National Supercomputing in DK 2015 to 2019, and the 17 Sustainability Development Goals from UN

Birgitte Vedel Thage, Dorte Drongstrup,
Desirée Suhr Pérez, Emil Rendbæk Nygaard
Myhanh Nguyen, Jeannette Ekstrøm, Tom Olsen

Webinar, November 5th 2020

Motivation for Collecting National HPC Publications

1. Know our HPC users

- Scientific Disciplines
- Universities
- Industry
- ”Regionerne” / Hospitals
- Collaboration patterns

2. World-Class Research

- In top10% most cited
- Field-Weighted Citataion Impact (FWCI)
- Top10% Journals by SNIP
- Journal Impact Factor (JIF)
- Open Access
- Sustainability and Development Goals (SDG) from UN

3. Outreach

- Inspiration for new users
- Display scientific output from the HPC investment
- Global interaction
- Advantage: Publications that made use of HPC was substantially above the world average FWCI

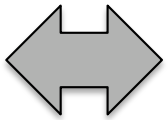
DeiC > Measure of Science from National HPC

835

Count & Metrics

2015-2019

412



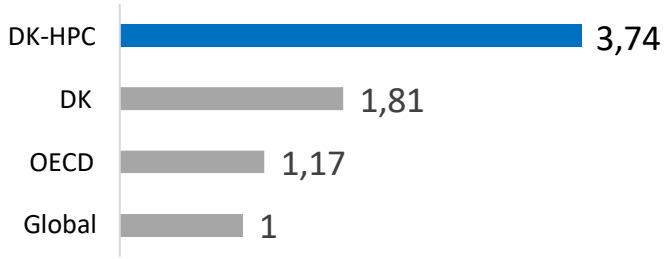
Credit: Azote Images for Stockholm Resilience Centre

DeiC > Highlights from National DK-HPC

In top 10% Most Cited Worldwide

40%

Field-Weighted Citation Impact



Published Open Access

61%

68% International Collaboration

Contribution to SDGs

44%

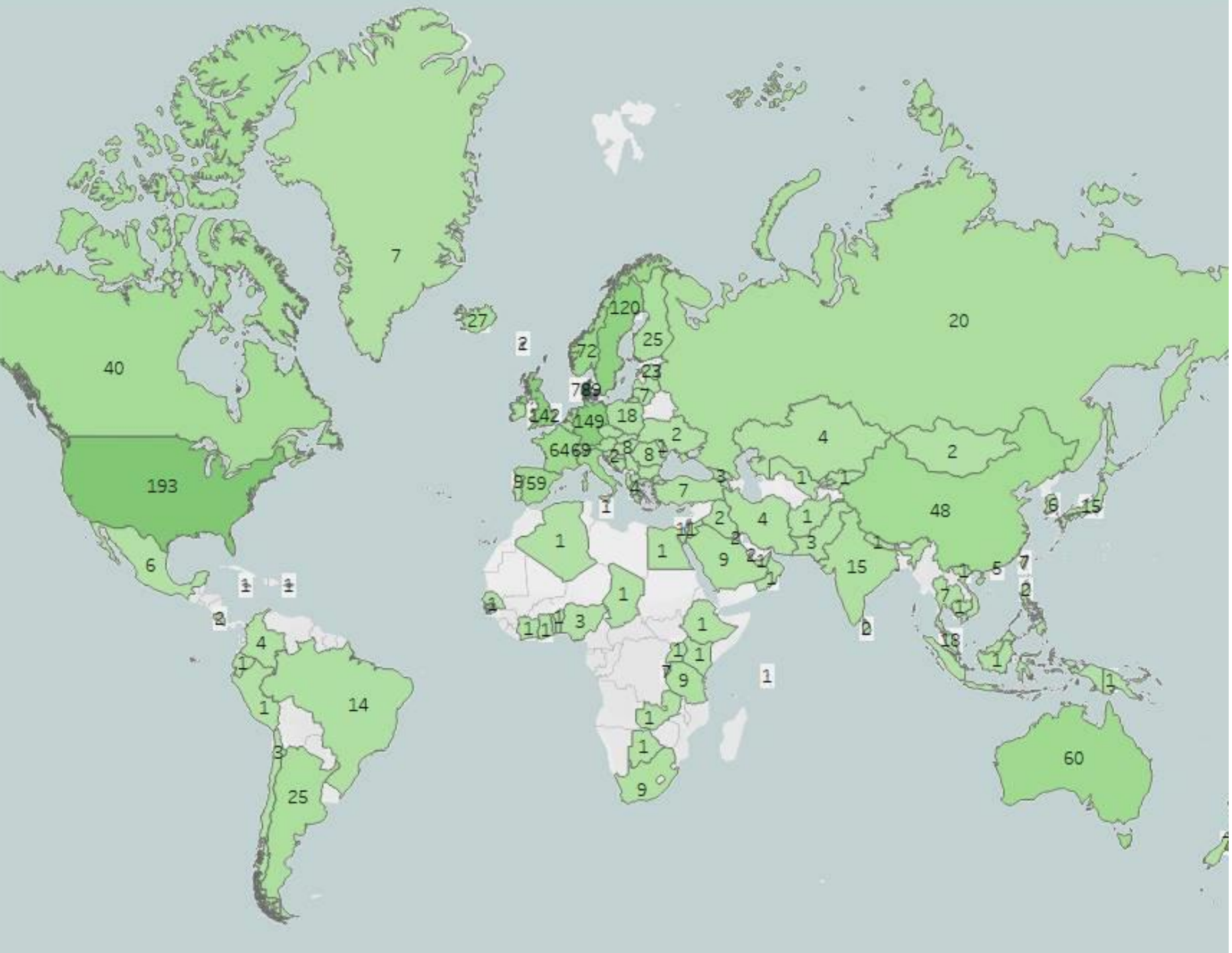
THE GLOBAL GOALS

Count of Publications

290 2015-2017

576 2015-2018

835 2015-2019



> #Publications

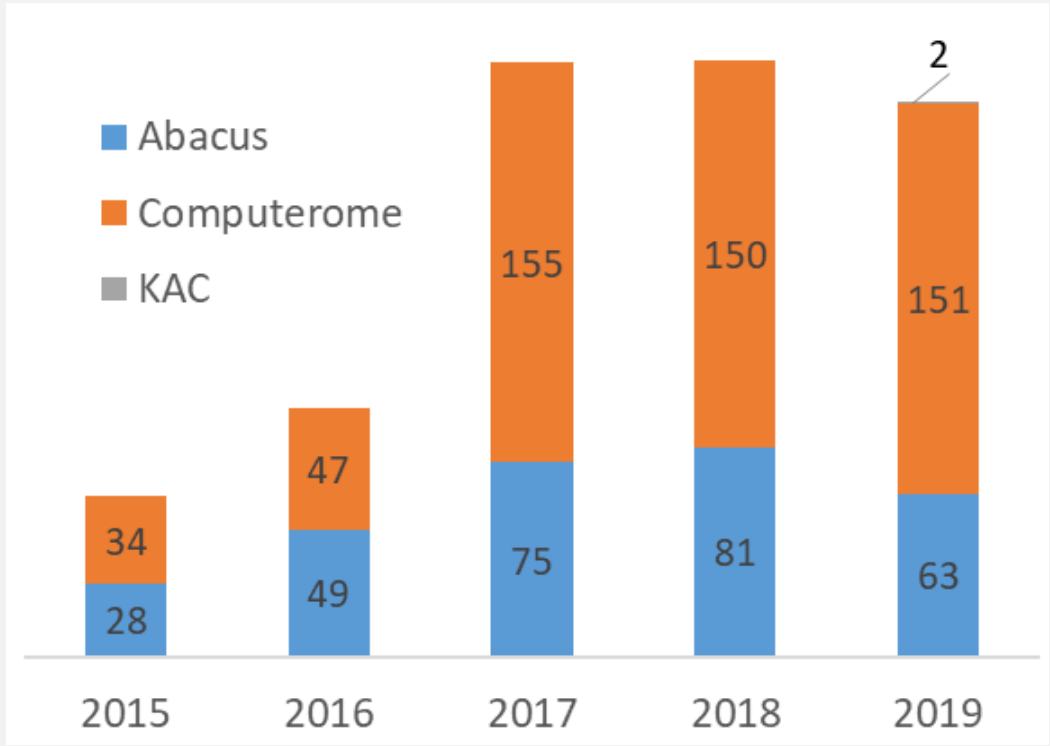
2015-2019

DeiC National HPC

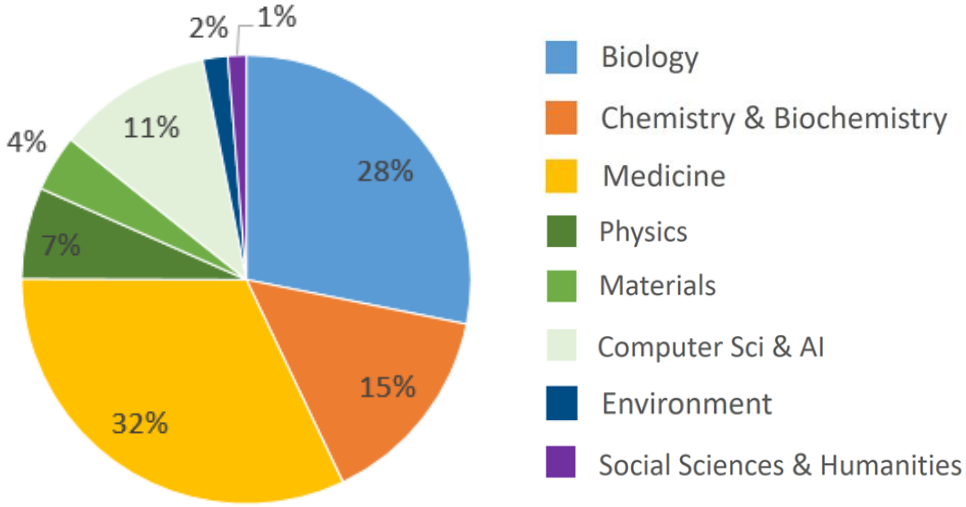
- Knowledge Exchange
- 110 Countries
- >3500 Research Units
  > 500 Institutions
- 68% International Collaboration

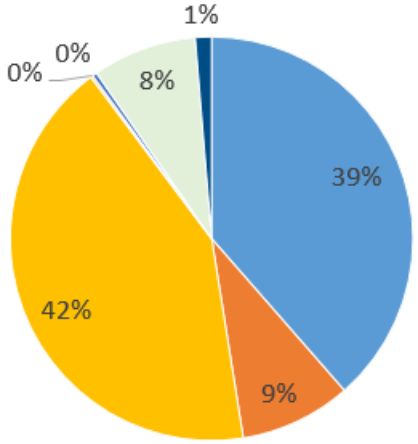
SciVal Data, Dorte Drongstrup, SDU

Puplication Level and HPC Facilities

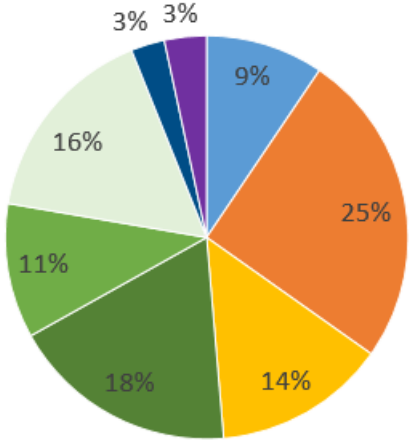


A. Total
N=835

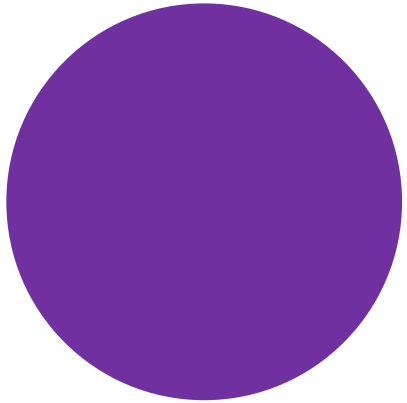




B. COMPUTEROME
N= 537

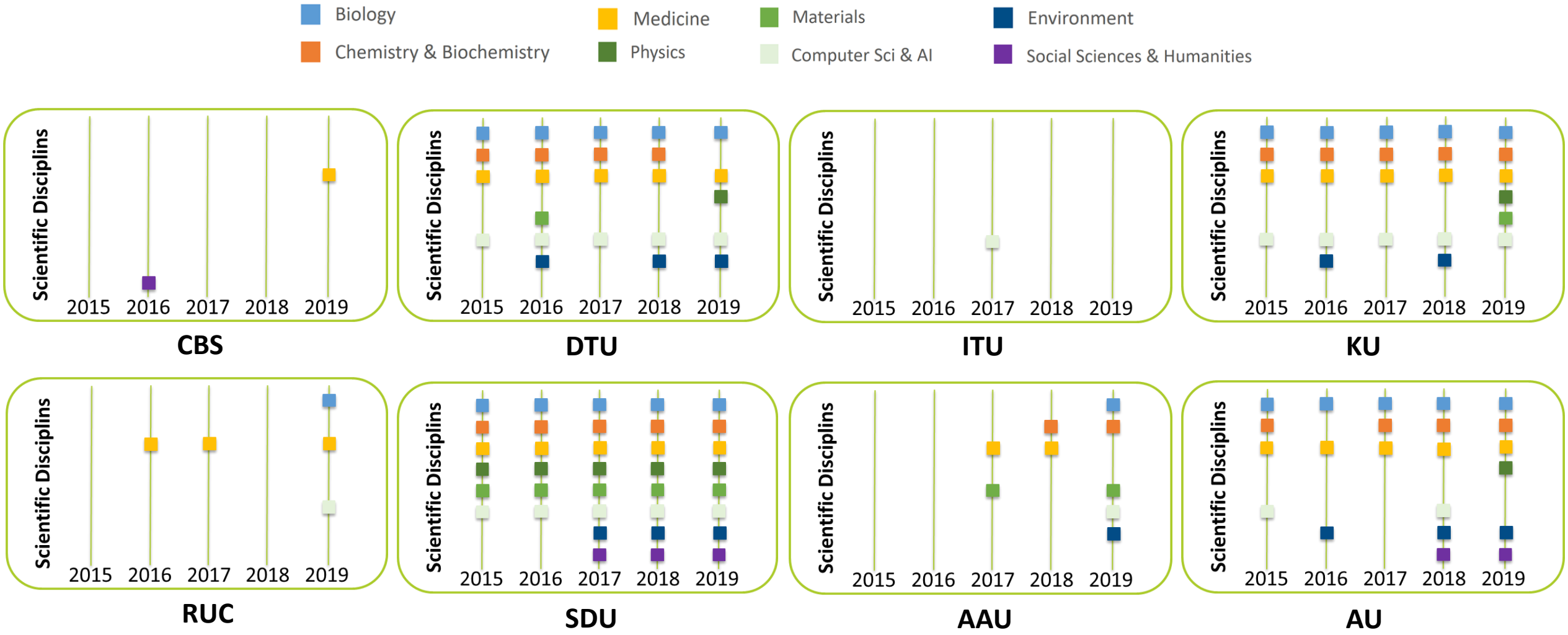


C. ABACUS2.0
N= 296

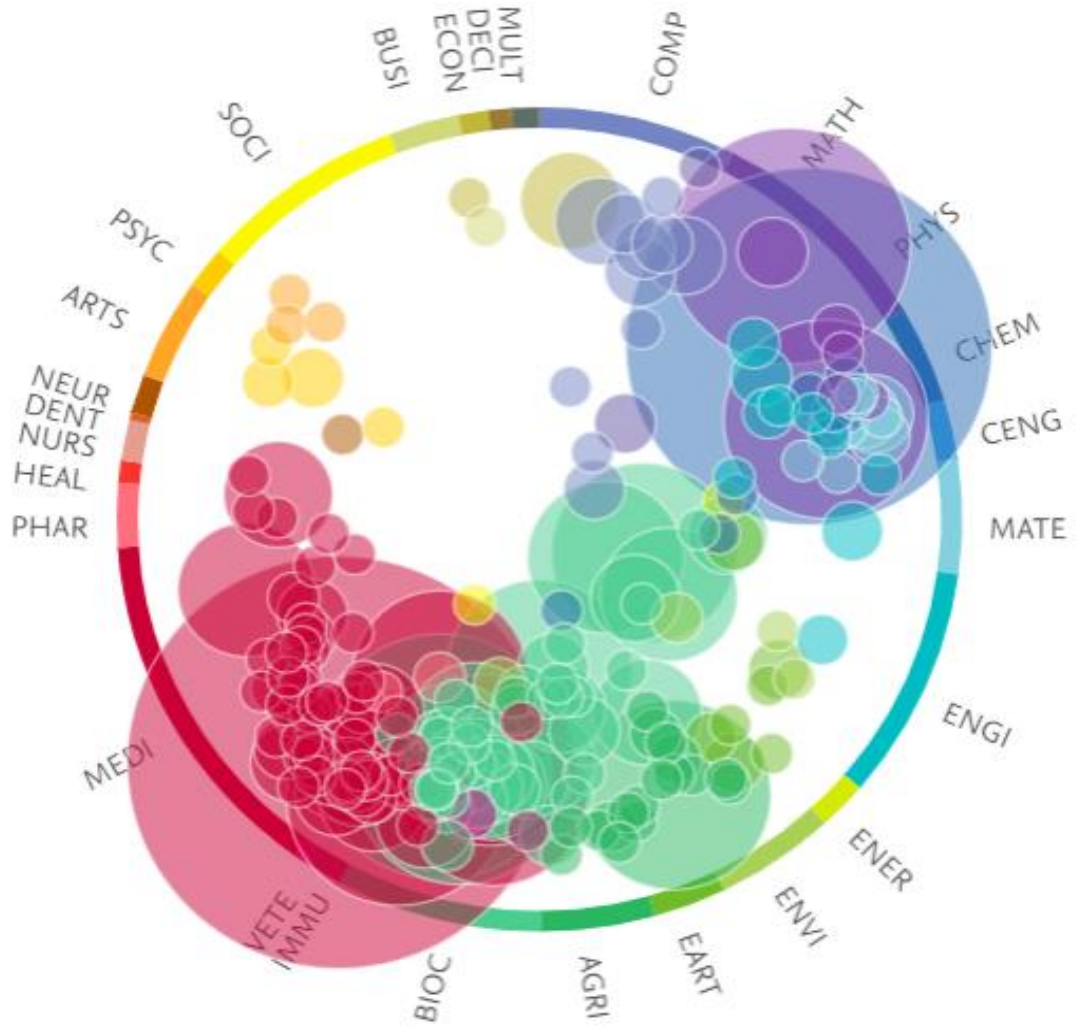


D. KAC
N= 2

Disciplins from Universities that used National HPC



Topic Prominence Clusters 2015-2019

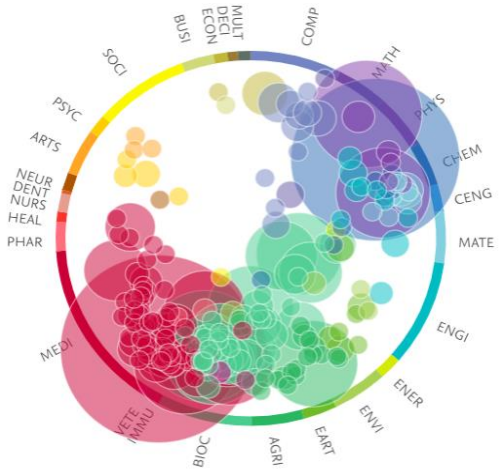


COMP	Computer Science
MATH	Mathematics
PHYS	Physics and Astronomy
CHEM	Chemistry
CENG	Chemical Engineering
MATE	Materials Science
ENGI	Engineering
ENER	Energy
ENVI	Environmental Science
EART	Earth and Planetary Sciences
AGRI	Agricultural and Biological Sciences
BIOC	Biochemistry, Genetics and Molecular Biology
IMMU	Immunology and Microbiology
VETE	Veterinary
MEDI	Medicine
PHAR	Pharmacology, Toxicology and Pharmaceutics
HEAL	Health Professions
NURS	Nursing
DENT	Dentistry
NEUR	Neuroscience
ARTS	Arts and Humanities
PSYC	Psychology
SOCI	Social Sciences
BUSI	Business, Management and Accounting
ECON	Economics, Econometrics and Finance
DECI	Decision Sciences
MULT	Multidisciplinary

SciVal Data, Dorte Drongstrup, SDU

Largest Topic Prominence Clusters using National HPC

Hot topics: Ten of the largest TCs are in the top10% topic prominence percentile!



"Topic prominence" can be calculated from the number of citations, citescore and "views" in Scopus.

TC, Topic Cluser

TOPIC CLUSTER (TC)	TC NUMBER	N	FWCI	WORLDWIDE PROMINENCE PERCENTILE
ANTI-BACTERIAL AGENTS; INFECTION; METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS	TC.16	41	3.33	98.260
QUANTUM CHEMISTRY; DENSITY FUNCTIONAL THEORY; MOLECULAR ORBITALS	TC.145	35	1.11	91.365
DNA METHYLATION; EPIGENOMICS; NEOPLASMS	TC.478	23	2.59	91.968
DECAY; QUARKS; NEUTRINOS	TC.6	22	3.32	98.394
T-LYMPHOCYTES; NEOPLASMS; IMMUNOTHERAPY	TC.12	20	6.11	99.665
MICRORNAS; LONG UNTRANSLATED RNA; NEOPLASMS	TC.219	19	1.23	99.398
PLASMONS; METAMATERIALS; SURFACE PLASMON RESONANCE	TC.47	18	3.35	99.531
BIRDS; NESTS; SEABIRDS	TC.41	17	1.69	89.759
PROTEINS; MOLECULAR DYNAMICS SIMULATION; MOLECULAR DYNAMICS	TC.108	16	1.86	94.846
GENOME; NEOPLASMS; GENES	TC.436	16	2.41	94.043
SALMONELLA; ESCHERICHIA COLI; LISTERIA MONOCYTOGENES	TC.40	16	2.51	93.641

SciVal Data, Dorte Drongstrup, SDU

DeiC > Examples of Mashine Learning using DK-HPC

Risk Analysis, Vol. 39, No. 6, 2019 DOI: 10.1111/risa.13239

Machine Learning Methods as a Tool for Predicting Risk of Illness Applying Next-Generation Sequencing Data

Patrick Murigu Kamau Njage,[1,*] Clementine Henri,[2] Pimlapas Leekitcharoenphon,[1] Michel-Yves Mistou,[2] Rene S. Hendriksen,[1] and Tine Hald[1]

AMIA Annu Symp Proc. 2015; 2015: 1296–1305.
Published online 2015 Nov 5.
PMCID: PMC4765575
PMID: 26958270

Finding Cervical Cancer Symptoms in Swedish Clinical Text usir Machine Learning Approach and NegEx

Rebecka Weegar, M.Sc,[1] Maria Kvist, MD, PhD,[1,2] Karin Sundström, MD, PhD,[3] Søren Brunak, P
Hercules Dalianis, PhD[1]

MDPI

molecules
DOI: 10.3390/molecules24152747

Article

Combined Ensemble Docking and Machine Learning in Identification of Therapeutic Agents with Potential Inhibitory Effect on Human CES1

Eliane Briand [1], Ragnar Thomsen [2], Kristian Linnet [2], Henrik Berg Rasmussen [3,4], Søren Brunak [5] and Olivier Taboureau [1,*]

Bioinformatics, 33(22), 2017, 3685–3690
doi: 10.1093/bioinformatics/btx531
Advance Access Publication Date: 23 August 2017
Review

OXFORD

Sequence analysis

An introduction to deep learning on biological sequence data: examples and solutions

Vanessa Isabell Jurtz[1], Alexander Rosenberg Johansen[2], Morten Nielsen[1,3], Jose Juan Almagro Armenteros[1], Henrik Nielsen[1], Casper Kaae Sønderby[4], Ole Winther[2,4,*] and Søren Kaae Sønderby[4,*]

Contents lists available at ScienceDirect

International Journal of Food Microbiology

journal homepage: www.elsevier.com/locate/ijfoodmicro

ELSEVIER

Improving hazard characterization in microbial risk assessment using next generation sequencing data and machine learning: Predicting clinical outcomes in shigatoxigenic *Escherichia coli*

Patrick Murigu Kamau Njage*, Pimlapas Leekitcharoenphon, Tine Hald

Research Group for Genomic Epidemiology, National Food Institute, Technical University of Denmark, Kemitorvet, Building 204, 2800 Kgs. Lyngby, Denmark

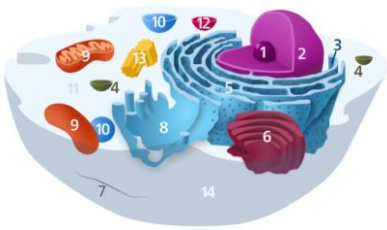
–3395
btx431
2017
Paper

OXFORD

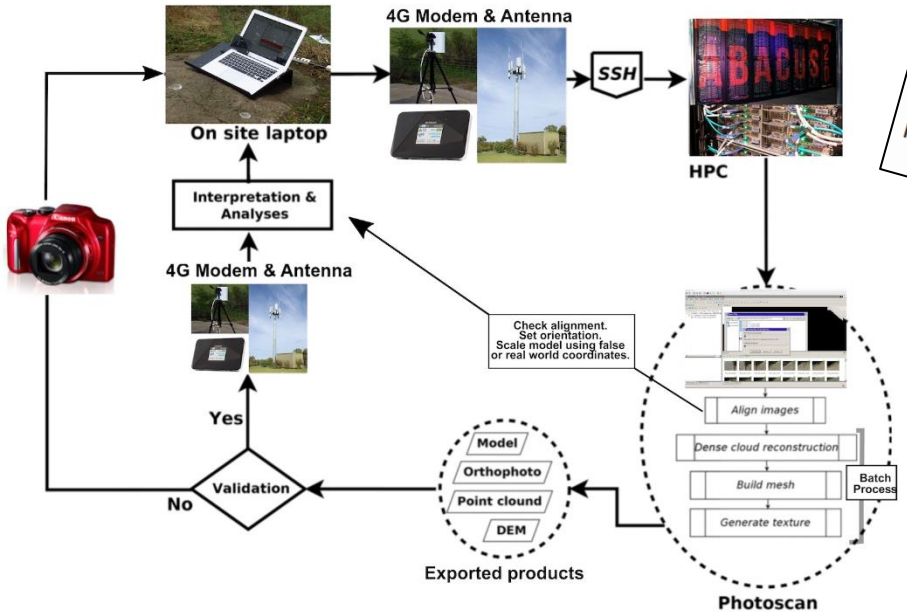
Sequence analysis

DeepLoc: prediction of protein subcellular localization using deep learning

José Juan Almagro Armenteros[1,2,*], Casper Kaae Sønderby[2], Søren Kaae Sønderby[2], Henrik Nielsen[1] and Ole Winther[2,3]



Examples from Social Sciences & Humanities



Dodd, J. (2018) Adoranten: 92-104.
The application of **high performance computing** in rock art documentation and research

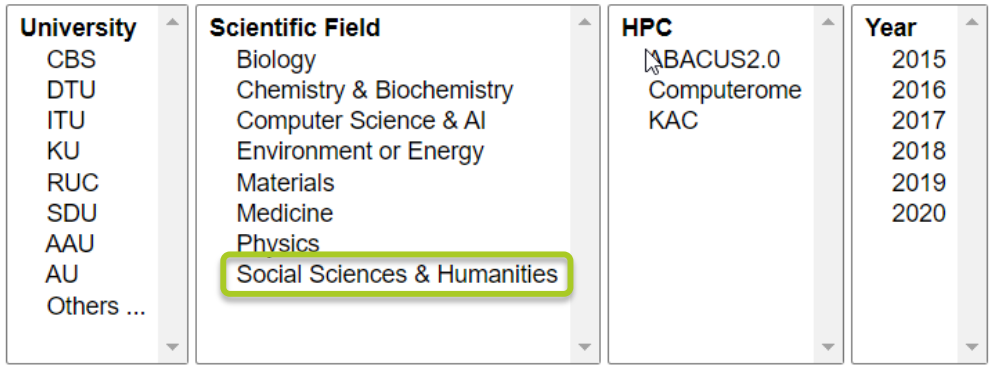
Archaeology:
Rock carvings
in the field

NEW!

Brügger, N. et al. (2019) Establishing a corpus of the archived web: the case of the Danish web from 2005 to 2015. In The historical web and digital humanities. The case of national web domains, ISBN 978-1-138-29431-8

Explore More using our search function:

https://vidensportal.deic.dk/en/HPC/literature/search



Milstreu, G. and Prøhl, H. (eds.) (2020) Documentation and Registration of Rock Art in Tanum World Heritage No. 4. Tanumshede: Tanums Hällristningsmuseum Underslös, Scandinavian Society for Prehistoric Art.

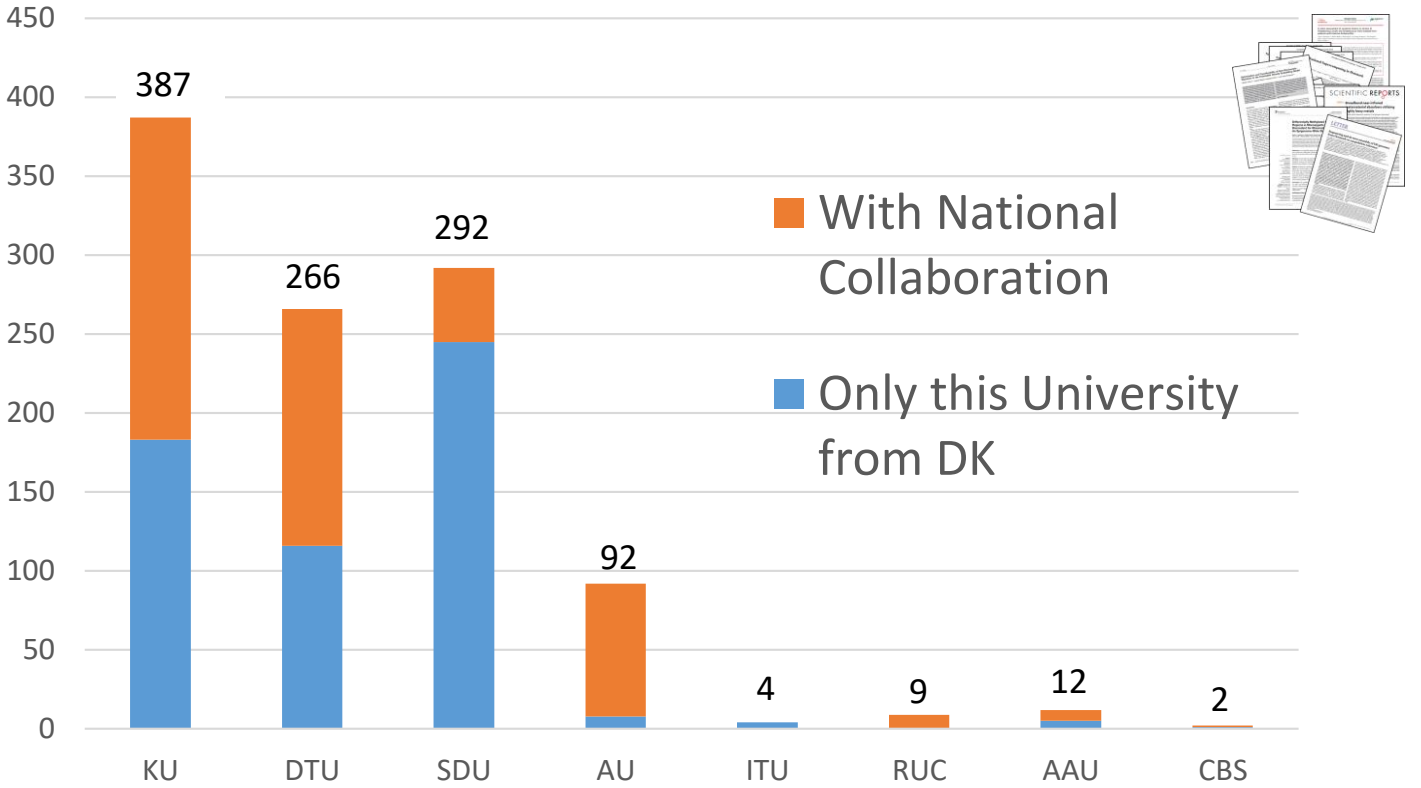
Archaeology: **NEW!**
Prehistoric art

DeiC > Collaboration Patterns: Academia

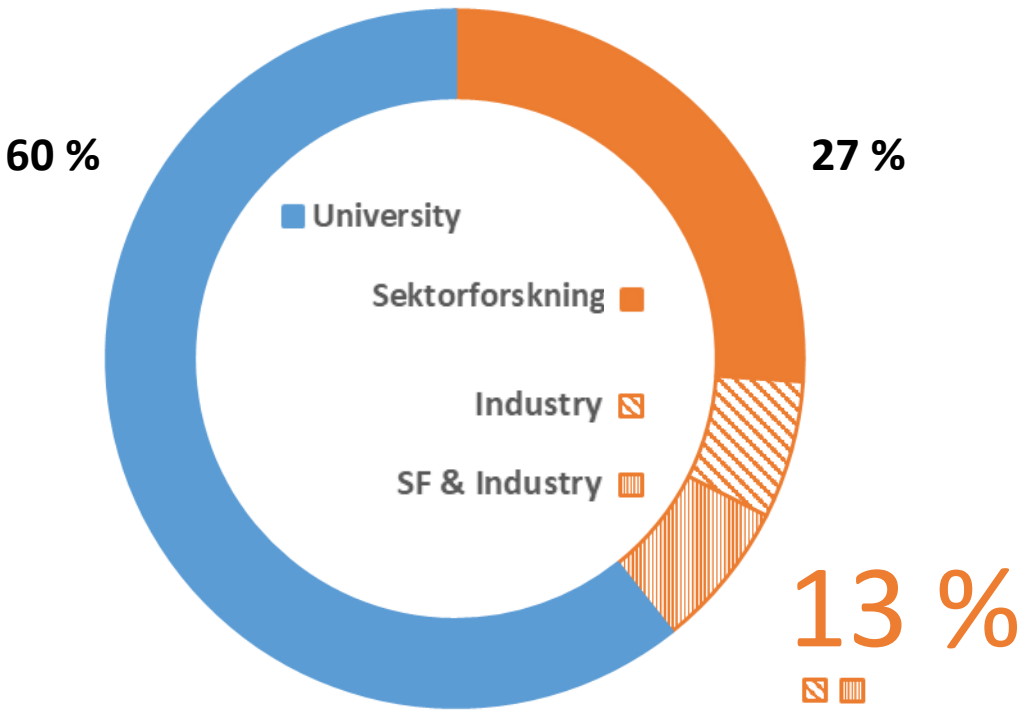
1. Know our National HPC users

- ✓ Scientific Disciplines
- ✓ Global collaboration
- Universities
- Industry
- ”Regionerne” / Hospitals

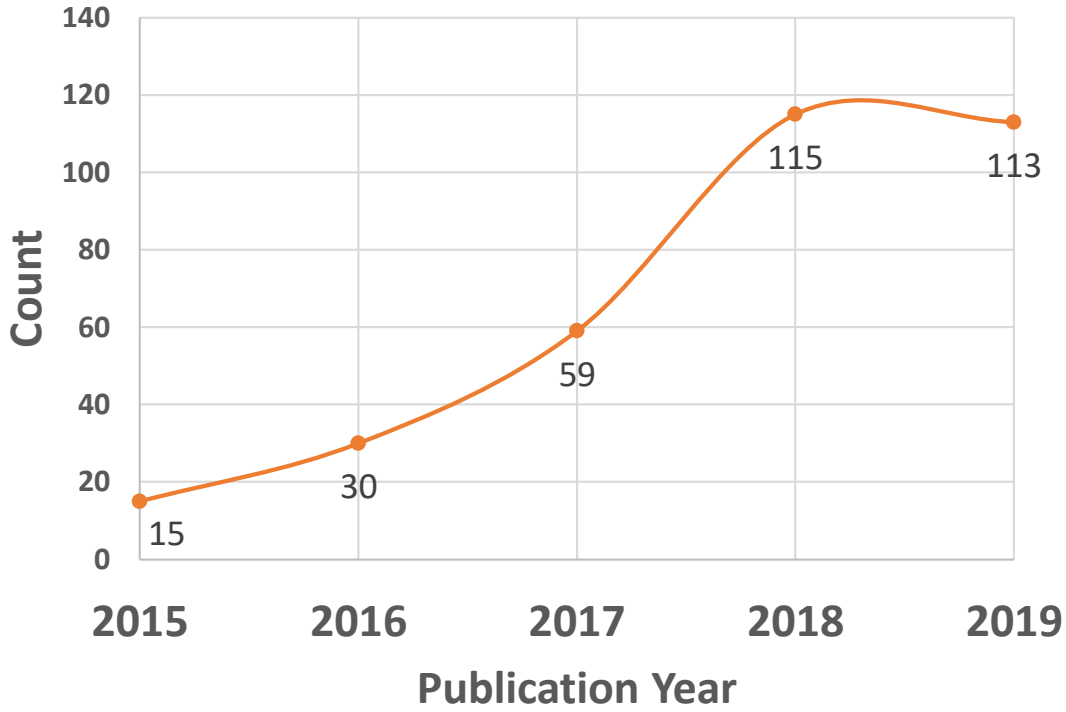
Authorship
Total, N=835



Collaboration with Industry Plateaued



A total of 332 (40%) of the 835 publications included Industry and ”Sektorforskning” (SF)

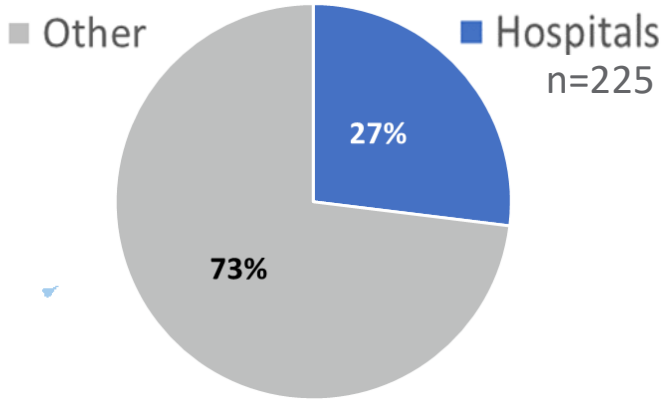


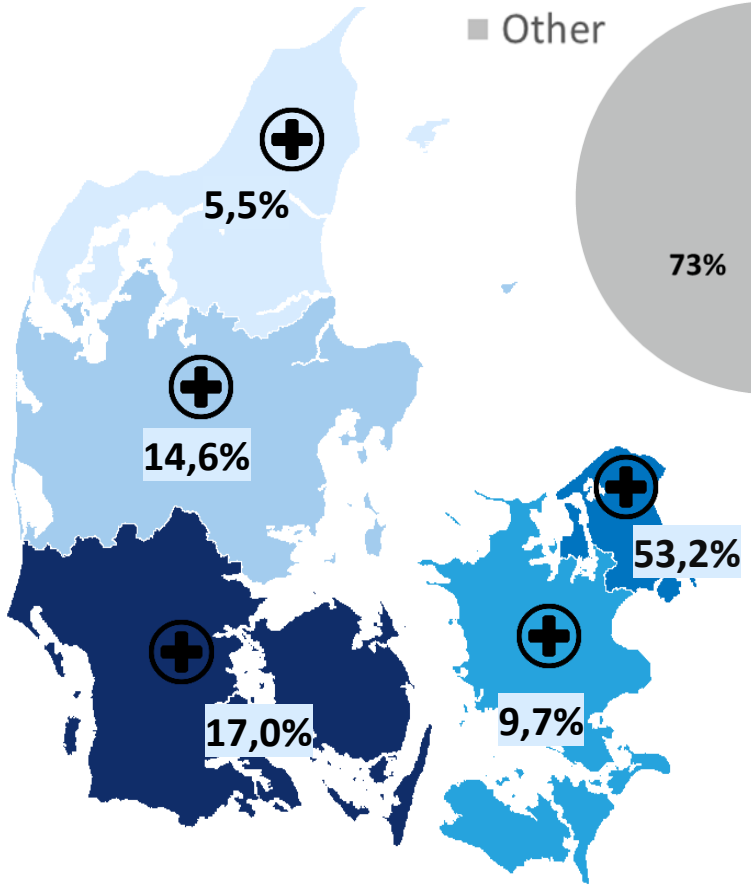
SF, ”Sektorforskning” such as Hospitals, Statens Serum Institut, Kræftens bekæmpelse, Fødevarestyrelsen m.m.

DeiC > Collaboration with Industry

DeiC > DK-HPC to Regional Hospitals

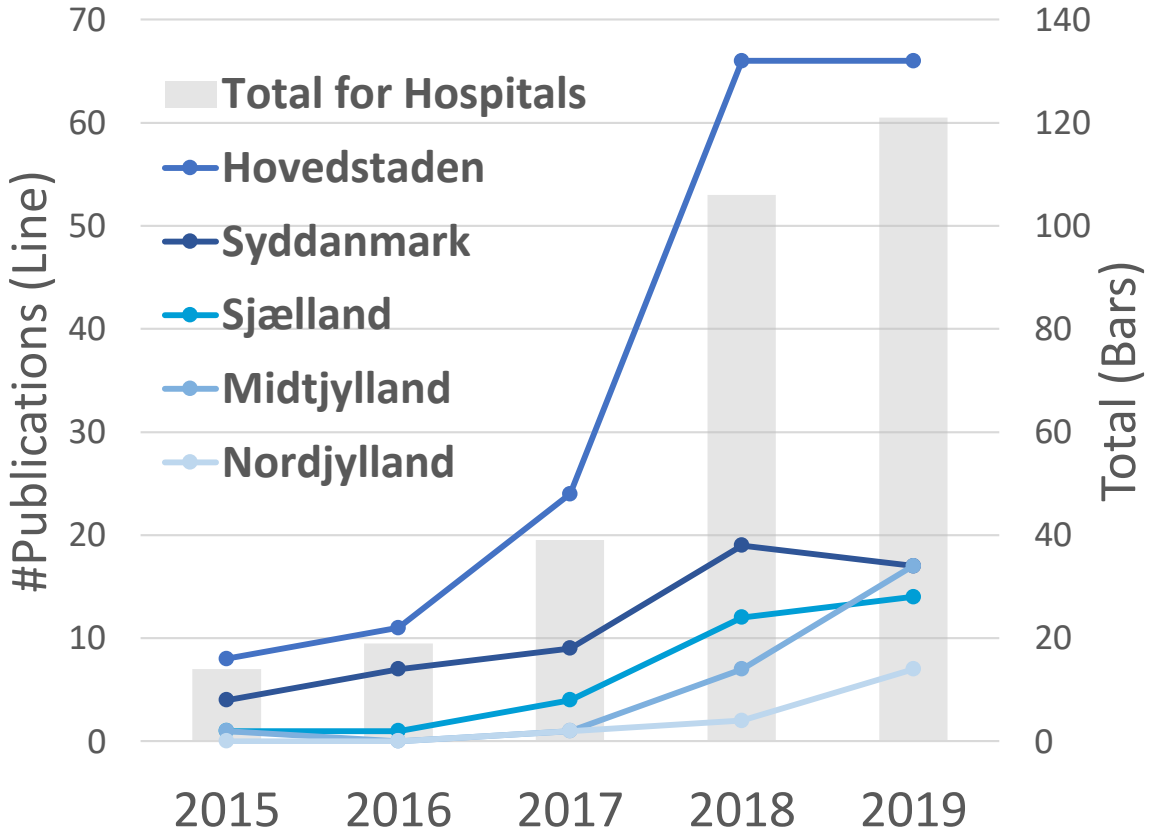
How many incl. hospitals?





If a publication has authors from several hospitals, then each of these hospitals would get one credit for the publication.

> 10-Fold Increase 2015 to 2019



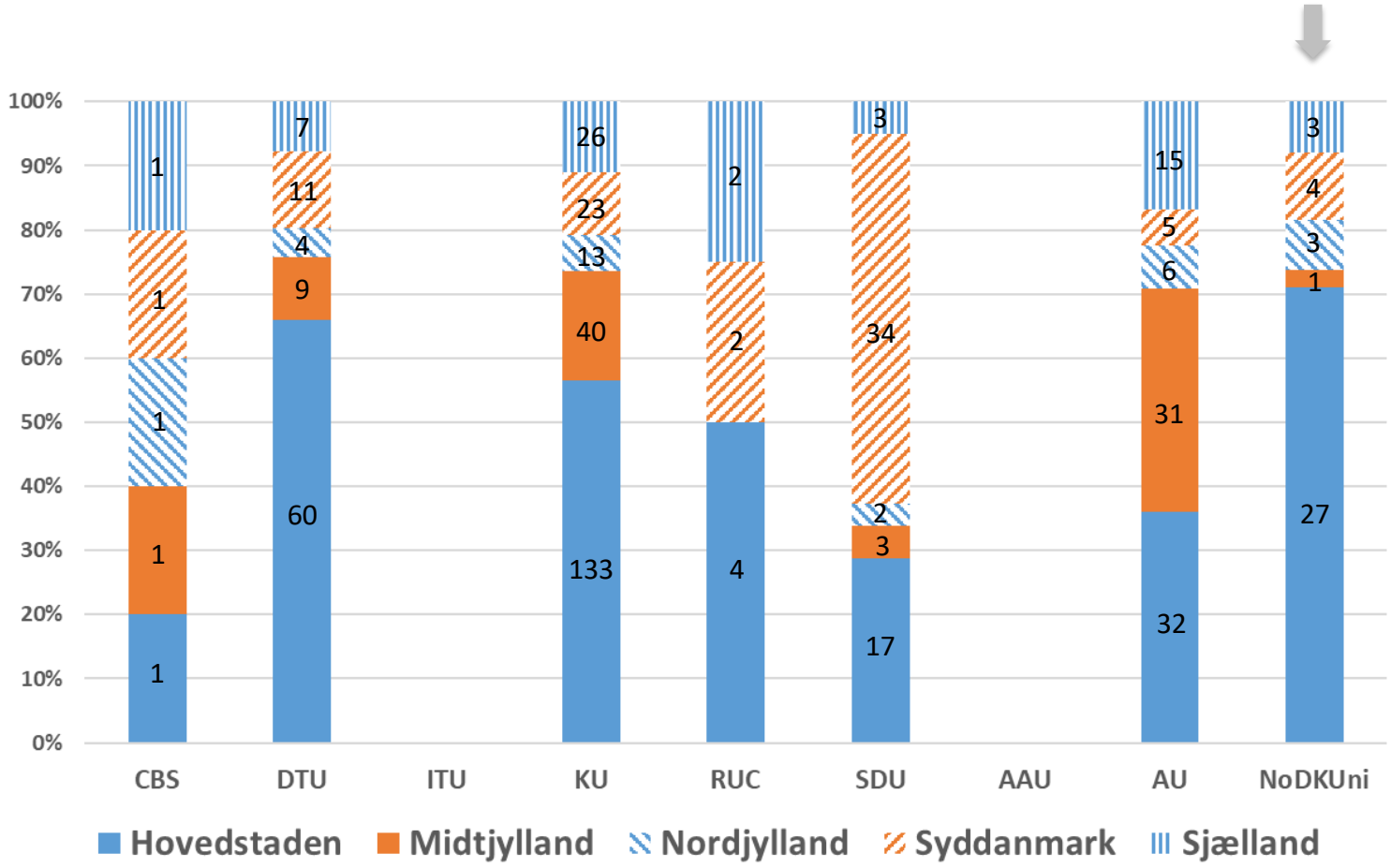
DeiC > DK-HPC and Regional Hospitals

1. Know our National HPC users

- ✓ Scientific Disciplines
- ✓ Global collaboration
- ✓ Universities
- ✓ Industry
- ✓ ”Regionerne” / Hospitals

If a publication has authors from several universities, then each of these universities would get one credit for the publication.

Regional Hospitals also access DK-HPC on their own (NoDKUni)



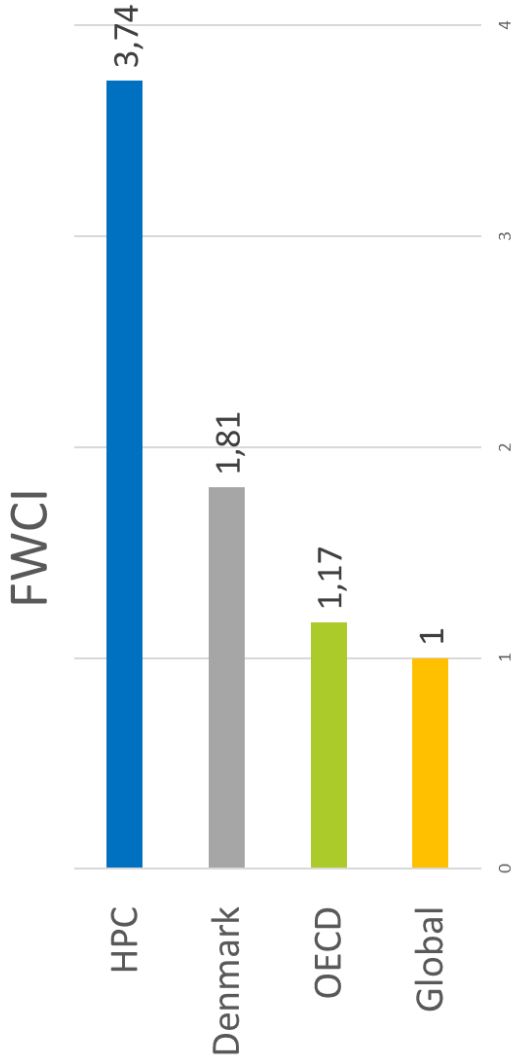
Impact - FWCI

2. World-Class Research

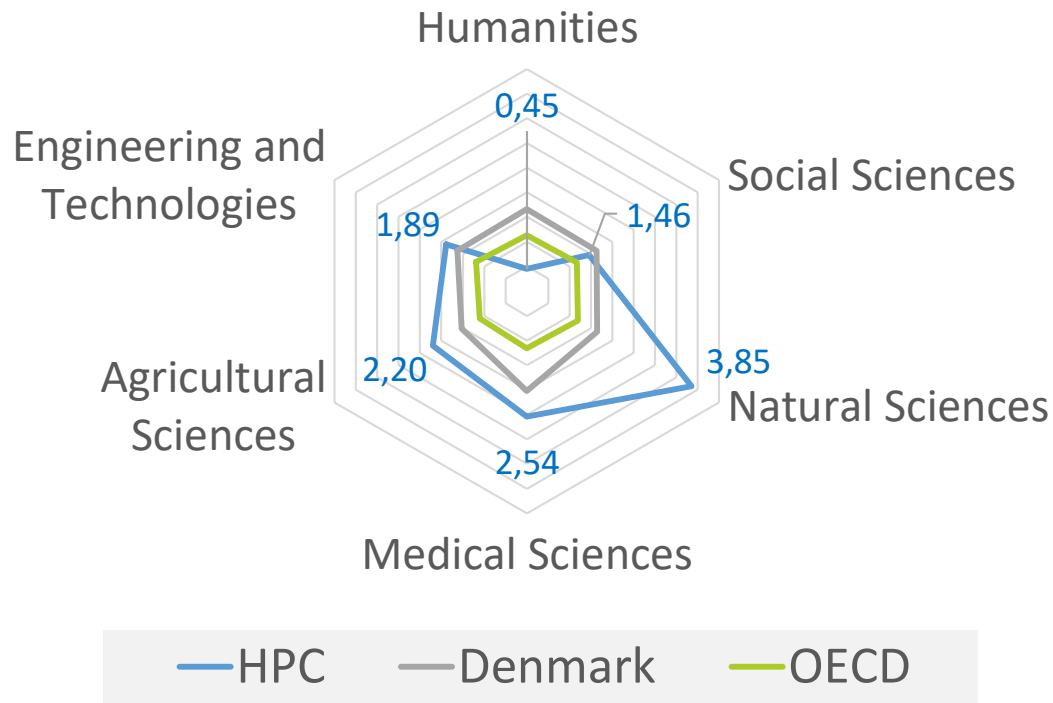
- Field-Weighted Citataion Impact (FWCI)
- Advantage: Publications that made use of HPC was substantially above the world average FWCI

Benchmark

2015-2019

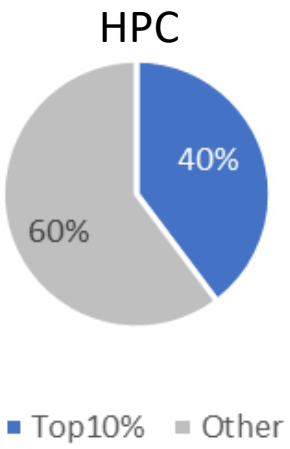


PUBLICATIONS	UNIQUE AUTHORS	CITATIONS	AVERAGE CITATION PER PUBLICATION	FWCI
805 (Scopus)	7,022	24,302	30.2	3.74

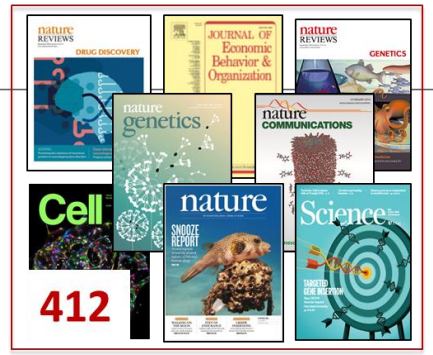


> Impact - Visibility

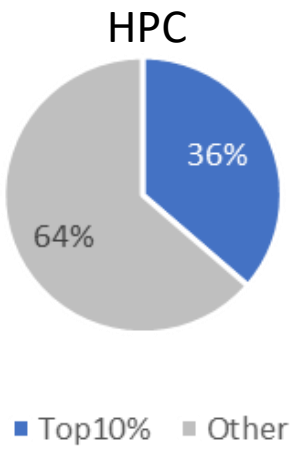
Share of 2015-2019 Publications in top 10% most cited worldwide



Denmark: 22%

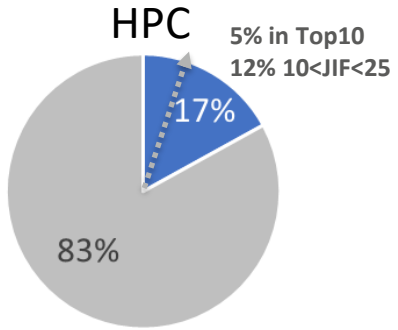


Publications in top 10% Journals by SNIP



Denmark: 23%

Journal Impact Factor
JIF > 10



Journal (Top10 highest JIF)	#	JIF
New England Journal of Medicine	2	70,67
Nature Reviews Drug Discovery	1	57
Nature Biotechnology	1	41,667
Nature Reviews Genetics	1	40,282
Nature	13	40,137
Science	5	37,205
Cell	6	30,41
Nature Genetics	11	27,959
Cancer Cell	1	27,407
Nature Methods	2	25,062

2. World-Class Research

- 40% in top10% most cited
- In Top10% Journals by SNIP
- High Journal Impact Factor (JIF)
- Advantage: Publications that made use of HPC was substantially above the average values for DK

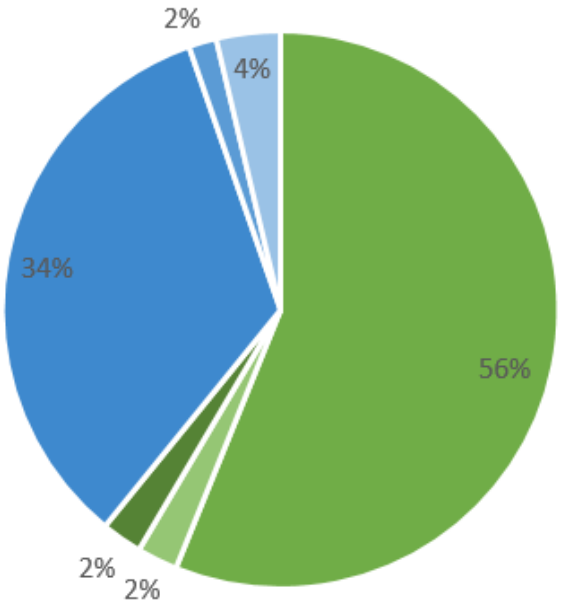
DeiC > Open Access

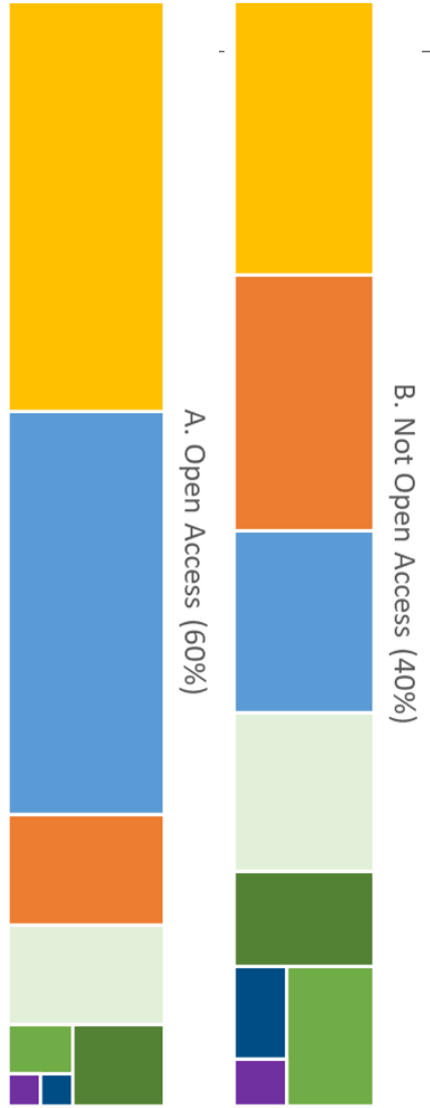
A total of 61%

- OA: Articles
- OA: Reviews
- OA: Other publications

Part of publications

N=805 of 835 in Scopus





Scientific Field

- Medicine
- Chemistry & Biochemistry
- Biology
- Computer Sci & AI
- Physics
- Materials
- Environment
- Social Sciences & Humanities

Life Science publish OA

……..and is also the largest scientific area that does NOT publish OA!

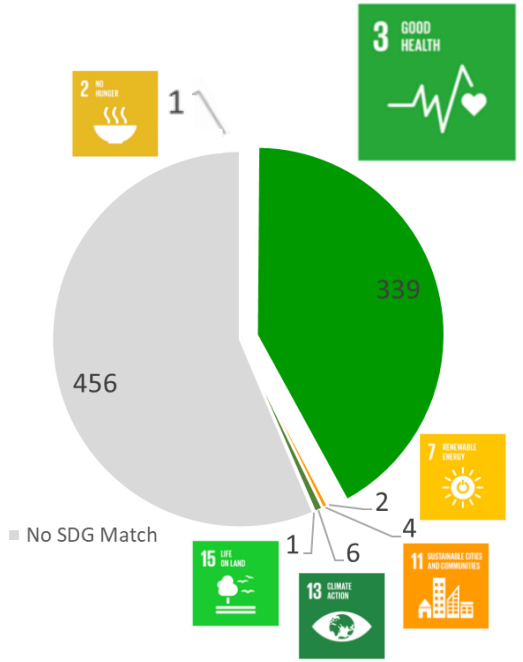
National Supercomputing in DK 2015 to 2019, and UN's 17 SDG's

- How to test this?
- Display scientific output
- Some publications that made use of HPC were feeding into the global agenda

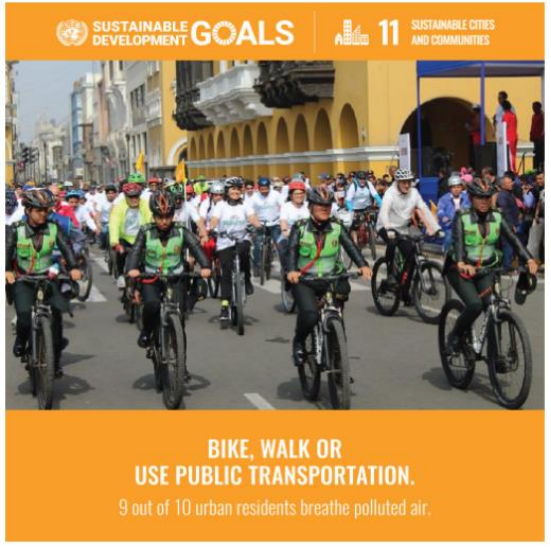
Global challenges formulated in the UN's 17 Sustainable Development Goals

UN Sustainability Development Goals

In total, we matched
353 publications
to a SDG goal



N=805 of 835 in Scopus



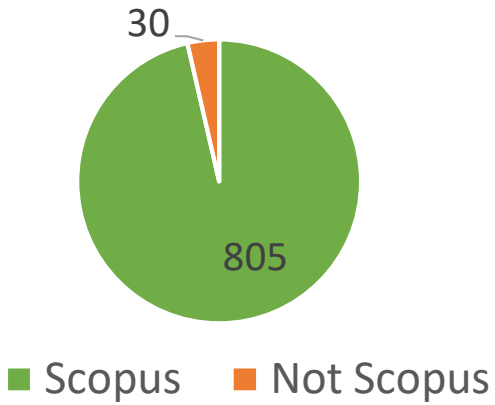
https://www.un.org/sustainabledevelopment/sustainable-development-goals/

SDG3 Match to DK-HPC Publications

Diseases,
Genome sequencing
& Epigenetics

INFLAMMATION
ENDOMETRIOSIS
MALARIA
PARKINSON
LUPUS
LEUKEMIA
PRETERM BIRTH
DISEASE PROGRESSION PATTERNS
INFECTIONS
BIPOLAR DISORDER
CANCER
DIABETES
AGING
AUTISM
DEPRESSION
PTSD
ASTHMA
LIVER DISEASE
OBESITY
ADHD
SCHIZOPHRENIA
GUT
CARDIOVASCULAR DISEASE
MICROBIOME
CORONARY HEART DISEASE
! Nb Not Corona virus
RHEUMATOID ARTHRITIS
CORONARY ATERY DISEASE
THROMBOSIS
TUBERCULOSIS
! Nb Not Corona virus

DeiC > SDG Search Queries



Used in this study:

Jayabalasingham, B. et al. (2019) Identifying research supporting the United Nations Sustainable Development Goals, Mendeley Data (1 ed.). **Scopus search queries developed by Elsevier**, DOI: 10.17632/87txkw7khs.1

"Too premature to trust commercial SDG-analyses for anything other than exploratory purposes at this stage in their development".

Armitage, C. S. et al. (2020) Mapping scholarly publications related to the Sustainable Development Goals: Do independent bibliometric approaches get the same results? Quantitative Science Studies. Advance Publication. DOI: 10.1162/qss_a_00071

DeiC > Other SDG Search Candidates

Suggestion

Seach Result

www.nature.com/scientificreports

SCIENTIFIC REPORTS

OPEN

Genomic and metagenomic signatures of giant viruses are ubiquitous in water samples from sewage, inland lake, waste water treatment plant, and municipal water supply in Mumbai, India

6 CLEAN WATER AND SANITATION

11 SUSTAINABLE CITIES AND COMMUNITIES

Anirvan Chatterjee[1], Thomas Sicheritz-Pontén[2], Rajesh Yadav[1] & Kiran Kondabagil[1]

We report the detection of genomic signatures of giant viruses (GVs) in the metagenomes of three environment samples from Mumbai, India, namely, a pre-filter of a household water purifier, a sludge sample from wastewater treatment plant (WWTP), and a drying bed sample of the same WWTP. The *de novo* assembled contigs of each sample yielded 700 to 2000 maximum unique matches with the GV genomic database. In all three samples, the maximum number of reads aligned to Pandoraviridae, followed by Phycodnaviridae, Mimiviridae, Iridoviridae, and other Megaviruses. We also isolated GVs from every environmental sample (n = 20) we tested using co-culture of the sample with *Acanthomoeba castellanii*. From this, four randomly selected GVs were subjected to the genomic characterization that showed remarkable cladistic homology with the three GV families viz., Mimiviridae (*Mimivirus Bombay [MVB]*), Megaviruses (*Powai lake megavirus [PLMV]* and *Bandra megavius [BAV]*), and Marseilleviridae (*Kurlavirus [KV]*). All 4 isolates exhibited remarkable genomic identity with respective GV families. Functionally, the genomes were indistinguishable from other previously reported GVs, encoding nearly all COGs across extant family members. Further, the uncanny genomic homogeneity exhibited by individual GV families across distant geographies indicate their yet to be ascertained ecological significance.

The discovery of *Acanthamoeba polyphaga mimivirus* (APMV)[1,2] galvanized the search for other giant viruses (GVs). Subsequently, GVs have been isolated from diverse environmental niches, including cooling towers, sewage, fresh water, and coastal water[3]. In fact, nucleocytoplasmic large DNA viruses (NCLDVs) in the photic layer of oceans were thought to outnumber the eukaryotic organisms[4]. Metagenomic identification of *Klosneuvirus*, a new GV family, from wastewater treatment plant (WWTP) and their detection in the existing environmental metagenomes indicated their previously undetected presence[5]. Despite the discovery of several GV families, very little is known about their natural hosts, their role in the ecology, and biogeochemical pathways. While the Phycodnaviridae members are believed to control the planktonic communities[6], the role of other GVs in their environment is largely unknown.

The current classification of NCLDVs consists of six closely related families of amoebal megaviruses, namely, Mimiviridae, Marseilleviridae, Pandoraviridae, Pithoviridae, Faustoviridae, and Mollivirida[7]. While the evolutionary genealogy of NCLDVs remains highly debated[7–11], the comparative genomics of several new amoebal NCDLV genomes from diverse geographies have augmented their accurate familial classification[12–17]. Both genome *expansion*[18,19] and *reduction*[20] models have been explored for explaining the evolution of the large

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nature COMMUNICATIONS

ARTICLE

https://doi.org/10.1038/s41467-019-08853-3 OPEN

Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage

Rene S. Hendriksen[1], Patrick Munk[1], Patrick Njage[1], Bram van Bunnik[2], Luke McNally[3], Oksana Lukjancenko[1], Timo Röder[1], David Nieuwenhuijse[4], Susanne Karlsmose Pedersen[1], Jette Kjeldgaard[1], Rolf S. Kaas[1], Philip Thomas Lanken Conradsen Clausen[1], Josef Korbinian Vogt[1], Pimlapas Leekitcharoenphon[1], Milou G.M. van de Schans[5], Tina Zuidema[5], Ana Maria de Roda Husman[6], Simon Rasmussen[7], Bent Petersen[7], The Global Sewage Surveillance project consortium[#], Clara Amid[8], Guy Cochrane[8], Thomas Sicheritz-Ponten[9], Heike Schmitt[6], Jorge Raul Matheu Alvarez[10], Awa Aidara-Kane[10], Sünje J. Pamp[1], Ole Lund[7], Tine Hald[1], Mark Woolhouse[2], Marion P. Koopmans[4], Håkan Vigre[1], Thomas Nordahl Petersen[1] & Frank M. Aarestrup[1]

Antimicrobial resistance (AMR) is a serious threat to global public health, but obtaining representative data on AMR for healthy human populations is difficult. Here, we use metagenomic analysis of untreated sewage to characterize the bacterial resistome from 79 sites in 60 countries. We find systematic differences in abundance and diversity of AMR genes between Europe/North-America/Oceania and Africa/Asia/South-America. Antimicrobial use data and bacterial taxonomy only explains a minor part of the AMR variation that we observe. We find no evidence for cross-selection between antimicrobial classes, or for effect of air travel between sites. However, AMR gene abundance strongly correlates with socio-economic, health and environmental factors, which we use to predict AMR gene abundances in all countries in the world. Our findings suggest that global AMR gene diversity and abundance vary by region, and that improving sanitation and health could potentially limit the global burden of AMR. We propose metagenomic analysis of sewage as an ethically acceptable and economically feasible approach for continuous global surveillance and prediction of AMR.

6 CLEAN WATER AND SANITATION

3 GOOD HEALTH

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frontiers in Microbiology

3 GOOD HEALTH

14 LIFE BELOW WATER

No SDG Hit

ORIGINAL RESEARCH
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Surveillance and Genomics of Toxigenic *Vibrio cholerae* O1 From Fish, Phytoplankton and Water in Lake Victoria, Tanzania

Yaovi M. Gildas Hounmanou[1], Pimlapas Leekitcharoenphon[2], Rene S. Hendriksen[2], Tamegnon V. Dougnon[3], Robinson H. Mdegela[4], John E. Olsen[1] and Anders Dalsgaard[1]*

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The occurrence of toxigenic *Vibrio cholerae* O1 during a non- outbreak period in Lake Victoria was studied and genetic characteristics for environmental persistence and relatedness to pandemic strains were assessed. We analyzed 360 samples of carps, phytoplankton and water collected in 2017 during dry and rainy seasons in the Tanzanian basin of Lake Victoria. Samples were tested using PCR (*ompW* and *ctxA*) with DNA extracted from bacterial isolates and samples enriched in alkaline peptone water. Isolates were screened with polyvalent antiserum O1 followed by antimicrobial susceptibility testing. Whole genome sequencing and bioinformatics tools were employed to investigate the genomic characteristics of the isolates. More *V. cholerae* positive samples were recovered by PCR when DNA was obtained from enriched samples than from isolates (69.0% vs. 21.3%, $p < 0.05$), irrespectively of season. We identified ten *V. cholerae* O1 among 22 *ctxA*-positive isolates. Further studies are needed to serotype the remaining *ctxA*-positive non-O1 strains. Sequenced strains belonged to El Tor atypical biotype of *V. cholerae* O1 of MLST ST69 harboring the seventh pandemic gene. Major virulence genes, *ctxA*, *ctxB*, *zot*, *ace*, *tcpA*, *hlyA*, *rtxA*, *ompU*, *toxR*, *T6SS*, *alsD*, *makA* and pathogenicity islands VPI-1, VPI-2, VSP-1, and VSP-2 were found in all strains. The strains contained *Vibrio* polysaccharide biosynthesis enzymes, the *mshA* gene and two-component response regulator proteins involved in stress response and autoinducers for quorum sensing and biofilm formation. They carried the SXT integrative conjugative element with phenotypic and genotypic resistance to aminoglycoside, sulfamethoxazole, trimethoprim, phenicol, and quinolones. Strains contained a multidrug efflux pump component and were resistant to toxic compounds with copper homeostasis and cobalt-zinc-cadmium resistance proteins. The environmental strains belonged to the third wave of the seventh pandemic and most are genetically closely related to recent outbreak strains from

What About the Climate?

DeiC > DK-HPC & SDGs: Climate / Energy (<2%)

Contamination of the Arctic reflected in microbial meta-genomes from the Greenland ice sheet

Hauptmann A.L. et al. (2017)

DOI: 10.1088/1748-9326/aa7445.

1.31

Upstream freshwater and terrestrial sources are differentially reflected in the bacterial community structure along a small Arctic river and its estuary

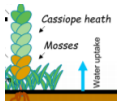
Hauptmann A.L. et al. (2016)

DOI: 10.3389/fmicb.2016.01474.

1.17

1.19

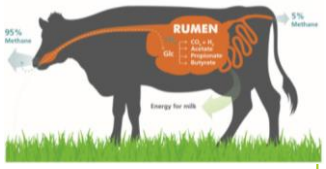
Process-Oriented Modeling of a High Arctic Tundra Eco-system: Long-Term Carbon Budget & Ecosystem Respon-ses to Interannual Variations of Climate



Zhang W. et al. (2018)

DOI: 10.1002/2017JG003956

Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows



Difford G.F. et al. (2018)

DOI: 10.1371/journal.pgen.1007580.

3.95

Meta-genomic analysis of toilet waste from long distance flights; A step towards global surveillance of infectious diseases and antimicrobial resistance.

Petersen T.N. et al. (2015)

DOI: 10.1038/srep11444.

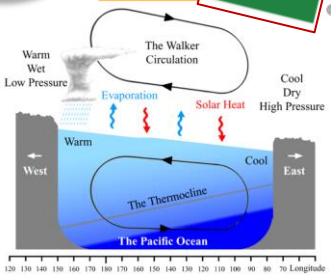
1.26

1.15

Slowdown of the Walker circulation at solar cycle maximum

Misios S. et al. (2019)

DOI: 10.1073/pnas.1815060116.

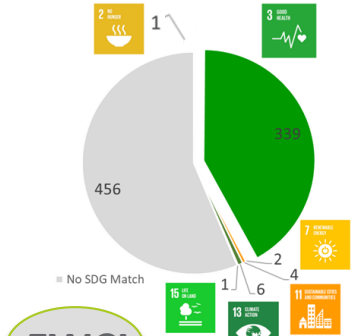


A testing procedure for wind turbine generators based on the power grid statistical model

Farajzadeh S. et al. (2018)

DOI: 10.1016/j.renene.2017.03.073.

0.37



FWCI

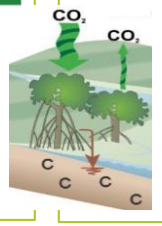
N=805 in Scopus

Drivers of dissolved organic carbon export in a subarctic catchment: Importance of microbial decomposition, sorption-desorption, peatland and lateral flow

Tang J. et al. (2018)

DOI: 10.1016/j.scitotenv.2017.11.252.

1.16



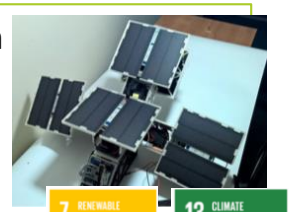
Climate Sensitivity Controls Uncertainty in Future Terrestrial Carbon Sink

Schurgers G. et al. (2018)

DOI: 10.1029/2018GL077528.

0.64

Toward energy autonomy in heterogeneous modular plant-inspired robots through artificial evolution



Veenstra F. et al. (2017)

DOI: 10.3389/frobt.2017.00043.

ND

No SDGs matched and yet some hits.....

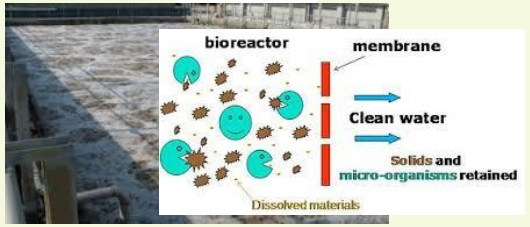
FWCI

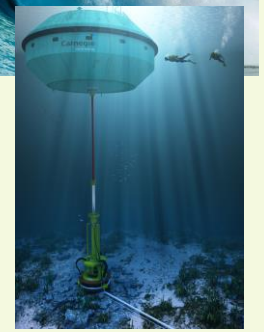
- Farajzadehbibalan, S. et al. (2017) Statistical modeling of the power grid from a wind farm standpoint. DOI: 10.1016/j.epsr.2016.11.020 **0.34**
- Herp, J. et al. (2018) Bayesian state prediction of wind turbine bearing failure. DOI: 10.1016/j.renene.2017.02.069 **1.69**
- Dahl, C. M. et al. (2019) Nonparametric wind power forecasting under fixed and random censoring. DOI: 10.1016/j.eneco.2019.104520 **ND**

2.95 Wendt, F. et al. (2019) Ocean energy systems wave energy modelling task: Modelling, verification and validation of wave energy converters. DOI: 10.3390/jmse7110379

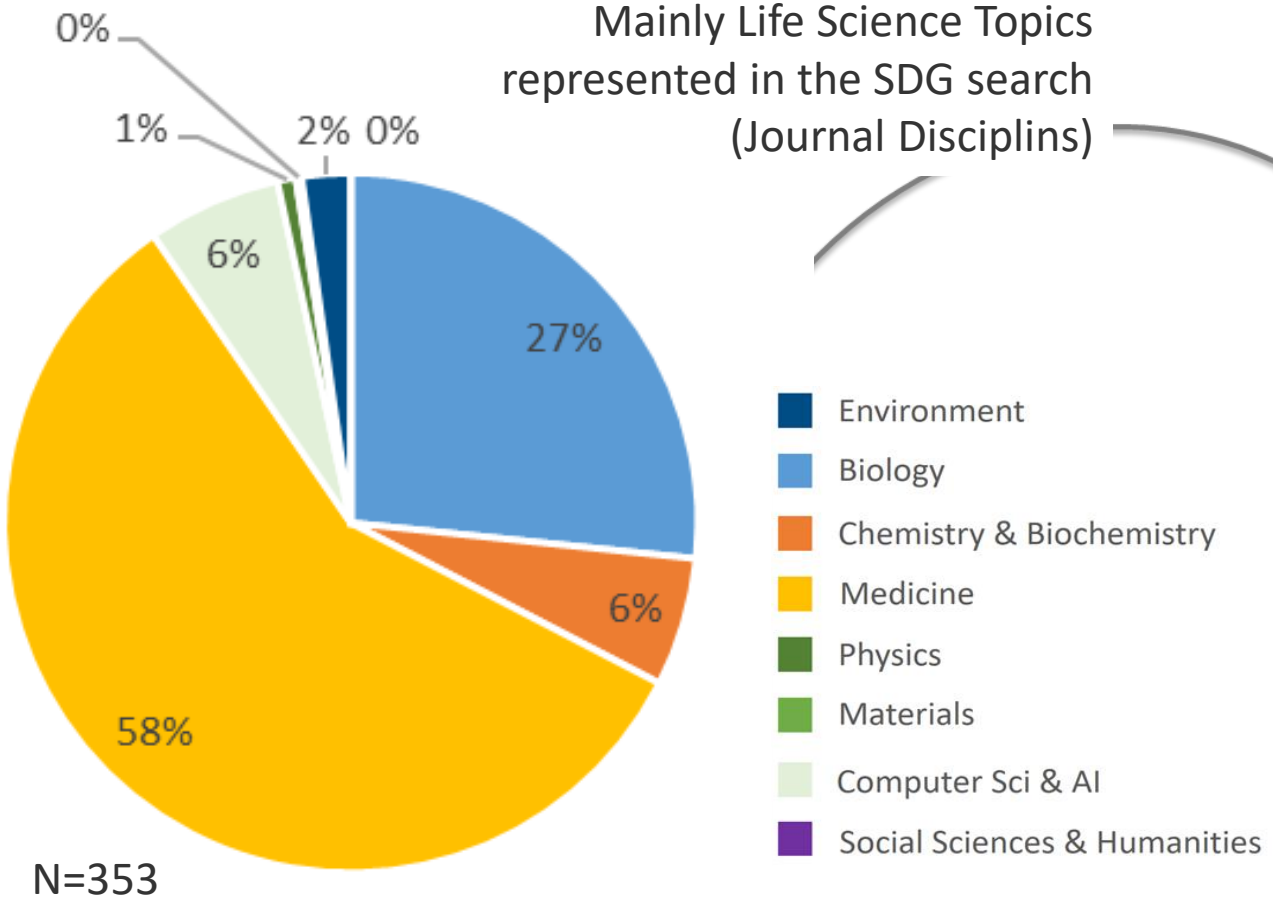
4.69 Alexandersen, J. et al. (2018) Design of passive coolers for light-emitting diode lamps using topology optimization. DOI: 10.1016/j.ijheatmasstransfer.2018.01.10

1.09 Torresi, E. et al. (2018) Reactor staging influences microbial community composition and diversity of denitrifying MBBRs - Implications on pharmaceutical removal. DOI: 10.1016/j.watres.2018.03.014





SDGs and Disciplines related to DK-HPC papers



N=353

Mainly Life Science Topics represented in the SDG search (Journal Disciplins)

44%

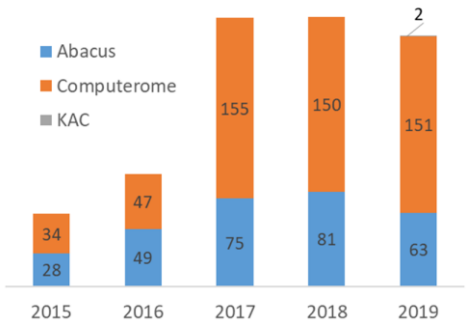
Majority of the 353 publications matched **SDG3** or 5 other SDGs

2 additional SDGs

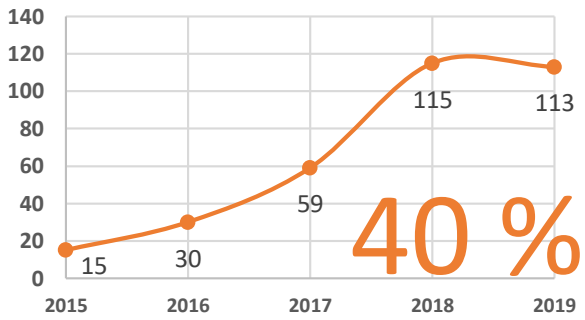
9 SDGs NOT represented

National DK-HPC: Peaks and Potentials

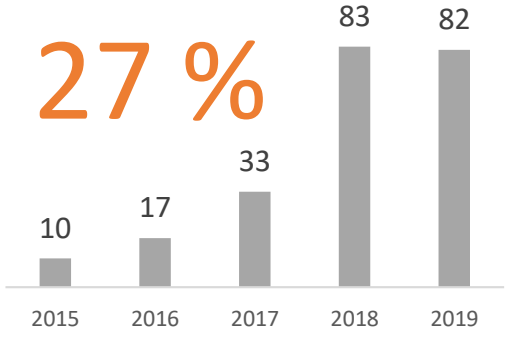
Publication Plateau Reached



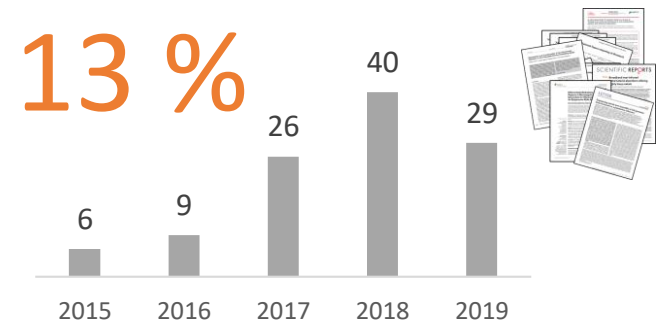
…… also for Industry & SF



…… and Hospitals



……. as well as Corporate Industry



44 %

THE GLOBAL GOALS

<2%

13 CLIMATE ACTION

Majority

3 GOOD HEALTH

Unused Potential

New HPC landscape from Ultimo 2020

Type 1 Interactive (VM/Docker)
Type 2 A la Computerome
Type 3 Large memory > 4TByte
Type 4 Experimental architechture
Type 5 LUMI

Platform Access

DeiC > Conclusions for National HPC 2015-2019

1. Know our HPC users

YES!

- Scientific Disciplines
- Universities
- Industry
- ”Regionerne” / Hospitals
- Collaboration patterns: High degree of knowledge exchange

2. World-Class Research

YES!

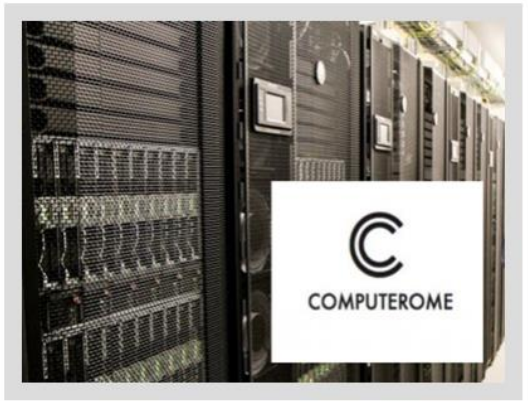
- 40% of peer-reviewed research from Danish National HPC are among the top 10% most cited world wide
- 61% use Open Access
- 44% feed into SDGs (#3 Health)
  (Algorithm not optimal)
- FWCI above world average!
  (DK-HPC: 3,74)

3. Outreach

YES!

- Inspiration for new users
- HPC investment: Plateau reached for publications
- High Global interaction (68%)
- Advantage: Publications that made use of HPC was substantially above the world average FWCI

Acknowledgements



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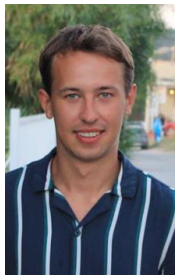
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