Translating a trillion points of data into therapies, diagnostics, and new insights into disease

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Disclosures

• Scientific founder and advisory board membership
  – Genstruct
  – NuMedii
  – Personalis
  – Carmenta

• Honoraria for talks
  – Lilly
  – Pfizer
  – Siemens
  – Bristol Myers Squibb
  – AstraZeneca
  – Roche
  – Genentech

• Past or present consultancy
  – Lilly
  – Johnson and Johnson
  – Roche
  – NuMedii
  – Genstruct
  – Tercica
  – Ecoeos
  – Ansh Labs
  – Prevendia
  – Samsung

  – Assay Depot
  – Regeneron
  – Verinata
  – Geisinger
  – Covance

• Corporate Relationships
  – Northrop Grumman
  – Aptalis
  – Thomson Reuters

• Speakers’ bureau
  – None

• Companies started by students
  – Carmenta
  – Serendipity
  – NuMedii
  – Stimulomics
  – NunaHealth
  – Praedicat
  – MyTime
  – Flipora
The data deluge

AND HOW TO HANDLE IT: A 14-PAGE SPECIAL REPORT
The data deluge
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Big Data in Biomedicine

Data's shameful neglect

Research cannot flourish if data are not maximally available. Brooks Hanson is Deputy Editor for Physical Sciences at nature.

Making Data Maximally Available

Sharing research data to improve public health

The purpose of medical research is to analyse and understand health and disease. A key and expensive element is the study of populations to explore how interactions between behaviour and environment, in the context of genetic diversity, determine causation and variation in health. Ensuring data are made widely available to the research community accelerates the pace of discovery and enhances the efficiency of the research enterprise.
John Holdren, Director of the Office of Science and Technology Policy, “has directed Federal agencies with more than $100M in R&D expenditures to develop plans to make the published results of federally funded research freely available to the public within one year of publication and requiring researchers to better account for and manage the digital data resulting from federally funded scientific research.”
**Gene data to hit milestone**

By MONICA RIVER

With close to one million gene-expression data sets in publicly available databases, the number of gene-expression data sets has climbed to nearly one million over the past decade.

**DATA DUMP**

The number of gene-expression data sets in publicly available databases has climbed to nearly one million over the past decade.

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<th>ArrayExpress</th>
<th>GEO</th>
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<td>2012</td>
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*as of 13 July*
Nearly 1.4 million microarrays available
Doubles every 2-3 years

Results: 1 to 20 of 46046

1. Leukemia inhibitory factor effect on Sin3a-silenced MCF7 breast cancer cell line
   Analysis of SIN3 transcription regulator homolog A (Sin3a)-depleted MCF7 cells stimulated with LIF cytokine to activate signal transducer and activator of transcription 3 (STAT3). STAT3 transcription factor is a potent oncogene. Results provide insight into role of Sin3a in mediating STAT3 activity.
   Organism: Homo sapiens
   Type: Expression profiling by array, transformed count, 2 agent, 2 genotype/variation sets
   Platform: GPL570 Series: GSE35966 11 Samples
   Download data: GEO (CEL)
   DataSet Accession: GDS4388 ID: 4388
   PubMed Full text in PMC Similar studies GEO Profiles Analyze DataSet

2. Co-expression of tyrosine kinase receptors HER2 and HER3 in mammary epithelial cells MCF10A grown in three-dimensional cultures
   Analysis of MCF10A mammary epithelial cells expressing HER2, HER3, or HER2/HER3 heterodimer. Co-expression of HER2 and HER3 induced migration and invasion of MCF10A cells. Results provide insight into the role of HER2 and HER3 in breast cancer.
   Organism: Homo sapiens
   Type: Expression profiling by array, transformed count, 4 genotype/variation sets
Public big data = retroactive crowd-sourcing
17-year-old programs artificial 'brain' to diagnose breast cancer

Published July 25, 2012 / InnovationWaves/Daily Staff

A high school junior has created a computer brain that can diagnose breast cancer with 99 percent sensitivity.

Seventeen-year-old Brittany Wenger of Sarasota, Fla., wrote a breast cancer-diagnosing app based on an artificial neural network, basically a computer program whose structure is inspired by the way brain cells connect with one another. She won grand prize at the Google Science Fair for her invention in a ceremony held in Palo Alto, Calif. last night (July 23).

Like other artificial intelligence programs, artificial neural networks "learn" what to do by analyzing sample training cases and then perform better if they get

Teen develops algorithm to diagnose leukaemia

May 22, 2013 - 8:44AM
Vignesh Ramachandran

Brittany Wenger isn't your average high-school student: she taught a computer how to diagnose leukaemia.

"The most amazing part about science is you can answer questions and really revolutionise the world and our knowledge base..."
Trees in Biomedicine

- Linnaeus 1707-1778
- Promoted binomial nomenclature for taxonomy
  - *Homo sapiens, Mus musculus*
- But 300 year old trees need crutches!
- Species are commonly rearranged based on DNA
  - *Pneumocystis jiroveci* and *Pneumocystis carinii*
Trees of disease: Nosology

• Linnaeus also co-founder of systematic nosology
  – Nosology = classification of disease
  – *Genera Morborum* (1763)

• Why not classify diseases based on genomics?
  – Could reshuffle thinking about diseases and drugs
  – Use public big data to do this!

<table>
<thead>
<tr>
<th>Exanthematic</th>
<th>Feverish, with skin eruptions</th>
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<tbody>
<tr>
<td>Critical</td>
<td>Feverish, with urinary problems</td>
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<tr>
<td>Phlogistic</td>
<td>Feverish, with heavy pulse and topical pain</td>
</tr>
<tr>
<td>Dolorous</td>
<td>Painful</td>
</tr>
<tr>
<td>Mental</td>
<td>With alienation of judgment</td>
</tr>
<tr>
<td>Quietal</td>
<td>With loss of movement</td>
</tr>
<tr>
<td>Motor</td>
<td>With involuntary motion</td>
</tr>
<tr>
<td>Suppressorial</td>
<td>With impeded motions</td>
</tr>
<tr>
<td>Evacuatorial</td>
<td>With evacuation of liquids</td>
</tr>
<tr>
<td>Deformities</td>
<td>Changed appearance of solid parts</td>
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<tr>
<td>Blemishes</td>
<td>External and palpable</td>
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</tbody>
</table>

Bramley M. Coding Matters 2001, 8:1.
• 39 Cancer of the buccal cavity
• 40 Cancer of stomach and liver
• 41 Cancer of peritoneum, intestines, rectum
• 42 Cancer of female genital organs
• 43 Cancer of breast
• 44 Cancer of skin
• 45 Cancer of other organs or not specified

*Lung is an "other organ"; Brain is an "other organ"*
- 50 Diabetes
  - *No type 1 or type 2*
- **Endocrine diseases were under General Diseases**
- 88 Disease of the thyroid body
  - *Under Disease of the Respiratory System*
- 5 Smallpox, 13 Cholera, 15 Plague, 21 Glanders, 22 Anthrax
  - *All bioterroristic today*
- 189 Visitation from God
Human Disease Gene Expression Collection

~300 Diseases and Conditions

Blue: gene goes down in disease
Yellow: gene goes up in disease

20k+ Genes
The Truly Staggering Cost Of Inventing New Drugs

During the Super Bowl, a representative of the pharmaceutical company Eli Lilly posted on the company's corporate blog that the average cost of bringing a new drug to market is $1.3 billion, a price that would buy 371 Super Bowl ads, 16 million official NFL footballs, two pro football stadiums, pay of almost all NFL football players, and every seat in every NFL stadium for six weeks in a row. This is, of course, ludicrous.

The average drug developed by a major pharmaceutical company costs at least $1 billion to complete. And that's before it ever hits the market.
## Research Spending Per New Drug

<table>
<thead>
<tr>
<th>Company</th>
<th>Ticker</th>
<th>Number of drugs approved</th>
<th>R&amp;D Spending Per Drug ($Mil)</th>
<th>Total R&amp;D Spending 1997-2011 ($Mil)</th>
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<tbody>
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<td>AZN</td>
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<td>11,790.93</td>
<td>58,955</td>
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<tr>
<td>GlaxoSmithKline</td>
<td>GSK</td>
<td>10</td>
<td>8,170.81</td>
<td>81,708</td>
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<tr>
<td>Sanofi</td>
<td>SNY</td>
<td>8</td>
<td>7,909.26</td>
<td>63,274</td>
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<tr>
<td>Roche Holding AG</td>
<td>RHHBY</td>
<td>11</td>
<td>7,803.77</td>
<td>85,841</td>
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<tr>
<td>Pfizer Inc.</td>
<td>PFE</td>
<td>14</td>
<td>7,727.03</td>
<td>108,178</td>
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<tr>
<td>Johnson &amp; Johnson</td>
<td>JNJ</td>
<td>15</td>
<td>5,885.65</td>
<td>88,285</td>
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<tr>
<td>Eli Lilly &amp; Co.</td>
<td>LLY</td>
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<td>4,577.04</td>
<td>50,347</td>
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<tr>
<td>Abbott Laboratories</td>
<td>ABT</td>
<td>8</td>
<td>4,496.21</td>
<td>35,970</td>
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<td>Merck &amp; Co Inc</td>
<td>MRK</td>
<td>16</td>
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<tr>
<td>Bristol-Myers Squibb Co.</td>
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<td>Novartis AG</td>
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<td>Amgen Inc.</td>
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<td>3,692.14</td>
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</table>

Sources: InnoThink Center For Research In Biomedical Innovation; Thomson Reuters Fundamentals via FactSet Research Systems
Pharma Summits Patent Cliff in 2012; $290B in Sales at Risk Through 2018

By Nuala Moran
Staff Writer

BOSTON – 2012 may be the year that the patent cliff reaches its height — with $33 billion of sales at risk — but the impact of loss of exclusivity will continue to reverberate across the decade, with more than $290 billion of prescription drugs sales due to be exposed to generic competition between now and 2018.

“This is the worst year, but it will also be bad in succeeding years,” said Jonathan de Pass, founder and CEO of EvaluatePharma, the consulting firm that compiled the data. The somewhat depressing conclusions of the report, World Preview 2018, were discussed at BIO 2012 on Tuesday, as the largest partnering-fest of the year got into its swing.

In the past 10 years, a huge amount of money has been thrown at acquisitions and the restructuring of R&D, in an attempt to replace the revenues that are under threat from patent expiries. Over the same time, EvaluatePharma estimated that $1.1 trillion has been invested in R&D in a bid to revitalize pipelines.

Pharma industry executives "have blown an awful lot of cash" in a bid to swerve around the patent cliff. Unfortunately, it looks as if "the response is not sufficient," de Pass said. The forecast returns from new drugs in 2018 "are not that great."
Anti-seizure drug works against a rat model of inflammatory bowel disease

Psychiatric Drug Imipramine Shows Significant Activity Against Small Cell Lung Cancer

Vehicle control  Imipramine

p53/Rb/p130 triple knockout model of SCLC

Mice dosed after tumor formation

Joel Dudley
Nadine Jahchan
Julien Sage
Alejandro Sweet-Cordero
Joel Neal
NuMedii
- Best seller
- Irma Rombauer
- 1152 pages
- $19.47 plus shipping

Credit: Amazon
Credit: Oxford Nanopore Technologies and Wired
Sequencing Excitement

- 454/Roche, Life Technologies
- Helicos: $30k genome
- Pacific Biosystems: sequence human genome in 15 minutes
- Run times in minutes at a cost of hundreds of dollars
- 20 TB in 15 minutes
- Complete Genomics: 80 genomes/day
- Ion Torrent and Illumina: ~$1500 per genome
September 28, 2011

How Low Can We Go? Molecules, Photons, and Bits

Photons. The cost of photons is the cost of the optical and fluidic instrument designed to generate and capture photons from the fluorescent molecules. We can reduce the instrument cost per genome by successfully using more, faster cameras. Our current instruments are equipped with two electron multiplying charge coupled device (EMCCD) cameras. There is a new generation of fast complementary metal oxide semiconductor (CMOS) cameras, developed for other industries that are about 15 times faster than our current cameras (and also less expensive). New sequencing instruments that successfully use four of these fast new cameras could reduce the instrument cost per genome by about a factor of 30, from < $1,000 to $1,000/(2 x 15) or approximately $33 per genome.
Figure 2: Patient pedigree
The arrow shows the patient. Diagonal lines show relatives who are deceased. Years are age at death or diagnosis. AAA = abdominal aortic aneurysm. ARMD = age-related macular degeneration. ARVD/C = arrhythmogenic right-ventricular dysplasia or cardiomyopathy. CAD = coronary artery disease. CHF = congestive heart failure. HC = hypercholesterolaemia. HTN = hypertension. OA = osteoarthritis. SCD = sudden cardiac death (presumed). VT = paroxysmal ventricular tachycardia.

Credit: Euan Ashley, Russ Altman, Steve Quake, Lancet
<table>
<thead>
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<th>Drug(s) affected</th>
<th>Summary of effects</th>
<th>Level of evidence</th>
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<td>HMG-CoA reductase inhibitors (statins)</td>
<td>No increased risk of myopathy</td>
<td>High\textsuperscript{23, 24}</td>
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<tr>
<td>Clopidogrel and CYP2C19 substrates</td>
<td>CYP2C19 poor metaboliser; many drugs might need adjustment</td>
<td>High\textsuperscript{15}</td>
</tr>
<tr>
<td>Warfarin</td>
<td>Reduced dose needed</td>
<td>High\textsuperscript{16}</td>
</tr>
<tr>
<td>Pravastatin</td>
<td>No reduced efficacy</td>
<td>Medium\textsuperscript{14}</td>
</tr>
<tr>
<td>Pravastatin, simvastatin</td>
<td>Patient might have good response</td>
<td>Medium\textsuperscript{14}</td>
</tr>
<tr>
<td>β blockers</td>
<td>Other treatment options might be preferable</td>
<td>Medium\textsuperscript{15}</td>
</tr>
<tr>
<td>Metformin</td>
<td>Reduced likelihood of response</td>
<td>Medium\textsuperscript{15}</td>
</tr>
<tr>
<td>Troglitazone</td>
<td>Reduced likelihood of response</td>
<td>Medium\textsuperscript{15}</td>
</tr>
</tbody>
</table>

Credit: Russ Altman and team
Association of IL23R, TNFRSFIA, and HLA-DRB5*01:03 Allele Variants with Inflammatory Bowel Disease Phenotypes in the Finnish Population

Miaoli Leppikainen, PhD, a, 1 Lena Uusima, MD, PhD, 1 Ulla Takala, MD, 2 Eija Saarela, PhD, 3 Eliott Saarela, PhD, 3 Petri Karhunen, MD, PhD, 4, 5 Kimmo Kankaanranta, MD, PhD, 5b, 6 and Pauliina Paavolainen Saikku, MD, PhD1, 6

Background: Crohn’s disease (CD) and ulcerative colitis (UC), 2 major forms of inflammatory bowel disease (IBD), are complex disorders with significant genetic predisposition. Three CD-associated loci (CARD15, IL23R, and TNFRSFIA) have received considerable attention since several susceptibility loci have been reported. We investigated IBD phenotype associations to genetic variants in IL23R, TNFRSFIA, and HLA in Finnish IBD patients.

Methods: A total of 699 Crohn’s disease patients were genotyped for the following variants by polymerase chain reaction–restriction fragment length polymorphism (PCR–RFLP) method: rs1800899, rs1800649, and rs750998 at the 5′-untranslated region of the IL23R gene; rs3812101 at the 5′-untranslated region of the TNFRSFIA gene; HLA-DRB5*01:03, HLA-DRB1*16:01, HLA-DRB1*11:01, HLA-DRB1*04:01, HLA-DRB1*07:01, and HLA-DRB1*03:01 among Finnish IBD patients.

Results: IL23R gene was associated with CD at the gene level (p = 4.1 × 10−4). The rare HLA-DRB5*01:03 allele was associated with UC (p = 5.0 × 10−3). A HLA-DRB5*01:03 variant was associated with UC (p = 4.4 × 10−3). HLA-DRB1*11:01 positivity was associated with CD (p = 4.0 × 10−3). The IL23R variants were detected in association with familial UC and not with UC in smokers. The IL23R variants were detected in association with familial UC and not with UC in smokers. HLA-DRB1*04:01 and HLA-DRB1*07:01 were more prevalent in the carriers of the minor variant (p = 8.3 × 10−2) and HLA-DRB1*16:01 was associated with the rare IL23R variant (p = 9.0 × 10−2).

Conclusions: We were able to replicate the association of the IL23R variants with CD at HLA-DRB5*01:03 while HLA-DRB1*11:01 was not associated in our study. HLA-DRB1*04:01 and HLA-DRB1*07:01 were more prevalent in the carriers of the IL23R variant. These results suggest that the IL23R gene is associated with the CD phenotype.

The initial discovery of the association of CARD15/NOD2 CD variants with Crohn’s disease (CD) and a novel susceptibility gene for inflammatory bowel disease (IBD) have been reported. In 2008, the positional cloning approach led to the identification of the associated variant in the IBD1 candidate family 32 (IBD2A) in the splice donor element of the CARD15 gene. These variants have implications in the regulation of innate immunity and are associated with the CD phenotype. These results suggest that the IL23R gene is associated with the CD phenotype.

Most of the studies have confirmed the association of CD with IL23R gene variants. These findings suggest that the CD phenotype may be regulated by IL23R through an innate immune response.

The association of IL23R with CD has been identified by many groups in different populations, which indicates a potential role for IL23R in the pathogenesis of CD.

Infant Dis 2008; 16: 1-115
Credit: Rong Chen, Optra Systems, and Personalis, Inc.
Credit: Rong Chen, Alex Morgan, Joel Dudley, Lancet
Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence

Frederick E. Dewey¹, Rong Chen², Segio P. Cordero³, Kelly E. Ormond⁴,⁵, Colleen Caleshu¹, Konrad J. Karczewski²,³, Michelle Whirl-Carrillo⁶, Matthew T. Wheeler¹, Joel T. Dudley²,³, Jake K. Byrnes⁷, Omar E. Cornejo⁸, Joshua W. Knowles¹, Mark Woon⁹, Katrin Sangkuhl⁹, Li Gong⁹, Caroline F. Thorn⁹, Joan M. Hebert⁹, Emidio Capriotti⁴, Sean P. David⁴, Aleksandra Pavlovic⁴, Anne West⁶, Joseph V. Thakuria⁷, Madeleine P. Ball⁸, Alexander W. Zaranek⁸, Heidi L. Rehm⁹, George M. Church⁸, John S. West¹⁰, Carlos D. Bustamante⁸, Michael Snyder⁴, Russ B. Altman¹,¹¹, Teri E. Klein⁹, Atul J. Butte², Euan A. Ashley¹

¹ Center for Inherited Cardiovascular Disease, Division of Cardiovascular Medicine, Stanford University, Stanford, California, United States of America, ² Division of Systems Medicine, Department of Pediatrics, Stanford University School of Medicine, Stanford, California, United States of America, ³ Biomedical Informatics Graduate Training Program, Stanford University School of Medicine, Stanford, California, United States of America, ⁴ Department of Genetics, Stanford University School of Medicine, Stanford, California, United States of America, ⁵ Center for Biomedical Ethics, Stanford University, Stanford, California, United States of America, ⁶ Molecular and Cell
The First Child Saved By DNA Sequencing

Since he was a toddler, six-year-old Nicholas Volker's intestine had been dangerously inflamed, necessitating a hundred surgeries including the removal of his colon. No one knew the cause, but it seemed certain that the boy was dying. In a desperate attempt to figure out what was wrong, doctors at the Medical College of Wisconsin did something desperate and unproven: they sequenced his DNA.

The doctors found a mutation that nobody expected, but that seemed to explain his condition and also dictated a treatment: a bone marrow transplant.
The most important story in cancer treatment just got a new chapter.

FoundationOne™ Heme
A fully informative genomic profile for hematologic malignancies, sarcomas and pediatric cancers.

Foundation Medicine (NASDAQ: FMI) is leading a transformation in cancer care, where each patient’s treatment is informed by a deep understanding of the molecular changes that contribute to their disease.

CAREERS
Find out more about career opportunities at Foundation Medicine.

ABOUT US
Find out more about how Foundation Medicine is changing the way molecular information is used in cancer care.

RECENT NEWS
Tuesday, December 10, 2013 | Novel And Previously Reported Genomic Alterations Identified in Clinical Multiple Myeloma Cases Using FoundationOne™ Heme

Monday, December 9, 2013 | FoundationOne™ Heme Enables Identification of Genomic Alterations Not Identified By Conventional Methods Across Hematologic Malignancies

Saturday, December 7, 2013 | Foundation Medicine Launches FoundationOne™ Heme, Developed in Collaboration with Memorial Sloan-Kettering Cancer Center
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<th>Code</th>
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<td>82340</td>
<td>Calcium in Urine</td>
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<td>82310</td>
<td>Calcium, Total</td>
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<td>80156</td>
<td>Carbamazepine, Total</td>
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<td>Carbon Dioxide</td>
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<td>82378</td>
<td>Carcinoembryonic Antigen (CEA)</td>
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<tr>
<td>86147</td>
<td>Cardiolipin (Phospholipid) Antibody</td>
<td>$17.49</td>
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<tr>
<td>85025</td>
<td>CBC / Auto Diff with reflex to Manual Diff or Smear</td>
<td>$5.35</td>
</tr>
<tr>
<td>85027</td>
<td>CBC / no Diff</td>
<td>$4.45</td>
</tr>
</tbody>
</table>
Scanadu Scout

A scanner packed with sensors designed to read your vital signs and send them wirelessly to your smartphone in a few seconds, any time, anywhere.

Mountain View, California, United States  Technology

Story  Updates 33  Comments 933  Funders 8,523  Gallery 13

Scanadu Scout™ - The first medical Tricorder

$1,664,574 USD
RAISED OF $100,000 GOAL

1,665% © 0 time left

TEMPERATURE

HEART RATE

OXIMETRY

ECG

HRV

PWTT

UA

STRESS
FDA NEWS RELEASE

For Immediate Release: Sept. 23, 2013
Media Inquiries: Symon Rivers, 301-796-8729, symon.rivers@fda.hhs.gov
Consumer Inquiries: 888-INFO-FDA

FDA issues final guidance on mobile medical apps

Tailored approach supports innovation while protecting consumer safety

Today, the U.S. Food and Drug Administration issued final guidance for developers of mobile medical applications, or apps, which are software programs that run on mobile communication devices and perform the same functions as traditional medical devices. The guideline outlines the FDA's tailored approach to mobile apps.

The agency intends to exercise enforcement discretion (meaning it will not enforce requirements under the Federal Drug & Cosmetic Act) for the majority of mobile apps as they pose minimal risk to consumers. The FDA intends to focus its regulatory oversight on a subset of mobile medical apps that present a greater risk to patients if they do not work as intended.

Mobile apps have the potential to transform health care by allowing doctors to diagnose patients with potentially life-threatening conditions outside of traditional health care settings, help consumers manage their own health and wellness, and also gain access to useful information whenever and wherever they need it.
WONKBLOG

One hospital charges $8,000 — another, $38,000

By Sarah Kliff and Dan Keating, Published: May 8, 2018

Consumers on Wednesday will finally get some answers to a long-standing and persistent mystery: how much medical care should cost.

For the first time, the federal government will publish prices for the 100 most common inpatient procedures, a closely held secret by facilities that see a competitive advantage in the numbers. What the numbers reveal is a seemingly random variation in the costs of care.
Study: Pediatric Kidney Transplant Without Calcineurin Inhibitors

Thirty-four children were entered into a pilot trial of calcineurin inhibitor avoidance after living-donor kidney transplantation. Patients were treated with anti-CD25 mAbs, prednisone, mycophenolate mofetil, and sirolimus. It is concluded that calcineurin inhibitor-free immunosuppression can be safe and effective in pediatric living-donor renal transplantation.

PubMed ID: 15887625

Flow Cytometry Analysis (FLOCK)

Flow cytometry analysis component includes:
- Automated cell population identification
- Result visualization in 2D and 3D
- Statistical analysis of population characteristics
- Automated mapping of populations across multiple samples

MHC Validation and Analysis

MHC Sequence Feature Variant Type (SFVT) Analysis enables genetic association analysis of classical HLA protein sub-regions defined with structural (e.g. helix) and functional (e.g. binding site) information.

MHC Alleles

Complete DNA and protein sequences, sequence features, and population frequencies of MHC, MIC and TAP alleles. Align MHC sequences horizontally to visualize extent of polymorphisms across all alleles in a locus.

New Data Release

August 16, 2013 - The National Institute of Allergy and Infectious Diseases (NIAID) released to the ImmPort user community new data from 6 clinical studies or trials and updates to 7 additional studies available here. Research areas include predictive influenza biomarkers, antibody responses to pH1N1 and oral immunotherapy for childhood allergies. This release brings the total number of shared studies to 60.

Data Summary

- Studies: 60
- Subjects: 13859
- Experiments: 569
- Total Results: 226998
- ELISA Results: 126976
How can we expect health care professionals to review 6 billion pieces of data in a 15 minute encounter?
We already ask health care professionals to review 1 GB of data in 15 minutes...
We already ask health care professionals to review 1 GB of data in 15 minutes...
We already ask health care professionals to review 1 GB of data in 15 minutes... ... but we give them tools to help them do this!
What is Big Data in Biomedicine?
Big Data in Biomedicine is...

- Algorithms?
- Programmers?
- Databases?
- High-performance computers?
- Mobile?
Big Data in Biomedicine is...

Predicting the disease before it strikes

Explaining the rare disease that defies experts

Finding drugs for diseases lacking attention

Making sure we do the right thing for patients

An amazing platform for biomedical innovation
Big Data in Biomedicine is Hope
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- California Institute for Regenerative Medicine
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