Documentation 15.7.2020

Digitalisation and agriculture - Search 6.0

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TITLE-ABS-KEY (({wireless sensor*} OR {digital twin} OR {future farm*} OR {data platform*} OR {autonomous W/4 vehicle} OR {automatisation} OR (robot*) OR (internet) OR {precision farming} OR {precision agriculture} OR (drone*) OR (digitalisation) OR {farming 4.0} OR {agriculture 4.0} OR {artificial intelligence} OR {big data} OR {model* W/5 climate} OR {model* W/10 yield} OR {model* W/10 productivity} OR {mobile device}) AND ((agricult*) OR (farm*) OR (grain) OR (cattle) OR (cow) OR (dairy) OR (milk) OR (swine) OR (pig) OR (fodder) OR (soil) OR {farm land} OR {agricultural land})) AND (PUBYEAR > 2011) AND (LIMIT-TO (DOCTYPE , "ar") OR LIMIT-TO (DOCTYPE , "cp") OR LIMIT-TO (DOCTYPE , "re") OR LIMIT-TO (DOCTYPE , "ch") OR LIMIT-TO (DOCTYPE , "cr")) AND (LIMIT-TO (LANGUAGE , "English"))

- ⇨ 25,763 documents (15.7.2020)

Control of the 10 most cited documents

1 Flicek, P., Amode, M.R., Barrell, D., (...), Zerbino, D.R., Searle, S.M.J. (2014) Ensembl 2014, *Nucleic Acids Research* 42(D1), pp. D749-D755

Cited by 948

Abstract: Ensembl (http://www.ensembl.org) creates tools and data resources to facilitate genomic analysis in chordate species with an emphasis on human, major vertebrate model organisms and farm animals. Over the past year we have increased the number of species that we support to 77 and expanded our genome browser with a new scrollable overview and improved variation and phenotype views. We also report updates to our core datasets and improvements to our gene homology relationships from the addition of new species. Our REST service has been extended with additional support for comparative genomics and ontology information. Finally, we provide updated information about our methods for data access and resources for user training. © 2013 The Author(s). Published by Oxford University Press.

2 Hornbeck, P.V., Kornhauser, J.M., Tkachev, S., (...), Latham, V., Sullivan, M. (2012) PhosphoSitePlus: A comprehensive resource for investigating the structure and function of experimentally determined post-translational modifications in man and mouse. *Nucleic Acids Research* 40(D1). pp. D261-D270

Cited by 936

Abstract: PhosphoSitePlus (http://www.phosphosite.org) is an open, comprehensive, manually curated and interactive resource for studying experimentally observed post-translational modifications, primarily of human and mouse proteins. It encompasses 1 30 000 non-redundant modification sites, primarily phosphorylation, ubiquitinylation and acetylation. The interface is designed for clarity and ease of navigation. From the home page, users can launch simple or complex searches and browse high-throughput data sets by disease, tissue or cell line. Searches can be restricted by specific treatments, protein types, domains, cellular components, disease, cell types, cell lines, tissue and sequences or motifs. A few clicks of the mouse will take users to substrate pages or protein pages with sites, sequences, domain diagrams and molecular visualization of side-chains known to be modified; to site pages with information about how the modified site relates to the functions of specific proteins and cellular processes and to curated information pages summarizing the details from one record. PyMOL and Chimera scripts that colorize reactive groups on residues that are modified can be downloaded. Features designed to facilitate proteomic analyses include downloads of modification sites, kinase-substrate data sets, sequence logo generators, a Cytoscape plugin and BioPAX download to enable pathway visualization of the kinase-substrate interactions in PhosphoSitePlus®. © The Author(s) 2011. Published by Oxford University Press.

3 Alexe, B., Deselaers, T., Ferrari, V. (2012) Measuring the objectness of image windows. *IEEE Transactions on Pattern Analysis and Machine Intelligence.* 34(11),6133291, pp. 2189-2202

Cited by 843

Abstract: We present a generic objectness measure, quantifying how likely it is for an image window to contain an object of any class. We explicitly train it to distinguish objects with a well-defined boundary in space, such as cows and telephones, from amorphous background elements, such as grass and road. The measure combines in a Bayesian framework several image cues measuring characteristics of objects, such as appearing different from their surroundings and having a closed boundary. These include an innovative cue to measure the closed boundary characteristic. In experiments on the challenging PASCAL VOC 07 dataset, we show this new cue to outperform a state-of-the-art saliency measure, and the combined objectness measure to perform better than any cue alone. We also compare to interest point operators, a HOG detector, and three recent works aiming at automatic object segmentation. Finally, we present two applications of objectness. In the first, we sample a small numberof windows according to their objectness probability and give an algorithm to employ them as location priors for modern class-specific object detectors. As we show experimentally, this greatly reduces the number of windows evaluated by the expensive class-specific model. In the second application, we use objectness as a complementary score in addition to the class-specific model, which leads to fewer false positives. As shown in several recent papers, objectness can act as a valuable focus of attention mechanism in many other applications operating on image windows, including weakly supervised learning of object categories, unsupervised pixelwise segmentation, and object tracking in video. Computing objectness is very efficient and takes only about 4 sec. per image. © 2012 IEEE.

4 Zhang, C., Kovacs, J.M. (2012) The application of small unmanned aerial systems for precision agriculture: A review *Precision Agriculture.* 13(6), pp. 693-712

Cited by 724

Abstract: Precision agriculture (PA) is the application of geospatial techniques and sensors (e. g., geographic information systems, remote sensing, GPS) to identify variations in the field and to deal with them using alternative strategies. In particular, high-resolution satellite imagery is now more commonly used to study these variations for crop and soil conditions. However, the availability and the often prohibitive costs of such imagery would suggest an alternative product for this particular application in PA. Specifically, images taken by low altitude remote sensing platforms, or small unmanned aerial systems (UAS), are shown to be a potential alternative given their low cost of operation in environmental monitoring, high spatial and temporal resolution, and their high flexibility in image acquisition programming. Not surprisingly, there have been several recent studies in the application of UAS imagery for PA. The results of these studies would indicate that, to provide a reliable end product to farmers, advances in platform design, production, standardization of image georeferencing and mosaicing, and information extraction workflow are required. Moreover, it is suggested that such endeavors should involve the farmer, particularly in the process of field design, image acquisition, image interpretation and analysis. © 2012 Springer Science+Business Media, LLC.

5 McArthur, A.G., Waglechner, N., Nizam, F., (...), Yu, T., Wright, G.D. 2013 The comprehensive antibiotic resistance database. *Antimicrobial Agents and Chemotherapy* 57(7), pp. 3348-3357

Cited by 684

Abstract: The field of antibiotic drug discovery and the monitoring of new antibiotic resistance elements have yet to fully exploit the power of the genome revolution. Despite the fact that the first genomes sequenced of free living organisms were those of bacteria, there have been few specialized bioinformatic tools developed to mine the growing amount of genomic data associated with pathogens. In particular, there are few tools to study the genetics and genomics of antibiotic resistance and how it impacts bacterial populations, ecology, and the clinic. We have initiated development of such tools in the form of the Comprehensive Antibiotic Research Database (CARD; http://arpcard.mcmaster.ca). The CARD integrates disparate molecular and sequence data, provides a unique organizing principle in the form of the Antibiotic Resistance Ontology (ARO), and can quickly identify putative antibiotic resistance genes in new unannotated genome sequences. This unique platform provides an informatic tool that bridges antibiotic resistance concerns in health care, agriculture, and the environment. Copyright © 2013, American Society for Microbiology.

6 Mulla, D.J. (2013) Twenty five years of remote sensing in precision agriculture: Key advances and remaining knowledge gaps. *Biosystems Engineering* 114(4), pp. 358-371

Cited by 583

Abstract: Precision agriculture dates back to the middle of the 1980's. Remote sensing applications in precision agriculture began with sensors for soil organic matter, and have quickly diversified to include satellite, aerial, and hand held or tractor mounted sensors. Wavelengths of electromagnetic radiation initially focused on a few key visible or near infrared bands. Today, electromagnetic wavelengths in use range from the ultraviolet to microwave portions of the spectrum, enabling advanced applications such as light detection and ranging (LiDAR), fluorescence spectroscopy, and thermal spectroscopy, along with more traditional applications in the visible and near infrared portions of the spectrum. Spectral bandwidth has decreased dramatically with the advent of hyperspectral remote sensing, allowing improved analysis of specific compounds, molecular interactions, crop stress, and crop biophysical or biochemical characteristics. A variety of spectral indices now exist for various precision agriculture applications, rather than a focus on only normalised difference vegetation indices. Spatial resolution of aerial and satellite remote sensing imagery has improved from 100's of m to sub-metre accuracy, allowing evaluation of soil and crop properties at fine spatial resolution at the expense of increased data storage and processing requirements. Temporal frequency of remote sensing imagery has also improved dramatically. At present there is considerable interest in collecting remote sensing data at multiple times in order to conduct near real time soil, crop and pest management. © 2012 IAgrE.

7 Zhang, X., Davidson, E.A., Mauzerall, D.L., (...), Dumas, P., Shen, Y. (2015) Managing nitrogen for sustainable development. *Nature* 528(7580), pp. 51-59

Cited by 428

Abstract: © 2015 Macmillan Publishers Limited. All rights reserved. Improvements in nitrogen use efficiency in crop production are critical for addressing the triple challenges of food security, environmental degradation and climate change. Such improvements are conditional not only on technological innovation, but also on socio-economic factors that are at present poorly understood. Here we examine historical patterns of agricultural nitrogen-use efficiency and find a broad range of national approaches to agricultural development and related pollution. We analyse examples of nitrogen use and propose targets, by geographic region and crop type, to meet the 2050 global food demand projected by the Food and Agriculture Organization while also meeting the Sustainable Development Goals pertaining to agriculture recently adopted by the United Nations General Assembly. Furthermore, we discuss socio-economic policies and technological innovations that may help achieve them.

8 Wolfert, S., Ge, L., Verdouw, C., Bogaardt, M.-J. (2017) Big Data in Smart Farming – A review. *Agricultural Systems.* 153, pp. 69-80

Cited by 401

Abstract: © 2017 The Authors Smart Farming is a development that emphasizes the use of information and communication technology in the cyber-physical farm management cycle. New technologies such as the Internet of Things and Cloud Computing are expected to leverage this development and introduce more robots and artificial intelligence in farming. This is encompassed by the phenomenon of Big Data, massive volumes of data with a wide variety that can be captured, analysed and used for decision-making. This review aims to gain insight into the state-of-the-art of Big Data applications in Smart Farming and identify the related socio-economic challenges to be addressed. Following a structured approach, a conceptual framework for analysis was developed that can also be used for future studies on this topic. The review shows that the scope of Big Data applications in Smart Farming goes beyond primary production; it is influencing the entire food supply chain. Big data are being used to provide predictive insights in farming operations, drive real-time operational decisions, and redesign business processes for game-changing business models. Several authors therefore suggest that Big Data will cause major shifts in roles and power relations among different players in current food supply chain networks. The landscape of stakeholders exhibits an interesting game between powerful tech companies, venture capitalists and often small start-ups and new entrants. At the same time there are several public institutions that publish open data, under the condition that the privacy of persons must be guaranteed. The future of Smart Farming may unravel in a continuum of two extreme scenarios: 1) closed, proprietary systems in which the farmer is part of a highly integrated food supply chain or 2) open, collaborative systems in which the farmer and every other stakeholder in the chain network is flexible in choosing business partners as well for the technology as for the food production side. The further development of data and application infrastructures (platforms and standards) and their institutional embedment will play a crucial role in the battle between these scenarios. From a socio-economic perspective, the authors propose to give research priority to organizational issues concerning governance issues and suitable business models for data sharing in different supply chain scenarios.

9 Grotzinger, J.P., Crisp, J., Vasavada, A.R., (...), Welch, R.V., Wiens, R.C. (2012) Mars Science Laboratory mission and science investigation. *Space Science Reviews* 170(1-4), pp. 5-56

Cited by 394

Abstract: Scheduled to land in August of 2012, the Mars Science Laboratory (MSL) Mission was initiated to explore the habitability of Mars. This includes both modern environments as well as ancient environments recorded by the stratigraphic rock record preserved at the Gale crater landing site. The Curiosity rover has a designed lifetime of at least one Mars year (∼23 months), and drive capability of at least 20 km. Curiosity's science payload was specifically assembled to assess habitability and includes a gas chromatograph-mass spectrometer and gas analyzer that will search for organic carbon in rocks, regolith fines, and the atmosphere (SAM instrument); an x-ray diffractometer that will determine mineralogical diversity (CheMin instrument); focusable cameras that can image landscapes and rock/regolith textures in natural color (MAHLI, MARDI, and Mastcam instruments); an alpha-particle x-ray spectrometer for in situ determination of rock and soil chemistry (APXS instrument); a laser-induced breakdown spectrometer to remotely sense the chemical composition of rocks and minerals (ChemCam instrument); an active neutron spectrometer designed to search for water in rocks/regolith (DAN instrument); a weather station to measure modern-day environmental variables (REMS instrument); and a sensor designed for continuous monitoring of background solar and cosmic radiation (RAD instrument). The various payload elements will work together to detect and study potential sampling targets with remote and in situ measurements; to acquire samples of rock, soil, and atmosphere and analyze them in onboard analytical instruments; and to observe the environment around the rover. The 155-km diameter Gale crater was chosen as Curiosity's field site based on several attributes: an interior mountain of ancient flat-lying strata extending almost 5 km above the elevation of the landing site; the lower few hundred meters of the mountain show a progression with relative age from clay-bearing to sulfate-bearing strata, separated by an unconformity from overlying likely anhydrous strata; the landing ellipse is characterized by a mixture of alluvial fan and high thermal inertia/high albedo stratified deposits; and a number of stratigraphically/geomorphically distinct fluvial features. Samples of the crater wall and rim rock, and more recent to currently active surface materials also may be studied. Gale has a well-defined regional context and strong evidence for a progression through multiple potentially habitable environments. These environments are represented by a stratigraphic record of extraordinary extent, and insure preservation of a rich record of the environmental history of early Mars. The interior mountain of Gale Crater has been informally designated at Mount Sharp, in honor of the pioneering planetary scientist Robert Sharp. The major subsystems of the MSL Project consist of a single rover (with science payload), a Multi-Mission Radioisotope Thermoelectric Generator, an Earth-Mars cruise stage, an entry, descent, and landing system, a launch vehicle, and the mission operations and ground data systems. The primary communication path for downlink is relay through the Mars Reconnaissance Orbiter. The primary path for uplink to the rover is Direct-from-Earth. The secondary paths for downlink are Direct-to-Earth and relay through the Mars Odyssey orbiter. Curiosity is a scaled version of the 6-wheel drive, 4-wheel steering, rocker bogie system from the Mars Exploration Rovers (MER) Spirit and Opportunity and the Mars Pathfinder Sojourner. Like Spirit and Opportunity, Curiosity offers three primary modes of navigation: blind-drive, visual odometry, and visual odometry with hazard avoidance. Creation of terrain maps based on HiRISE (High Resolution Imaging Science Experiment) and other remote sensing data were used to conduct simulated driving with Curiosity in these various modes, and allowed selection of the Gale crater landing site which requires climbing the base of a mountain to achieve its primary science goals. The Sample Acquisition, Processing, and Handling (SA/SPaH) subsystem is responsible for the acquisition of rock and soil samples from the Martian surface and the processing of these samples into fine particles that are then distributed to the analytical science instruments. The SA/SPaH subsystem is also responsible for the placement of the two contact instruments (APXS, MAHLI) on rock and soil targets. SA/SPaH consists of a robotic arm and turret-mounted devices on the end of the arm, which include a drill, brush, soil scoop, sample processing device, and the mechanical and electrical interfaces to the two contact science instruments. SA/SPaH also includes drill bit boxes, the organic check material, and an observation tray, which are all mounted on the front of the rover, and inlet cover mechanisms that are placed over the SAM and CheMin solid sample inlet tubes on the rover top deck. © 2012 The Author(s).

10 Breuer, K., Foroushani, A.K., Laird, M.R., (...), Brinkman, F.S.L., Lynn, D.J. (2013) InnateDB: Systems biology of innate immunity and beyond - Recent updates and continuing curation. *Nucleic Acids Research* 41(D1), pp. D1228-D1233

Cited by 392

Abstract: InnateDB (http://www.innatedb.com) is an integrated analysis platform that has been specifically designed to facilitate systems-level analyses of mammalian innate immunity networks, pathways and genes. In this article, we provide details of recent updates and improvements to the database. InnateDB now contains >196000 human, mouse and bovine experimentally validated molecular interactions and 3000 pathway annotations of relevance to all mammalian cellular systems (i.e. not just immune relevant pathways and interactions). In addition, the InnateDB team has, to date, manually curated in excess of 18000 molecular interactions of relevance to innate immunity, providing unprecedented insight into innate immunity networks, pathways and their component molecules. More recently, InnateDB has also initiated the curation of allergy- and asthma-related interactions. Furthermore, we report a range of improvements to our integrated bioinformatics solutions including web service access to InnateDB interaction data using Proteomics Standards Initiative Common Query Interface, enhanced Gene Ontology analysis for innate immunity, and the availability of new network visualizations tools. Finally, the recent integration of bovine data makes InnateDB the first integrated network analysis platform for this agriculturally important model organism. © The Author(s) 2012.

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Import data sets to R

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library(readr)
scopus_2012 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2012.csv")
scopus_2013 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2013.csv")
scopus_2014 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2014.csv")
scopus_2015 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2015.csv")
scopus_2016 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2016.csv")
scopus_2017_1 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2017_art.csv")
scopus_2017_2 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2017_no_art.csv")
scopus_2018_1 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2018_art.csv")
scopus_2018_2 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2018_no_art.csv")
scopus_2019_1 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2019_art_1.csv")
scopus_2019_2 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2019_art_2.csv")
scopus_2019_3 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2019_no_art_engi.csv")
scopus_2019_4 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2019_no_art_rest.csv")
scopus_2020_1 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2020_cp.csv")
scopus_2020_2 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2020_art_engi.csv")
scopus_2020_3 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2020_art_envi.csv")
scopus_2020_4 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2020_art_rest.csv")
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scopus_2021 <- read_csv("C:\\Users\\Veronika Hannus\\LRZ Sync+Share\\Shared Jan Alshuth\\Data analysis\\Scopus data set 15.07.2020\\scopus_2021.csv")
total <- rbind(scopus_2012, scopus_2013, scopus_2014, scopus_2015, scopus_2016, scopus_2017_1, scopus_2017_2, scopus_2018_1, scopus_2018_2, scopus_2019_1, scopus_2019_2, scopus_2019_3, scopus_2020_1, scopus_2020_2, scopus_2020_3, scopus_2020_4, scopus_2020_5, scopus_2021)

write.table(total, file = "scopus_20200715.csv", sep = "t")
```

aPPENDIX.

Tip. it is best to copy the single search strings for documentation reasons for the final data export

e.g.

The content definition must always be included completely

TITLE-ABS-KEY (({wireless sensor*} OR {digital twin} OR {future farm*} OR {data platform*} OR {autonomous W/4 vehicle} OR {automatisation} OR (robot*) OR (internet) OR {precision farming} OR {precision agriculture} OR (drone*) OR (digitalisation) OR {farming 4.0} OR {agriculture 4.0} OR {artificial intelligence} OR {big data} OR {model* W/5 climate} OR {model* W/10 yield} OR {model* W/10 productivity} OR {mobile device}) AND ((agricult*) OR (farm*) OR (grain) OR (cattle) OR (cow) OR (dairy) OR (milk) OR (swine) OR (pig) OR (fodder) OR (soil) OR {farm land} OR {agricultural land})) AND (LIMIT-TO (LANGUAGE , "English"))

AND (LIMIT-TO (DOCTYPE , "ar") OR LIMIT-TO (DOCTYPE , "cp") OR LIMIT-TO (DOCTYPE , "re") OR LIMIT-TO (DOCTYPE , "ch") OR LIMIT-TO (DOCTYPE , "cr"))

AND (LIMIT-TO (PUBYEAR , 2019))

AND (EXCLUDE (DOCTYPE , "ar"))
AND (EXCLUDE (DOCTYPE , "cp")) respectively

AND (LIMIT-TO (SUBJAREA , "ENGI"))
AND (EXCLUDE (SUBJAREA , "ENGI")) respectively

AND (EXCLUDE (DOCTYPE , "ar"))