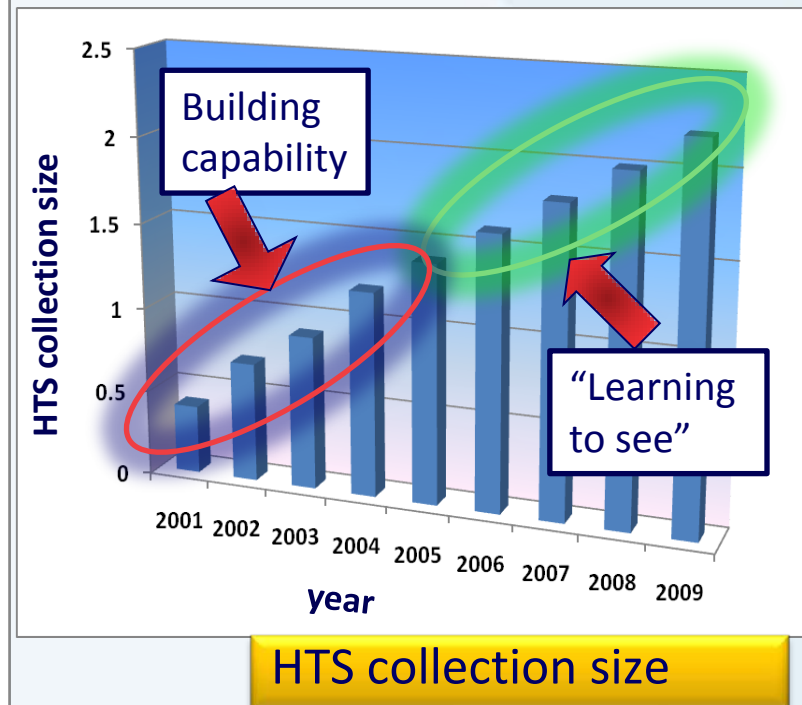
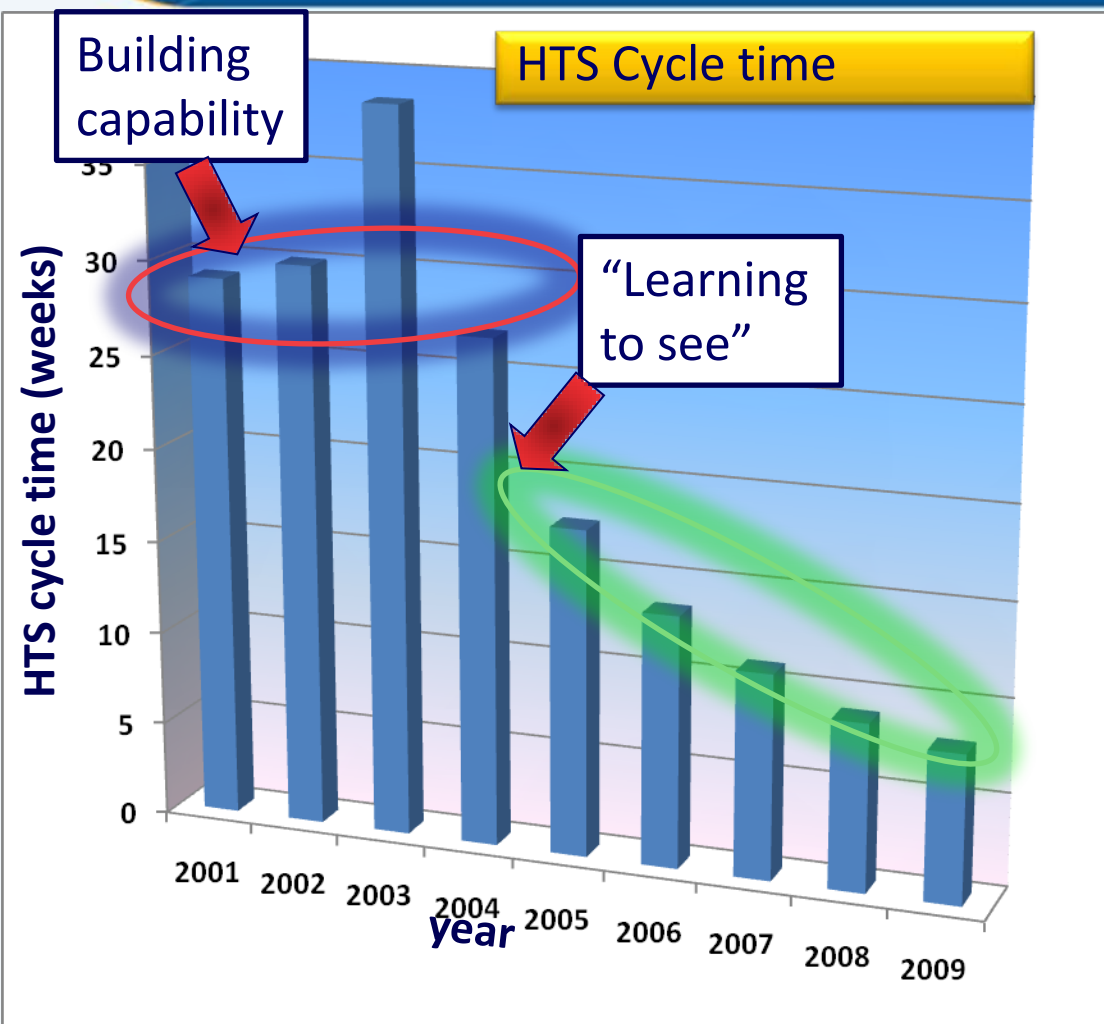
Overall spend



Cycle times and scale for HTS in the last decade



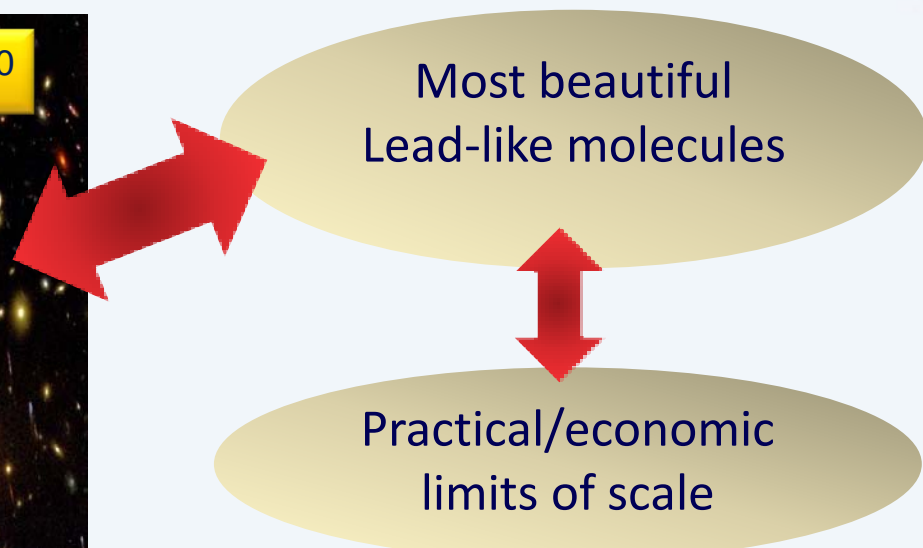
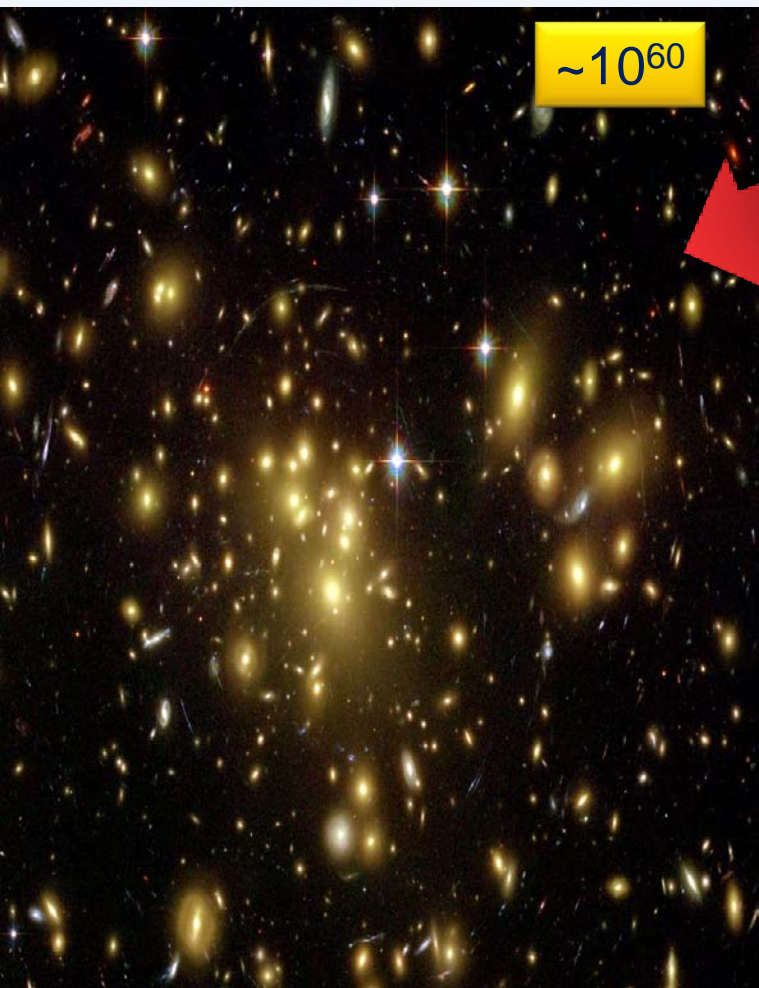
Cycle times and scale for HTS in the last decade



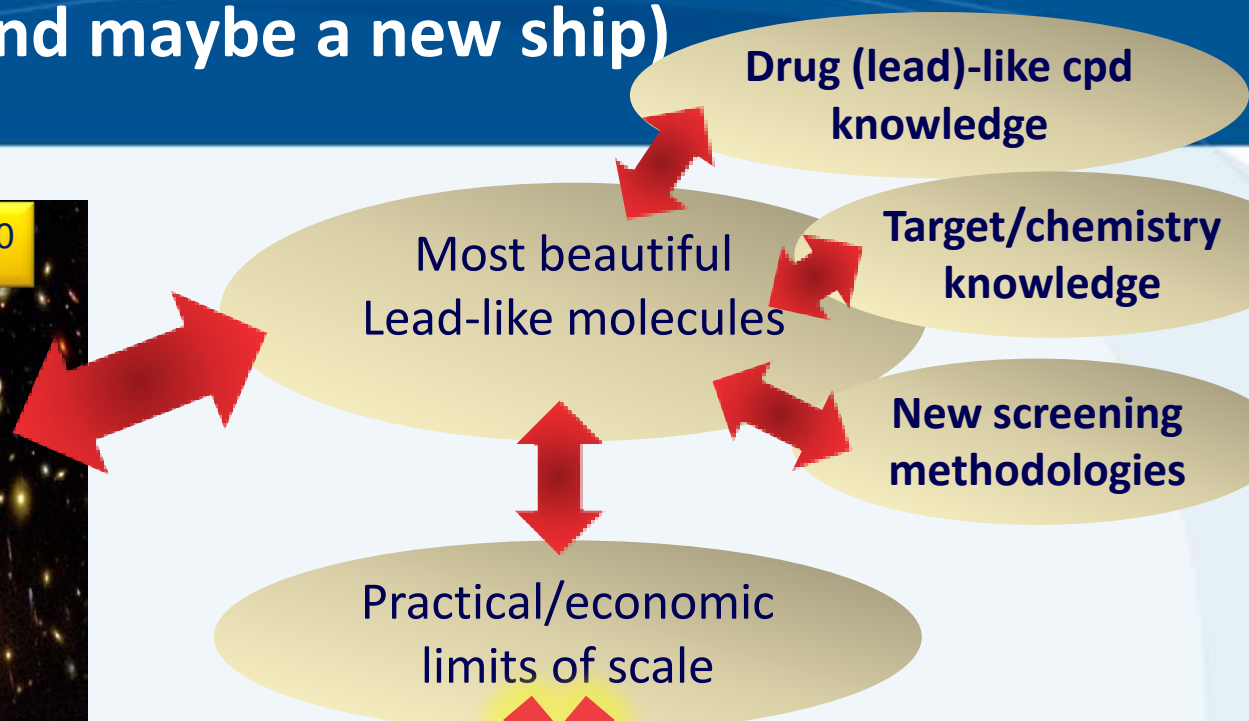
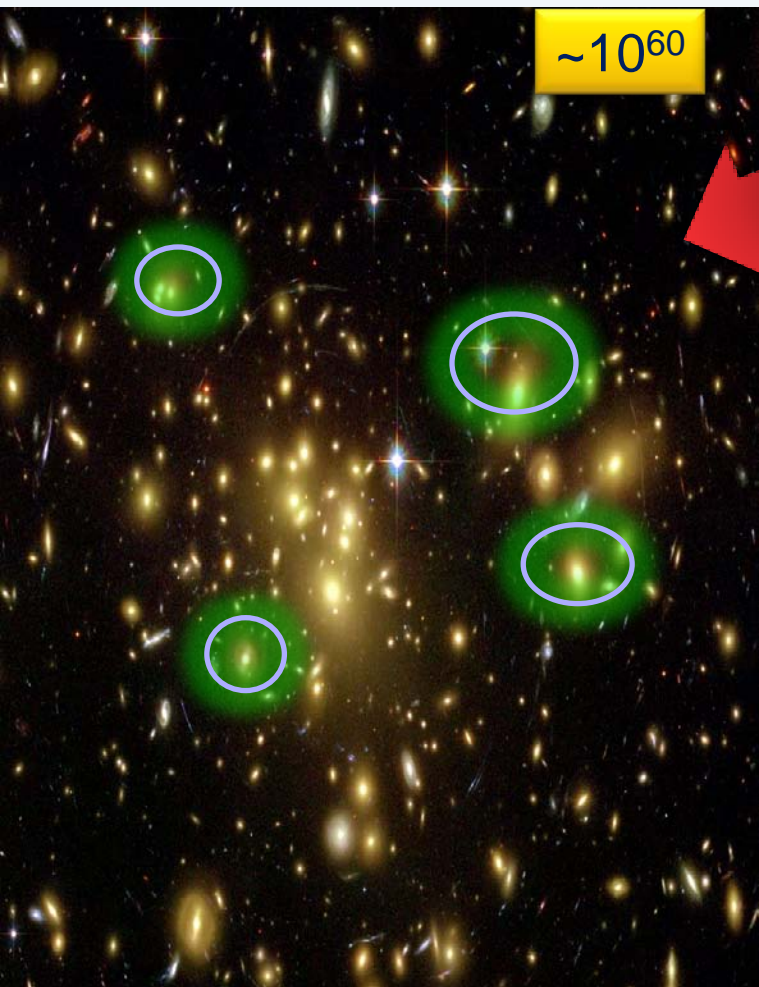
Looking back on the last 20 years..

- 1990 – Screening (as opposed to design) becomes the method of choice to discover drug starting points.**
- 1995 – Excitement builds around genome sequencing and combi-chem**
- 2000 - Major investments to “industrialize” drug discovery**
- 2005 - Major focus on time, cost, efficiency, quality (i.e. real data manufacturing)**
- 2008 - Focus on “re-personalizing” drug discovery, solving drug attrition, maximizing success on difficult targets, “new” biology**
- 2010 - Integration, flexibility and return on investment in a cost-constrained environment**

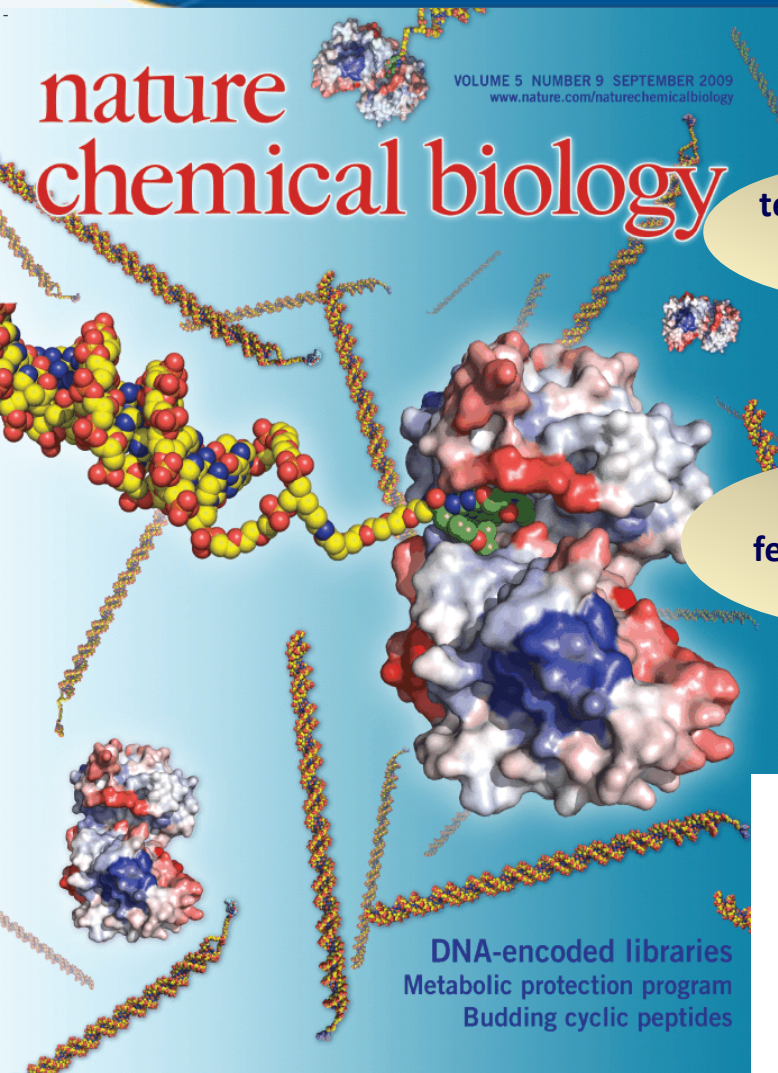
Drug-like space might be huge.....



We need a map...(and maybe a new ship)



A different screening paradigm...DNA Encoded Libraries



Library size $\sim 10^{10}$ compounds

test in biological assay

μg target protein + μL library pool

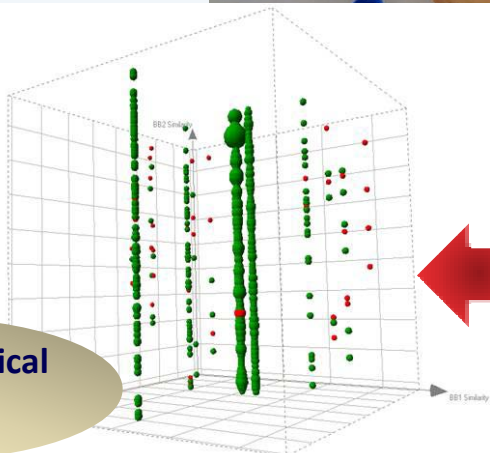


synthesize feature cpds off-DNA

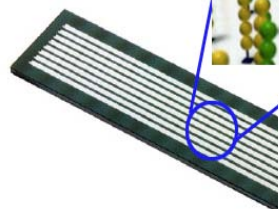


affinity-based selection

Sequence DNA tags



Identify chemical "features"



illumina®

ELT removes the infrastructure cost ceiling

HTS cpd store

- ~ 25,000 sq ft
- ~ 2.5×10^6 compounds
- ~ 11 full time staff, incl. engineer
- ~ max capacity ~3.5M



ELT cpd store

- 2 small freezers
- ready to use aliquots
- > 10^{10} compounds
- 1 part time person to maintain libraries
- No limit to capacity



..But, all chemical diversity needs to be synthesized in house..

..and all hits need off-DNA synthesis

Looking back on the last 20 years..

- 1990 – Screening (as opposed to design) becomes the method of choice to discover drug starting points.**
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Integration, choice & knowledge incorporation

- Key to increasing success and investment return

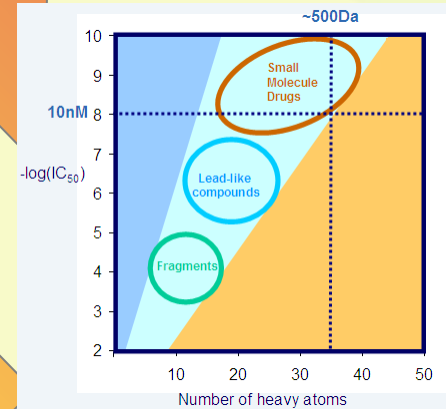
HTS

- maximize diversity, "lead likeness"
- big scale process (3M wells)
- cpds handled conventionally



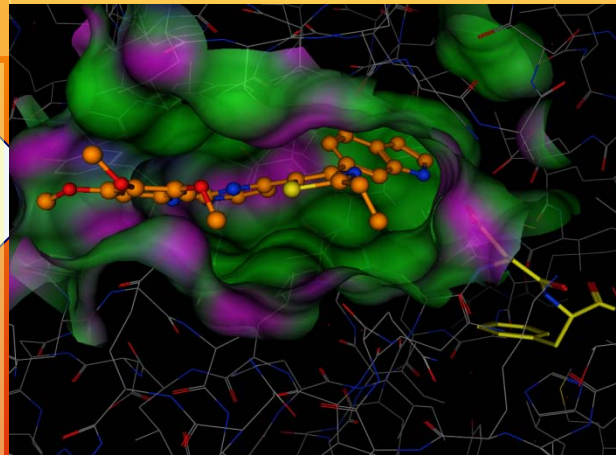
Fragment screening

- smallest, most efficient starting points for lead optimization



Structure-based design

- takes starting points from all other methods
- Xstallography of protein bound cpds
- Ab initio design methods



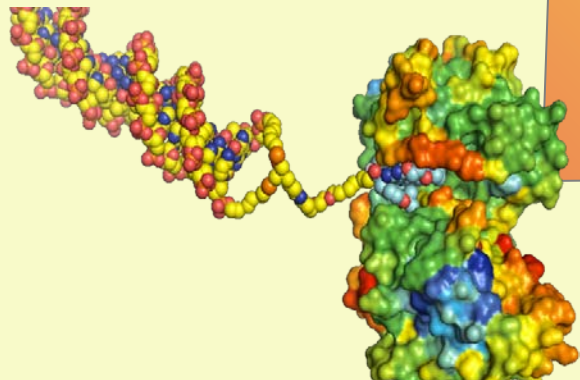
Focussed screening

- exploit chemical/biological connectivity of therapeutic targets
- biased to certain target types
- small scale process (quick, early)



ELT

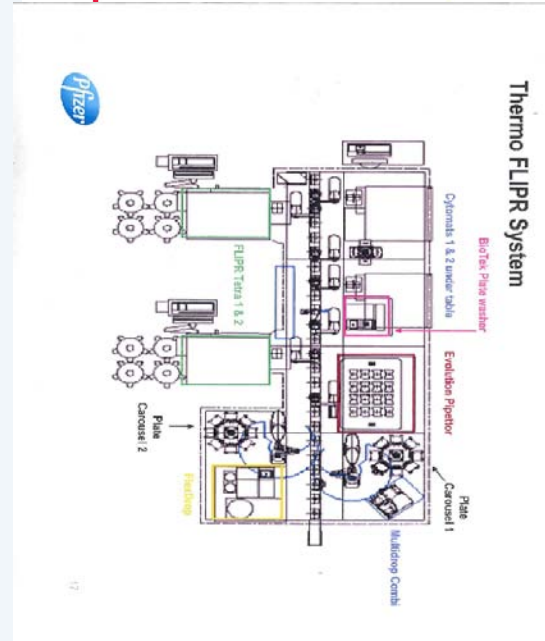
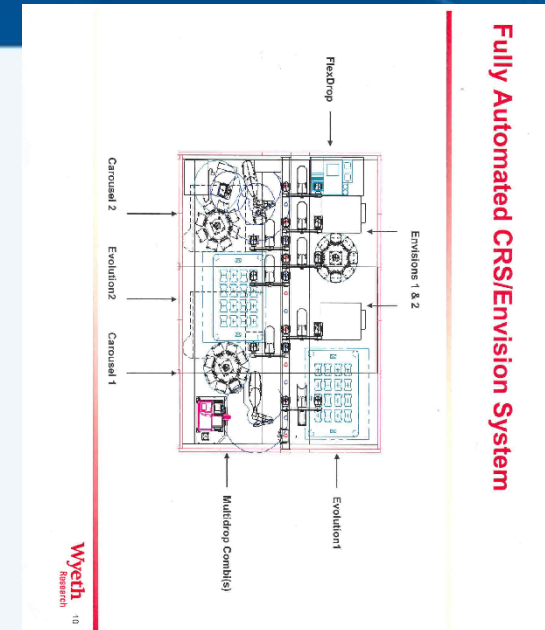
- maximize diversity, "lead-like cores"
- small flexible process
- cpds need to be made to follow up



2010 – Another visit to integrated automation



- Easy integration of components
- Plate motions not limiting
- Flexible design/re-tool
- Bucket brigade-like throughput



Summary



Automation has played a key role in the evolution of methods to discover new medicines



Within the existing paradigm, the HTS physical process is close to optimal, given sustainable investment levels

- *Focus on best possible chemical libraries*
- *Understanding chemical: biological relationships in data*
- *Screening novel disease biology in new ways*
- *Integration (or intelligent choice) of methods*



We will continue to need and to develop automation technology to help discover drugs...

- *Compound biological profiles*
- *Drug safety, efficacy and attrition-risk addressed early*



Timely discovery of chemical starting points (chemical probe or potential drug) are now well addressed

- *but there is a lot more involved in making a new medicine!*

Acknowledgements

Jeff Gross, Stan Martens, Zining Wu, Dwight Morrow, Tony Jurewicz, Glenn Hofmann, Christina Schulz-Pritchard, Mehul Patel and team members

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Ricardo Macarron, Sue Crimmin and colleagues (cpd supply)

Barry Morgan, Jeff Messer and colleagues (ELT)

Plus numerous other colleagues past and present.....