



Bioinformatics up to Date

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Inside.....

Cover story	1
Computers for Biologists	2
Bioserver	2
Molecule of the month	3
Bioinfo.	
Animation	3
Bioinfo. Patent	4
Upcoming Events	4
Contact Us	4

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Mitochondrial genome of *Hispaniolan solenodon*

An international team of scientists has completely sequenced the mitochondrial genome of the Hispaniolan solenodon (a venomous, insectivorous mammal that diverged from other living mammals 78 million years ago), filling in the last major branch of placental mammals on the tree of life.



The Hispaniolan solenodon (*Solenodon paradoxus*), also known as the Dominican solenodon, or *agouta*, is one of only a few mammal species capable of producing toxic saliva, which it uses to immobilize its invertebrate prey. The species is endemic to Hispaniola, the island shared by Haiti and the Dominican Republic. It is found in forests and brush country, as well as around plantations.

It looks much like a shrew. However, it is considerably larger. It measures between 11 and 13

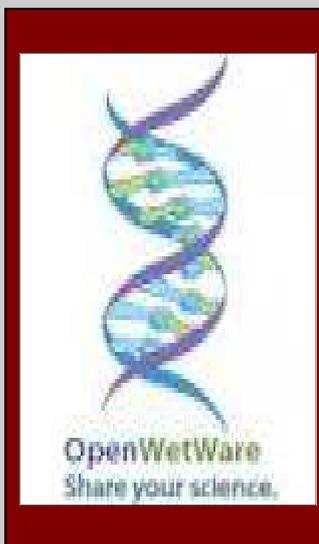
inches (28–33 cm), with the tail adding an additional 10 inches (25 cm). It weighs 600 g – 1 kg. A black to reddish-brown pelage covers the majority of the body, with the exception of the tail, feet, nose, and tips of the ears.

The new study, published in the journal *Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis*, confirmed that the Hispaniolan solenodon diverged from all other living mammals 78 million years ago, long before an asteroid wiped out the dinosaurs.

“It’s just impressive it’s survived this long. It survived the asteroid; it survived human colonization and the rats and mice humans brought with them that wiped out the solenodon’s closest relatives,” said lead author Dr. Adam Brandt, from the University of Illinois at Urbana-Champaign. The solenodon mitogenomes were 16,454–16,457 bp long and carried the expected repertoire of genes. A mitogenomic phylogeny confirmed the basal position of solenodons relative to shrews and moles, with solenodon mitogenomes estimated to have diverged from those of other mammals ca. 78 Mya. Control region sequences of solenodons from the northern ($n=3$) and southern ($n=5$) Dominican Republic grouped separately in a network, with $F_{ST} = 0.72$ ($p=0.036$) between north and south. The study also supports recent findings that the island of Hispaniola contains genetically distinct northern and southern populations that should be conserved as separate sub-species: *Solenodon paradoxus paradoxus* and *Solenodon paradoxus woodi*.

[Adam L. Brandt et al. Mitogenomic sequences support a north–south subspecies subdivision within *Solenodon paradoxus*. *Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis*, published online April 20, 2016]

1. **DPU Pune PhD Admissions 2016 in Biotech & Bioinformatics;** <http://www.dpu.edu.in/Forms/DPUPhD-Brochure-2016.pdf>
2. **ILS Bhubaneswar Computational Biology PhD Program 2016 ;** <https://www.ils.res.in/wp-content/uploads/2016/05/advt07-16.pdf>



GenSAS: Web-based Genome Sequence Annotation Server

GenSAS is a Web-based Genome Sequence Annotation Server that provides a one-stop website with a single graphical interface for running multiple structural and functional annotation tools, enabling visualization and manual curation of genome sequences. Users can upload sequences into their account and run gene prediction programs, protein homology searches, map ESTs, identify repeats, ORFs and SSRs with custom parameter settings. Each analysis is displayed on separate tracks of the graphical interface with custom editable tracks to select final annotation of features and create gff3 files for upload to genome browsers such as GBrowse. Additional programs can be easily added using this Drupal based software.



GenSAS was developed to help researchers in genome sequence analysis. It had the following goals.

- Develop a computational pipeline which incorporates multiple annotation tools (that is, working as an integration tool)
- Develop a visualization tool to display the output from annotation tools graphically
- Develop an intuitive web-based user interface to facilitate curation by biologists

GenSAS integrates with JBrowse and Apollo to provide visualization and editing. As experimental evidence such as cDNA, ESTs and proteins continues to grow and the accuracy of the existing and new annotation tools continue to improve, already annotated genomes can be revisited for further annotation. As GenSAS is flexible and has the capability of incorporating new data and improved/advanced tools relatively easily, GenSAS should be a very useful application in assisting researchers to generate high quality annotation of genome sequences. GenSAS can be retrieve at <http://www.bioinfo.wsu.edu/gensas/rosaceae/apl.cgi>.

New computer program developed to detect DNA mutations in single cancer cells

Researchers at The University of Texas MD Anderson Cancer Center have announced a new method for detecting DNA mutations in a single cancer cell versus current technology that analyzes millions of cells which they believe could have important applications for cancer diagnosis and treatment. The results are published in the April 18 online issue of *Nature Methods*. Existing technology, next-generation sequencing (NGS), measures genomes derived from millions of cells versus the newer method for single-cell sequencing, called Monovar. Developed by MD Anderson researchers, Monovar allows scientists to examine data from multiple single cells. The study was, in part, funded by MD Anderson's Moon Shots Program, an unprecedented effort to significantly reduce deaths from cancer. However, because NGS measures large numbers of cells, genomic variations within tissue samples are often masked."

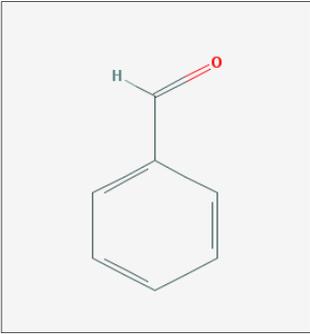
This led to development of newer technology, called single cell sequencing (SCS), that has had a major impact in many areas of biology, including cancer research, neurobiology, microbiology, and immunology, and has greatly improved understanding of certain tumor characteristics in cancer. Monovar improves further on the new SCS's computational tools which scientists found "lacking" by more accurately detecting slight alterations in DNA makeup known as single nucleotide variants (SNVs). "To improve the SNVs in SCS datasets, we developed Monovar," said Nicholas Navin, Ph.D., assistant professor of Genetics and co-author of the paper. "Monovar is a novel statistical method able to leverage data from multiple single cells to discover SNVs and provides highly detailed genetic data."

With the recent innovations in SCS methods to analyze thousands of single cells in parallel with RNA analysis which will soon be extended to DNA analysis, the need for accurate DNA variant detection will continue to grow," said Chen. "Monovar is capable of analyzing large-scale datasets and handling different whole-genome protocols, therefore it is well-suited for many types of studies.

[http://www.biologynews.net/archives/2016/04/18/first_computer_program_developed_to_detect_dna_mutations_in_single_cancer_cells.html]

Benzaldehyde

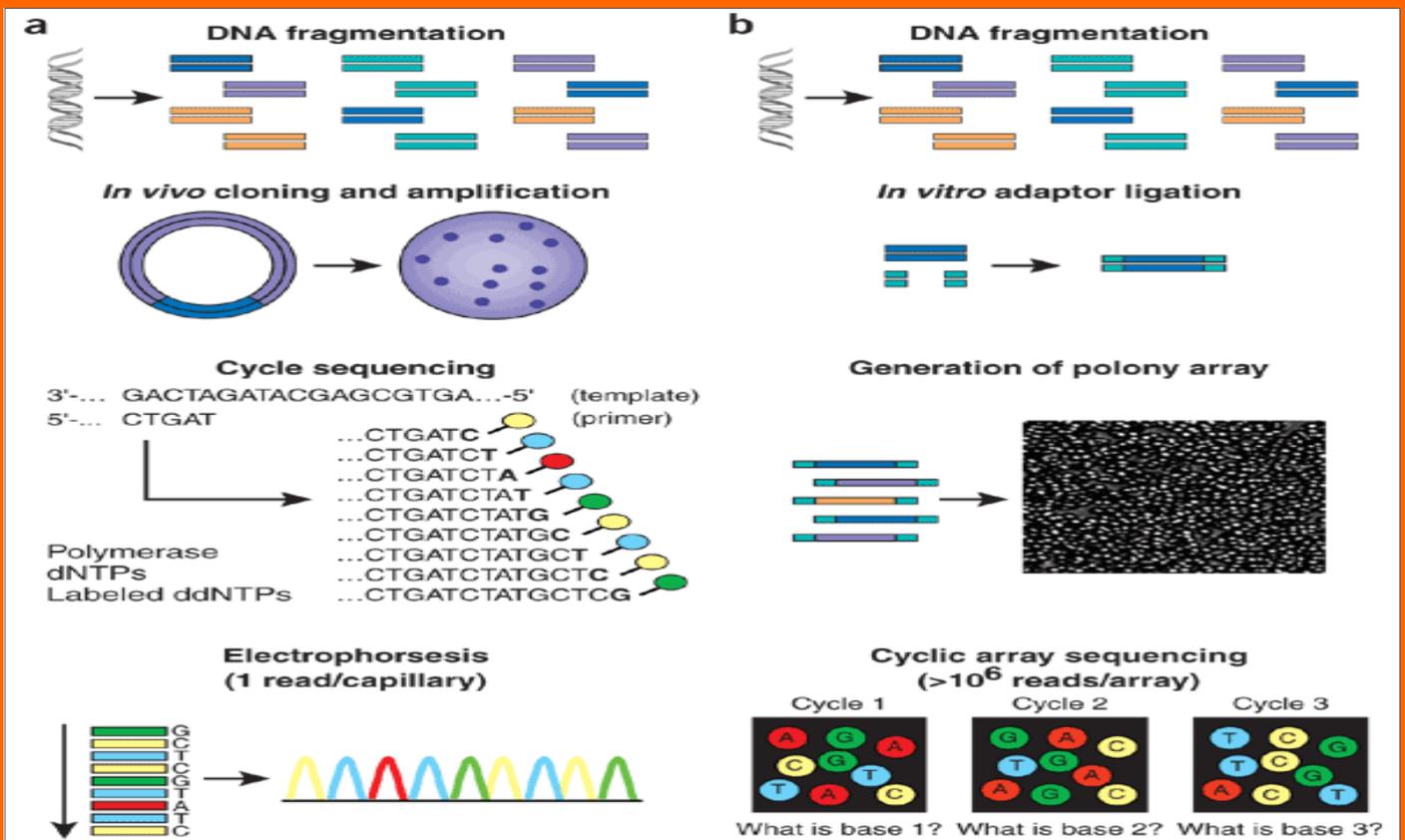
Benzaldehyde is a color liquid aldehyde with an almond odor. Benzaldehyde is found in many foods and is widely used in the chemical industry. In the chemical industry, this agent is used in the preparation of various aniline dyes, perfumes, flavorings, and pharmaceuticals. In addition, benzaldehyde has been associated with amygdalin (laetrile), since one of amygdalins breakdown products is benzaldehyde. Chronic benzaldehyde exposure is known to cause central nervous system (CNS) disturbances. It has shown that benzaldehyde causes the formation of reactive oxygen species (ROS) in rat synaptosomal fractions. Benzaldehyde has also been implicated in ROS formation in the CNS of rats treated with toluene.



Benzaldehyde's production and use as a food additive, as a fragrance in cosmetics, perfumes, and detergents, as an intermediate in the synthesis of a variety of pharmaceuticals and industrial chemicals, as well as its use as a solvent for resins, oils, and cellulose acetates and nitrates may result in its release to the environment through various waste streams. Benzaldehyde is also released to the environment in emissions from combustion processes such as gasoline and diesel engines, incinerators and wood burning. It is formed in the atmosphere through photochemical oxidation of toluene and other aromatic hydrocarbons.

PubChem CID	: 240
Chemical Names	: benzaldehyde, formyl-(14) C-labeled
Molecular Formula:	C_7H_6O
Molecular Weight	: 106.12194 g/mol
Smiles	: <chem>C1=CC=C(C=C1)C=O</chem>

Bioinfo. Animation



Next-generation DNA sequencing

Virtual network file server

US 6356863 B1

Inventor: Roger Anthony Sayle

Abstract

A virtual file server for generating content data in response to computer operating system requests involving a remote file system. According to a preferred embodiment, the virtual file server receives the request, which may be via any of a variety of standard protocols. Content data is generated or retrieved and translated into the format specified by the request. The virtual file content need not be maintained as a stored physical file in the requested format. The requested contents of this virtual file are encoded according to the protocol by which the request was initially received. Once so encoded, the requested content of the virtual file is transmitted in response to the request.

Upcoming events

Hands-on Workshop on Molecular Biotechnology and Bioinformatics Pune, India

ICSCCB, R.H. 2, Ujwal Regalia, Near Prabhatee Tech Park, Baner Road, Pune – 411045, India



Symposium on
Genomics in clinical practice: Future of precision medicine
June 1-2, 2016, Yenepoya University, Mangalore, India

Kindly send us your feedback to

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