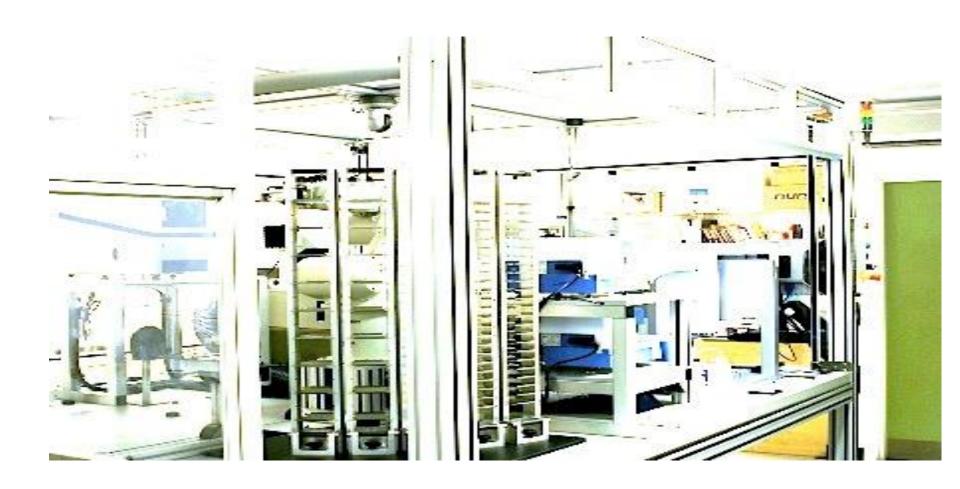
The Automation of Science

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Scientific Discovery

Technology Drivers

- n Improved computer hardware:
 - faster processors, more processors, GPUs, ...
- Improved data availability:
 - computers recording almost everything, deep data, ...
- Improved computer software:
 - new machine learning methods, deep mining, ...

Artificial Intelligence (AI)

- There have been multiple AI hype cycles, but this time it seems different.
- AI, especially machine learning, is now the hottest technology on the planet. Speed of Advance has surprised me.
- Machine Learning is the core technology of Google, Facebook, Amazon, ... Tencent, Alibaba, Baidu, ...

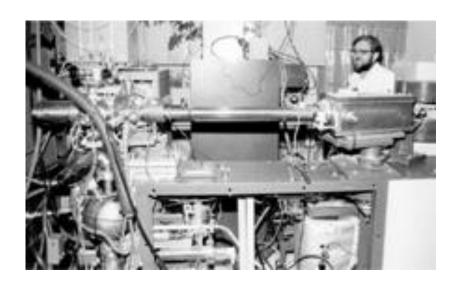
AI Systems have Superhuman Scientific Reasoning Powers

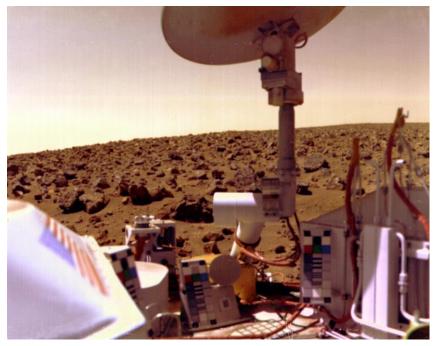
- Flawlessly remember vast numbers of facts
- Execute flawless logical reasoning
- Execute optimal probabilistic reasoning,
- Learn more rationally than humans
- Learn from vast amounts of data
- Extract information from millions of scientific papers.
- n Etc.

Scientific Discovery

- Scientific problems are abstract, but involve the real-world.
- Scientific problems are restricted in scope no need to know about "Cabbages and Kings".
- Nature is honest no malicious agents.
- Nature is a worthy object of our study.
- The generation of scientific knowledge is a public good.

Meta-Dendral

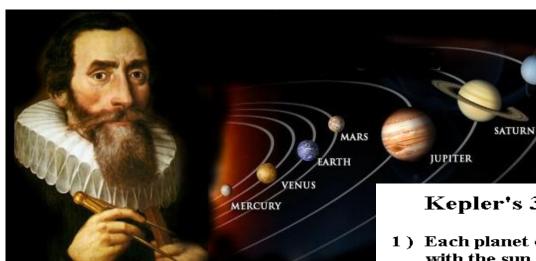




Analysis of mass-spectrometry data.

Joshua Lederburg, Ed. Feigenbaum, Bruce Buchanan, Karl Djerassi, *et al.* 1960-70s.

Bacon



Kepler's 3 Laws of Planetary Motion

- 1) Each planet orbits the sun in an elliptical path with the sun at one focus
- 2) The radius vector (from sun to planet) sweeps out equal areas in equal time intervals
- 3) The square of the period is proportional to the cube of the semi-major axis of the orbit

i.e.
$$T^2 = k a^3$$
 for some constant k

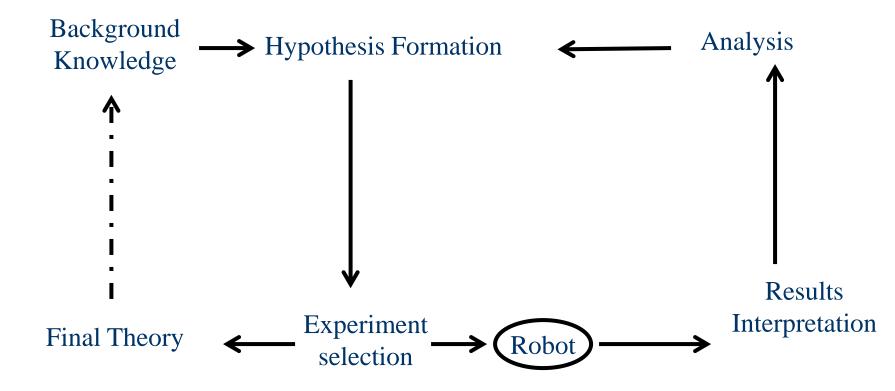
Figure 11.1

Rediscovering physics and chemistry: Langley, Bradshaw, Simon (1979).

Robot Scientists

The Concept of a Robot Scientist

Computer systems capable of originating their own experiments, physically executing them, interpreting the results, and then repeating the cycle.

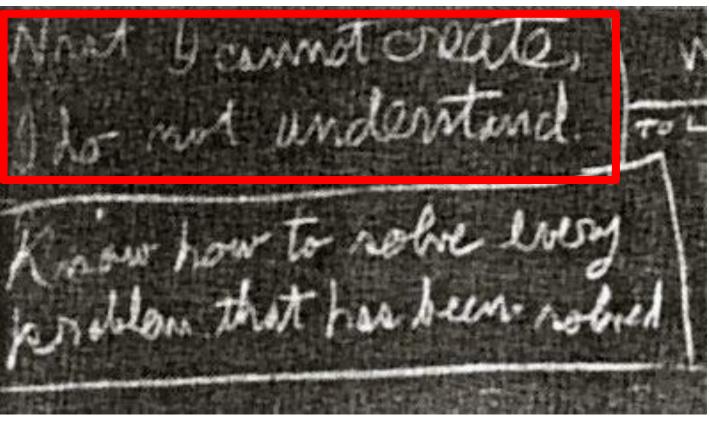


Motivation: Philosophical

- Mhat is Science?
- The question whether it is possible to automate scientific discovery seems to me central to understanding science.
- There is a strong philosophical position which holds that we do not fully understand a phenomenon unless we can make a machine which reproduces it.

Richard Feynman's Blackboard





"What I cannot create, I do not understand"

Motivation: Technological

- Robot Scientists have the potential to increase the productivity of science. They can work cheaper, faster, more accurately, and longer than humans. They can also be easily multiplied.
 - Enabling the high-throughput testing of hypotheses.
- Robot Scientists have the potential to improve the quality of science.
 - by enabling the description of experiments in greater detail and semantic clarity.

Robot Scientist Timeline

- n 1999-2004 Initial Robot Scientist Project
 - Limited Hardware: Collaboration with Douglas Kell (Aber Biology), Steve
 Oliver (Manchester), Stephen Muggleton (Imperial)

King et al. (2004) Nature, 427, 247-252

- 2004-2011 Adam Yeast Functional Genomics
 - Sophisticated Laboratory Automation: Collaboration with Steve Oliver (Cambridge).

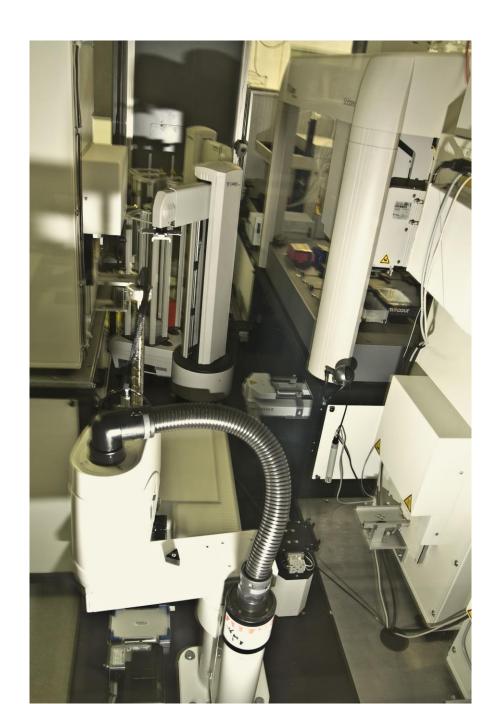
King et al. (2009) Science, 324, 85-89

- n 2008-2015 Eve Drug Design for Tropical Diseases
 - Sophisticated Laboratory Automation: Collaboration with Steve Oliver (Cambridge)

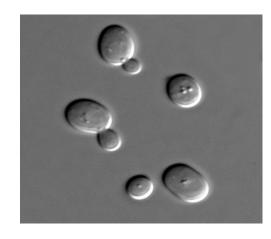
Williams et al. (2015) Royal Society Interface, DOI 10.1098/rsif.2014.1289

- n 2015-2018 Eve Human cells Cancer, Yeast Aging
 - DARPA, CHIST-ERA

Adam



The Application Domain



- Functional genomics
- n In yeast (*S. cerevisiae*) ~15% of the 6,000 genes still have no known function.
- EUROFAN 2 made all viable single deletant strains.
- Task to determine the "function" of a gene by growth experiments.

Formalising the Problem

- Use logic programming to represent background knowledge: metabolism modelled as a directed labeled hyper-graph.
- Use abduction to infer new hypotheses:
 - Abductive logic programming.
 - Techniques from Bioinformatics.
- Use active learning to decide efficient experiments: cost of compounds and time.
- Use machine learning to decide meaning of experimental results.

Deduction

Rule: All swans are white.

Fact: Daffy is a swan.

Daffy is white.

Abduction

Rule: All swans are white.

Fact: Daffy is white.

∴ Daffy is a swan.

Induction

Fact: Daffy is a swan and white.

Fact: Tweety is a swan and white

∴ All swans are white.

Deduction

Rule: All swans are white.

Fact: Daffy is a swan.

Daffy is white.

Abduction

Rule: All swans are white.

Fact: Daffy is white.

∴ Daffy is a swan. Daffy is a duck.

Induction

Fact: Daffy is a swan and white.

Fact: Tweety is a swan and white

:. All swans are white.

Deduction

Rule: All swans are white.

Fact: Daffy is a swan.

Daffy is white.

Abduction

Rule: All swans are white.

Fact: Daffy is white.

∴ Daffy is a swan.

Induction

Fact: Daffy is a swan and white.

Fact: Tweety is a swan and white

∴ All swans are white.

Deduction

Rule: All swans are white.

Fact: Daffy is a swan.

Daffy is white.

Abduction

Rule: All swans are white.

Fact: Daffy is white.

∴ Daffy is a swan.

Induction

Fact: Daffy is a swan and white.

Fact: Tweety is a swan and white

:. All swans are white.

Bruce is a black swan.

Novel Science

- Adam generated and confirmed novel functional-genomics hypotheses concerning the identify of genes encoding enzymes catalysing orphan reactions in the metabolic network of the yeast *S. cerevisiae*.
- Adam's conclusions have been manually verified using bioinformatic and biochemical evidence.
- Adam was the first machine to autonomously discover novel scientific knowledge: hypothesise, and experimentally confirm.

Novel Scientific Knowledge

Orphan Enzyme		Hypothesised Gene	Prob.	Acc.	No.	Existing Annotation	Dry	Wet
1	glucosamine-6-phosphate deaminase (3.5.99.6)	YHR163W (SOL3)	<10-4	97	8	'6-phosphogluconolactonase' ida	-	5
2	glutaminase (3.5.1.2)	YIL033C (BCY1)	<10-4	92	11	'cAMP-dependent protein kinase inhibitor' ida	x ?	*
3	L-threonine 3-dehydrogenase (1.1.1.103)	YDL168W (SFA1)	< 10-4	83	6	'alcohol dehydrogenase' ida	-	2
4	purine-nucleoside phosphorylase (2.4.2.1)	YLR209C (PNP1)	<10-4	82	11	'purine-nucleoside phosphorylase' ida	~	5
5	2-aminoadipate transaminase (2.6.1.39)	YGL202W (ARO8)	< 10-4	80	3	'aromatic-amino-acid transaminase' ida	1	1
6	5,10-methenyltetrahydrofolate synthetase (6.3.3.2)	YER183C (FAU1)	<10-4	80	4	'5,10 formyltetrahydrofolate cyclo-ligase' ida	✓	2
7	glucosamine-6-phosphate deaminase (3.5.99.6)	YNR034W (SOL1)	< 10-4	79	2	'possible role in tRNA export'		=:
8	pyridoxal kinase (2.7.1.35)	YPR121W (THI22)	< 10-4	78	1	'phosphomethylpyrimidine kinase' iss	-	4
9	mannitol-1-phosphate 5-dehydrogenase (1.1.1.17)	YNR073C	< 10-4	78	6	'putative mannitol dehydrogenase' iss	-	3
10	1-acylglycerol-3-phosphate O-acyltransferase (2.3.1.51)	YDL052C (SLC1)	0.0001	80	6	'1-acylglycerol-3-phosphate O-acyltransferase' ida	✓	
11	glucosamine-6-phosphate deaminase (3.5.99.6)	YGR248W (SOL4)	0.0002	78	2	'6-phosphogluconolactonase' ida	-	¥:
12	maleylacetoacetate isomerase (5.2.1.2)	YLL060C (GTT2)	0.0003	76	3	'glutathione S-transferase' ida	-	2
13	serine O-acetyltransferase (2.3.1.30)	YJL218W	0.0005	78	2	'unknown function'	-	-
14	L-threonine 3-dehydrogenase (1.1.1.103)	YLR070C (XYL2)	0.0052	75	6	'xylitol dehydrogenase' ida	-	2
15	2-aminoadipate transaminase (2.6.1.39)	YJL060W (BNA3)	0.0084	73	3	'kynurenine aminotransferase' ida	-	1
16	pyridoxal kinase (2.7.1.35)	YNR027W	0.0259	76	2	'involved in bud-site selection' iss	- 1	
17	polyamine oxidase (1.5.3.11)	YMR020W (FMS1)	0.0289	78	4	'polyamine oxidase' ida	1	2
18	2-aminoadipate transaminase (2.6.1.39)	YER152C	0.0332	74	3	'uncharacterized'	-	1
19	L-aspartate oxidase (1.4.3.16)	YJL045W	0.1300	72	1	'succinate dehydrogenase isozyme' iss	- 1	*
20	purine-nucleoside phosphorylase (2.4.2.1)	YLR017W (MEU1)	0.1421	72	6	'methylthioadenosine phosphorylase' ida	1	-

Formalising Science

Formalisation of Science

- The goal of science is to increase our knowledge of the natural world through the performance of experiments.
- This knowledge should be expressed in <u>formal logical</u> <u>languages</u>.
- Formal languages promote semantic clarity, which in turn supports the free exchange of scientific knowledge and simplifies scientific reasoning.

Robot Scientist & Formalisation

- Robot Scientists provide excellent test-beds for the development of methodologies for formalising science.
- Using them it is possible to completely capture and digitally curate all aspects of the scientific process.
- The ontology LABORS is designed to enable the open access of the Robot Scientist experimental data and metadata to the scientific community.

<u>Ontologies</u>

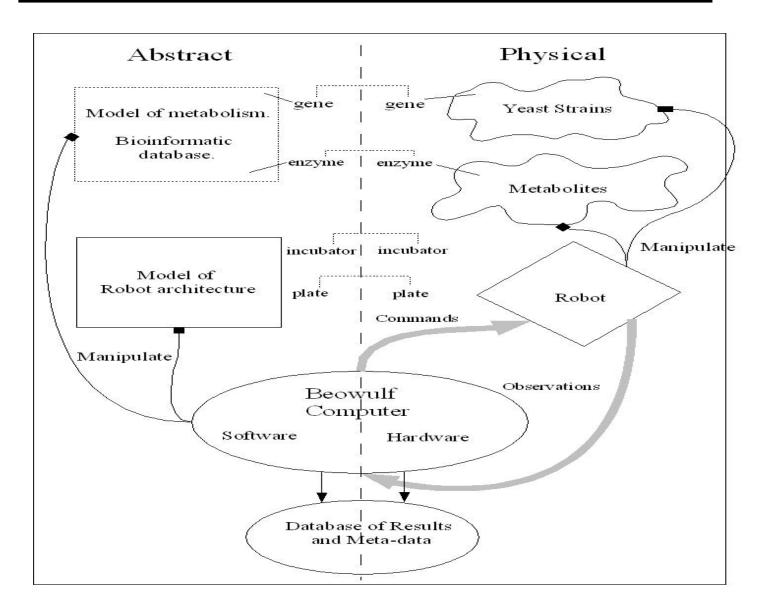
An ontology is "a concise and unambiguous description of what principal entities are relevant to an application domain and the relationship between them"*.

*Schulze-Kremer, S., 2001, Computer and Information Sci. 6(21)

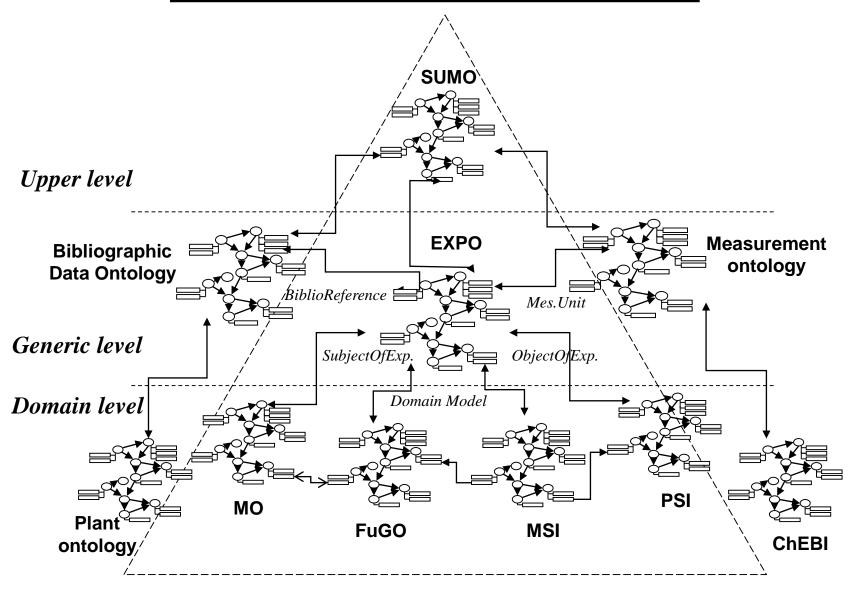
Dualism

- The most fundamental ontological division in our design of Adam is between <abstract> and <physical> objects
- We argue for this ontological division because it makes explicit the separation between models and reality.
- All the objects which Adam deals with computationally are <abstract>, and all the objects it deals with physically are <physical>.

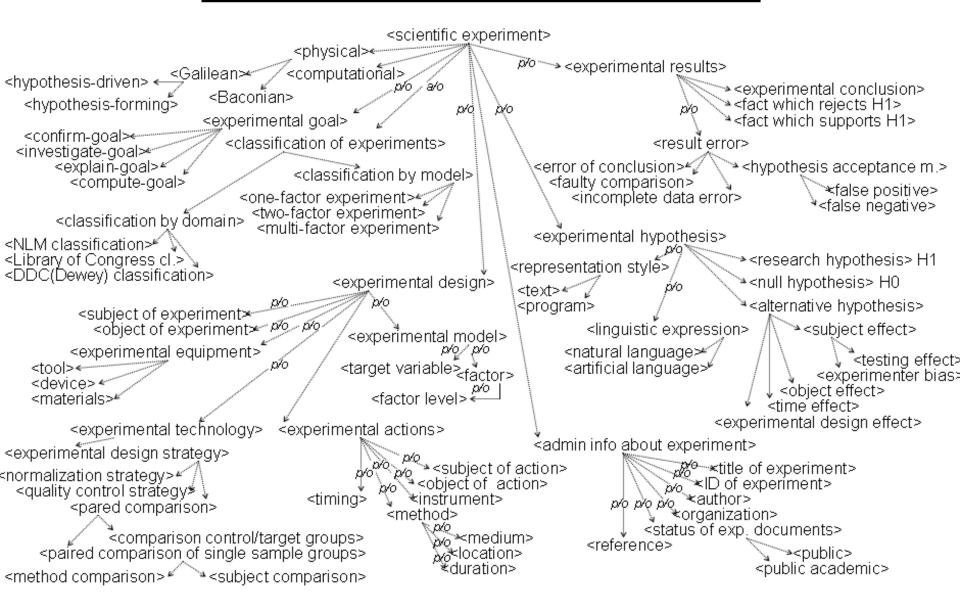
Overall View of the Universe



The Position of EXPO

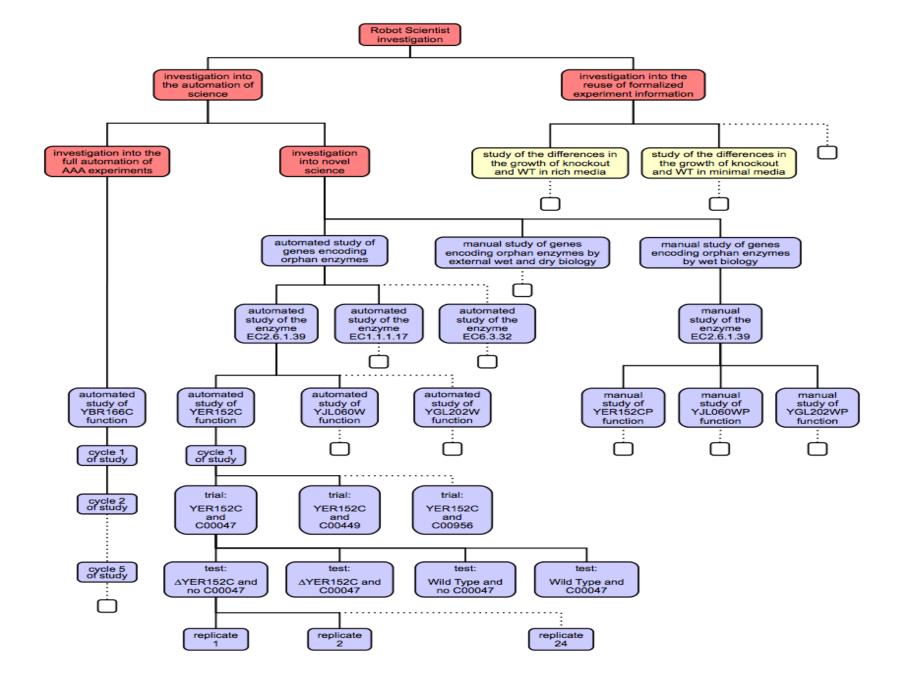


Small Section of EXPO



Adam's Investigations

- This formalisation involves >10,000 different research units in a nested tree-like structure 11 levels deep.
- It logically connects >6.6 million OD600_{nm} measurements to hypotheses, experimental goals, results, etc.
- No previous large-scale experimental work has been so comprehensively described and recorded.



Levels in the Formalisation

Investigation into the automation of Science

Investigation into the automation of novel science

<u>Investigation</u> into the automated discovery of genes encoding orphan enzymes

Automated <u>study</u> of E.C.2.6.1.39 encoding

Cycle 1 of automated study of YER152C function

YER152C and Lysine automated <u>trial</u>

Experiment 1 (wild-type no metabolite)

Replicate 1 (well)

Observation 1

automated study of yer152c function

has text representation:

automated study: automated study of yer152c_function

has domain of study: functional genomics

has investigate

has goal: 'To te with enzyme cl

has organism

has ncbi taxo

has hypothese

has negative

has cycle 1 of

has study resu encodes(yer15

highest

proporti

has study cond

has datalog representation:

a:automated study(X) :- a:automated_study_ a:hypotheses-set(X):- a:research_hypothesis a:cycle_of_study(X):-a:cycle_1_of_study_(X) a:hypotheses-set(X):- a:negative_hypothesis a:domain_of_study(Y) :- a: automated study(a:investigator(Y):- a: automated study(X), a:h a:goal(Y):- a: automated study(X), a:has_go a:organism_of_study (Y) :- a: automated stud a:hypotheses-set(Y):- a: automated study(X) a:cycle of study(Y):- a: automated study(X) a:study_result(Y):- a: automated study(X), a: a:study_conclusion(Y) :- a: automated study(a:domain_of_study(X) :- a:functional_genomi a: investigator(X) :- a:adam. a:goal(X):- a: to_test_the_hypothesis_that_g _encodes_an_enzyme_with_enzyme_class_

a:organism_of_study(X):-a:saccharomyces_

a:study_result(X):-a:the_strength_of_eviden

a:study_conclusion(X):-a:hypothesis_1_con

has OWL representation:

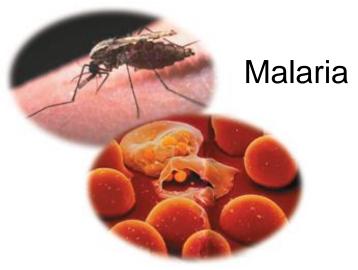
```
<?xml version="1.0"?>
<rdf:RDF
  xmlns="http://www.owl-ontologies.com/Ontology1204198571.owl#"
<owl: Class rdf:ID="goal"/>
 <owl:Class rdf:ID="study result"/>
 <owl:Class rdf:ID="ncbi taxonomy ID"/>
 <owl: Class rdf:ID="cycle of study"/>
 <owl:Class rdf:ID="negative hypothesis">
  <rdfs:subClassOf>
   <owl:Class rdf:ID="hypotheses-set"/>
  </rdfs:subClassOf>
 </owl:Class>
 <owl:Class rdf:ID="domain of study"/>
 <owl:Class rdf:ID="organism of study"/>
 <owl:Class rdf:ID="cycle 1 of study ">
  <rdfs:subClassOf rdf:resource="#cycle_of_study"/>
 </owl:Class>
 <owl: Class rdf:ID="automated study">
  <rdfs:subClassOf>
   <owl:Restriction>
    <owl:someValuesFrom rdf:resource="#goal"/>
    <owl><owl>Property
      <owl!ObjectProperty rdf:ID="has goal"/>
    </owl>
   </owl:Restriction>
  </rdfs:subClassOf>
  <rdfs:subClassOf>
   <owl:Restriction>
    <owl:someValuesFrom rdf:resource="#organism of study"/>
    <owl><owl>Property
      <owl:ObjectProperty rdf:ID="has organism of study"/>
```

Eve



Drug Design

The Application Domain



Shistosomaisis





Leishmania Chagas



Why Tropical Diseases?

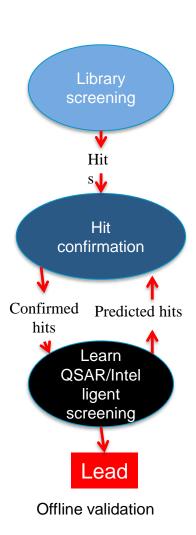
- Millions of people die of these diseases, and hundreds of millions of people suffer infection.
- It is clear how to cure these diseases kill the parasites.
- They are "neglected", so avoid competition from the Pharmaceutical industry.

Formalising the Problem

Use graphs and standard chemoinformatic methods to represent background knowledge - the use of relations is planned.

- Uses induction (quantitative structure activity relationship –
 QSAR learning) to infer new hypotheses.
- Use active learning to decide efficient experiments, and econometric model to decide what compounds to test.

Eve's Automation of Pipeline



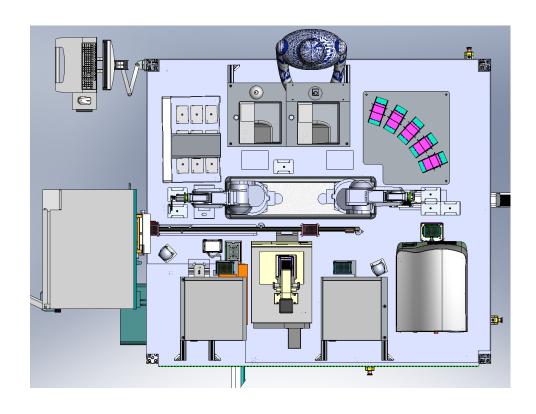
- Standard library screening is brute force:
- Eve uses intelligent screening

- In the standard "pipeline" the 3 processes are not integrated.
- In Eve automated and integrated.

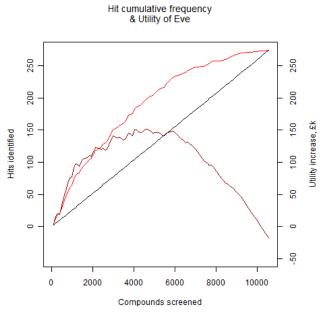
Eve's Hardware

Highlights of Eve's hardware:

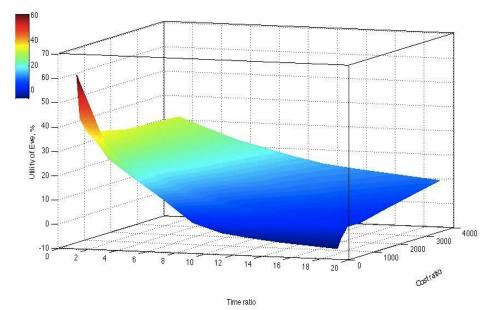
- Acoustic liquid handling
- High throughput 384 well plates
- Two industrial robot arms
- Automated 60x microscope
- Liquid handlers, fluorescence readers, barcode scanners, dry store, incubator, tube decapper ...



The Economics of Intelligent Screening



Uh



 $\Delta \, Utility \, of \, Eve = \sum_{i}^{Nm} (Tm + Cm) \, + \sum_{i}^{Nx} (Tc + Cc - Uh) \, + \sum_{i}^{Ne} (Tm - Tc + Cm - Cc)$

Nm	-	Number of compounds not assayed by Eve
Tm	-	Cost of the time to screen a compound using the mass screening assay
Cm	-	Cost of the loss of a compound in the mass screening assay
Nx	-	Number of hits missed by Eve
Tc	-	Cost of the time to screen a compound using a cherry-picking (confirmation or intelligent) assay
Cc	-	Cost of the loss of a compound in a cherry-picking assay

Utility of a hit

Ne - Number of compounds assayed by Eve

Triclosan Repositioned for Malaria

- Simple compound
- Known to be safe used in toothpaste.
- Targets both DHFR and FAS-II well established targets.
- Demonstrated activity using multiple wet experimental techniques.
- Works against wild-type and drug-resistant Plasmodium falciparum, and Plasmodium vivax.

Future Prospects

The Future?

- In Chess/Go there is a continuum of ability from novices up to Grandmasters.
- I argue that this is also true in science, from the simple research of Eve, through what most human scientists can achieve, up to the ability of a Newton or Einstein.
- If you accept this, then just as in Chess/Go, it is likely that advances in computer hardware and software will drive the development of ever smarter Robot Scientists.
- In favour of this argument are the ongoing development of Al and laboratory robotics.

Vision

- The collaboration between Human and Robot Scientists will produce better science than either can alone human/computer teams still play better chess that either alone.
- Scientific knowledge will be primarily expressed in logic with associated probabilities and published using the Semantic Web.
- The improved productivity of science leads to societal benefits: better food security, better medicines, etc.
- The Physics Nobel Frank Wilczek is on record as saying that in 100 years' time the best physicist will be a machine

Conclusions

- Science is a wonderful application area for AI.
- Automation is becoming increasingly important in scientific research e.g. DNA sequencing, drug design.
- The Robot Scientist concept is the logical next step in scientific automation.
- The Robot Scientist Adam was the first machine to have discovered novel scientific knowledge.
- The Robot Scientist Eve has found new lead compounds for neglected tropical diseases.
- The Robot Scientist Eve can accelerate systems biology modelling.

Acknowledgments

- The Robot Scientist team: Manchester, Aberystwyth, Cambridge, Brunel, Leuven, Thailand. (BBSRC)
- n Chicago Big Mechanism consortium. (DARPA)
- AdaLab consortium. (CHIST-ERA)
- AIST (Tokyo)