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Portuguese RDM Forum

Mark Hahnel, CEO  
@MarkHahnel

## Create co-occurrence networks

This notebook creates co-occurrence networks and exports them to .gexf-files, either at the start of a new book or chapter or one network for all selected books and chapters.

### User variables

```
In [22]: # which Bible passages to create co-occurrence networks for
# ~1 matches the last chapter/verse. Useful when selecting a
passages = {
    "Samuel_I": [1,1,-1,-1]
}
```

```
# what range the co-occurrence networks should have
```

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## Using social co-occurrence networks to analyze Biblical narrative

14.06.2016, 18:26 by [Frederik de Vree](#)

Results and code of MSc thesis Artificial Intelligence on VU Amsterdam, with the title "Using social co-occurrence networks to analyze Biblical narrative" by Frederik de Vree



01-Allosaur tooth rooted.stl (6.95 MB)

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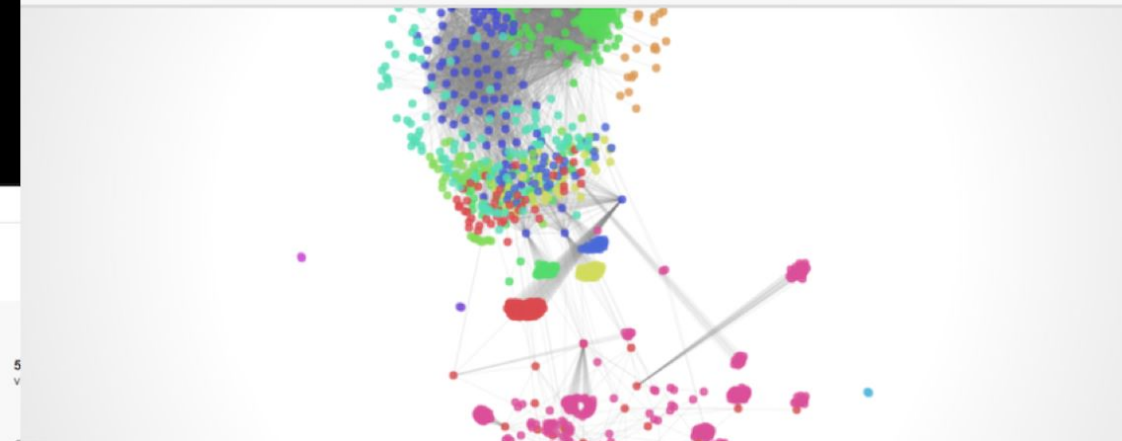
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## UWO-VPC-2013.001-Allosaur tooth rooted

21.02.2014, 21:55 by [Joseph Peterson](#)

Scanned with a Nextengine Desktop 3D Scanner and Scan Studio Pro (NextEngine) on high resolution settings. Model composed of 72,989 vertices and 145,758 faces. Saved as an \*.stl file in MeshLab (v.1.3.2).



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## Mapping the Structure of the Archaeological Web

Version 2 ▾ 29.04.2014, 17:03 by [Shawn Graham](#)

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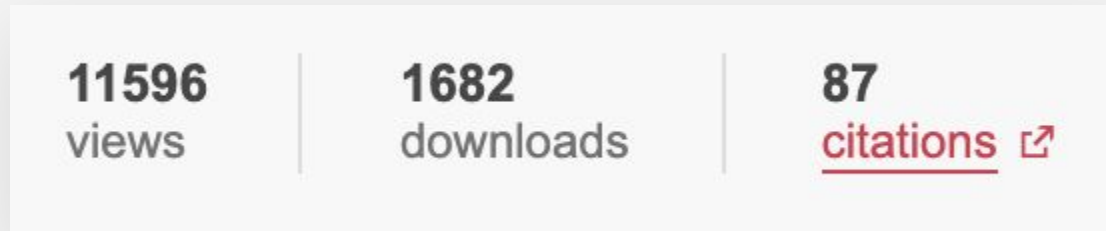
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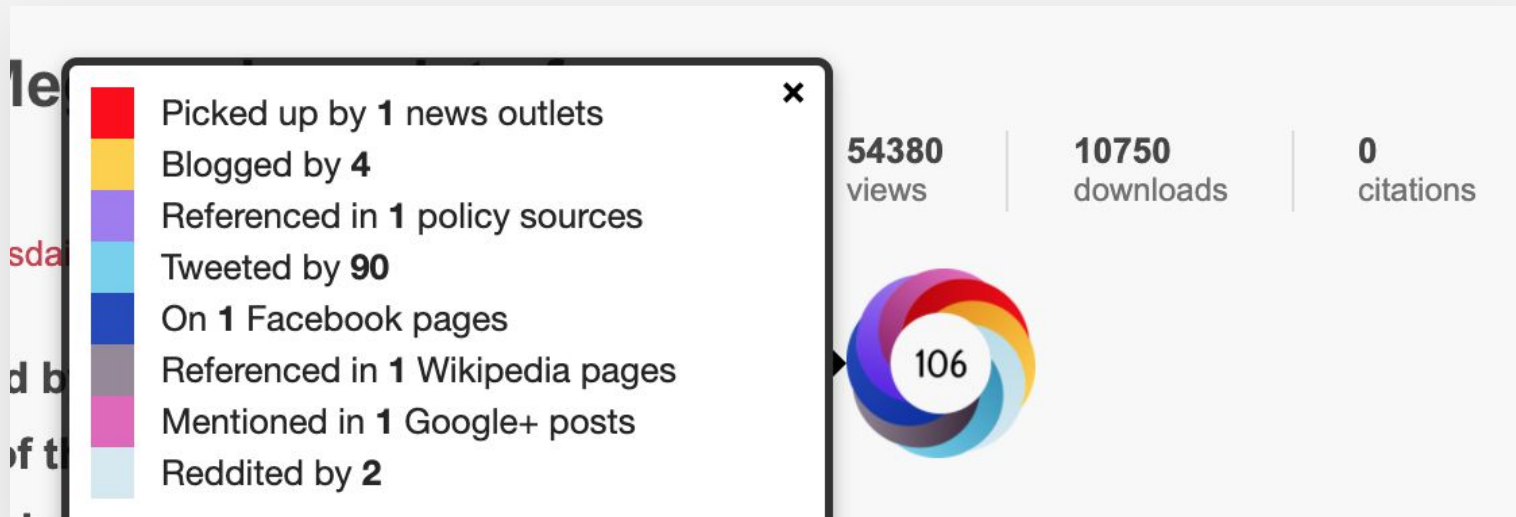
A filesset to accompany an article in a special issue of *Internet Archaeology*. In this article, I map the structure of the web to understand the context of archaeological blogging.

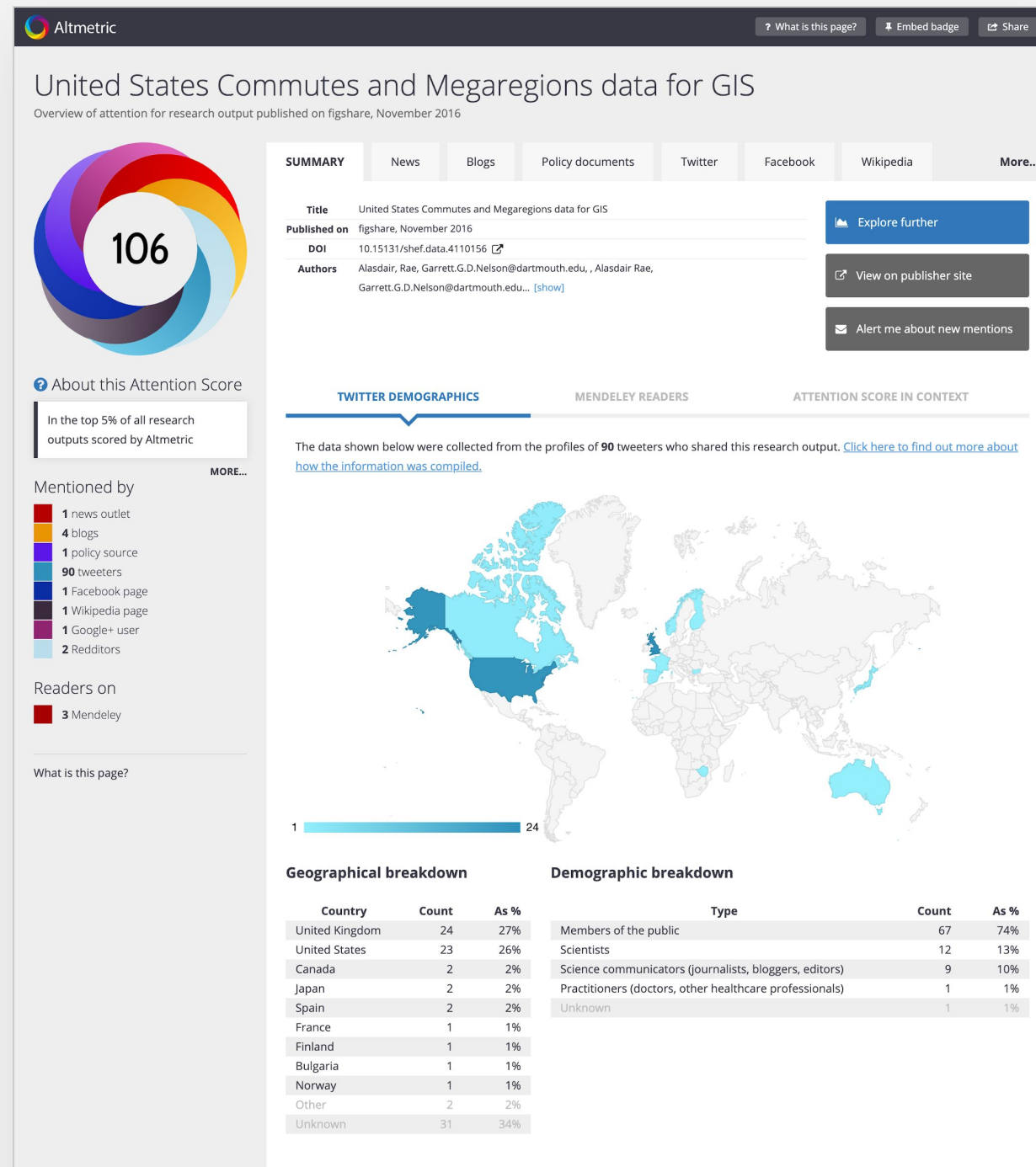
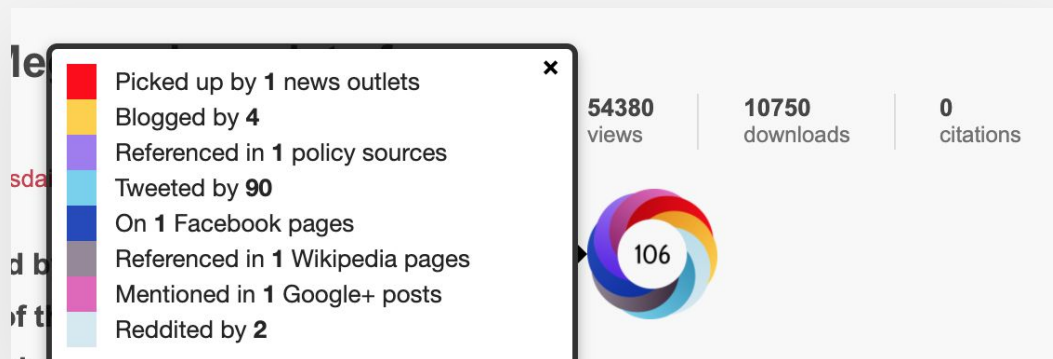


## Citations



## Altmetrics





SUMMARY

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Title

United States Commutes and Megaregions data for GIS

Published on

figshare, November 2016

DOI

10.15131/shef.data.4110156

Authors

Alasdair, Rae, Garrett.G.D.Nelson@dartmouth.edu, , Alasdair Rae, Garrett.G.D.Nelson@dartmouth.edu...[\[show\]](#)

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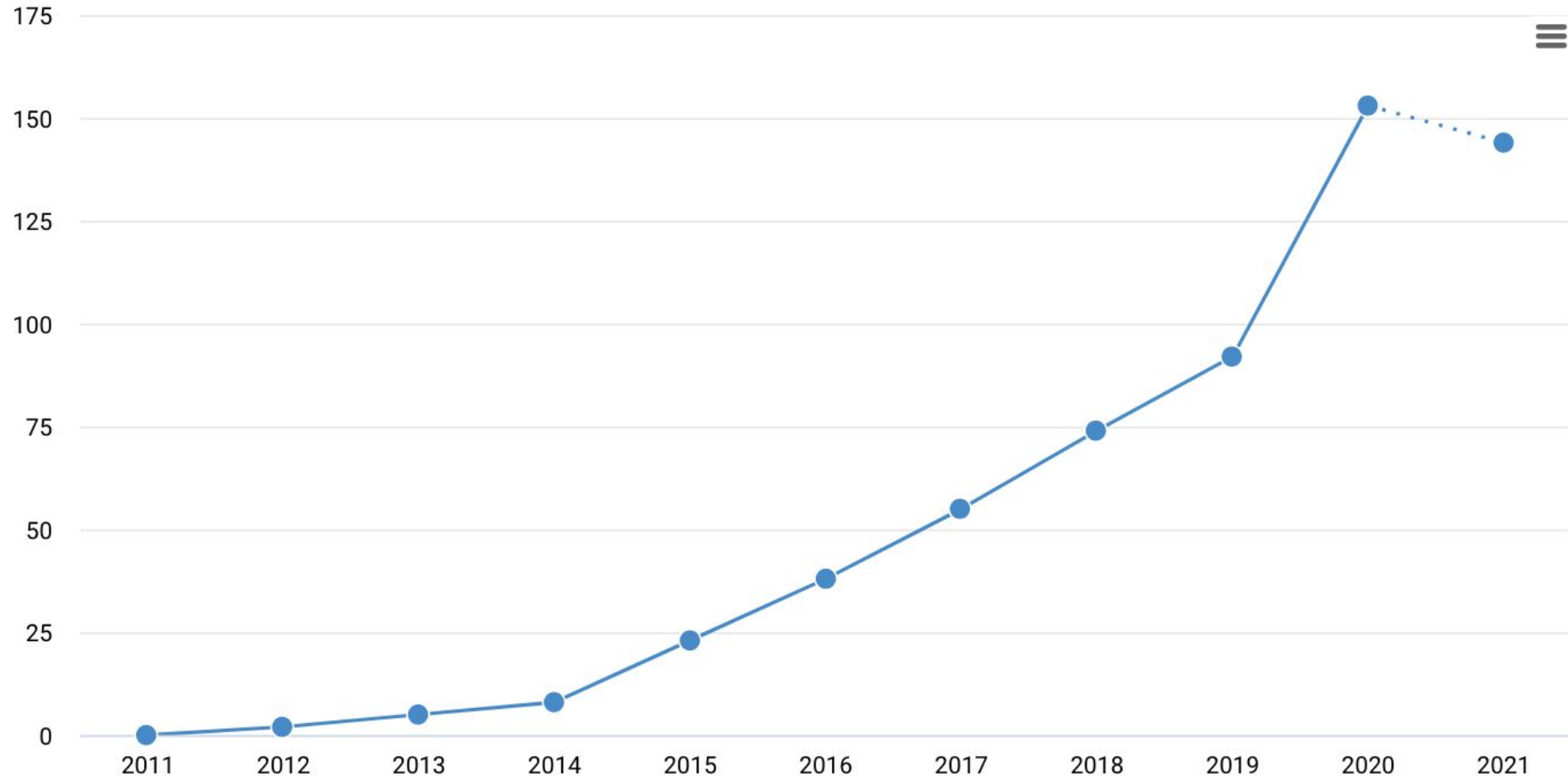
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Demographic breakdown

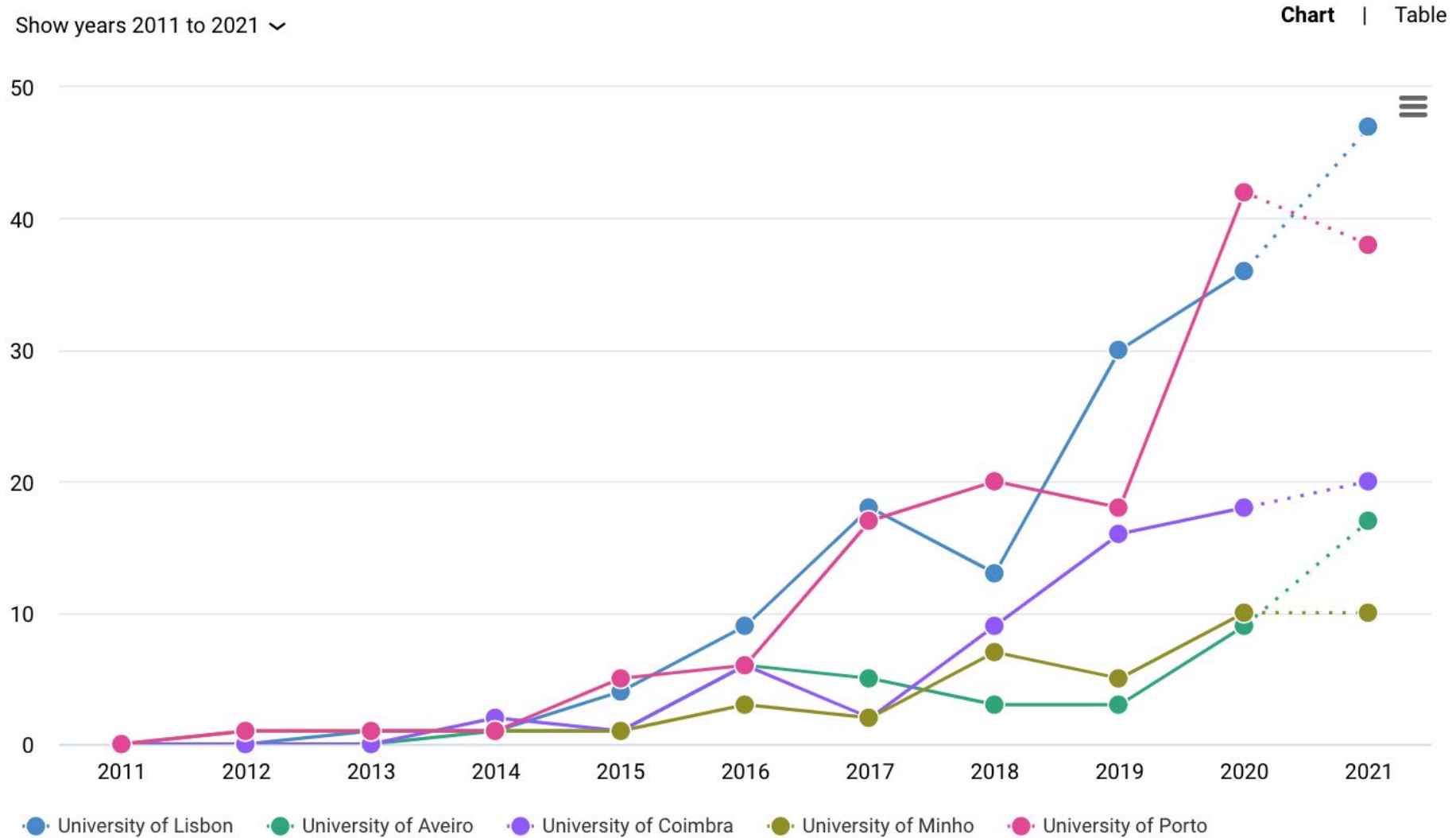
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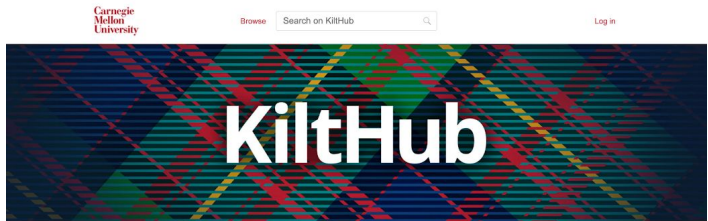
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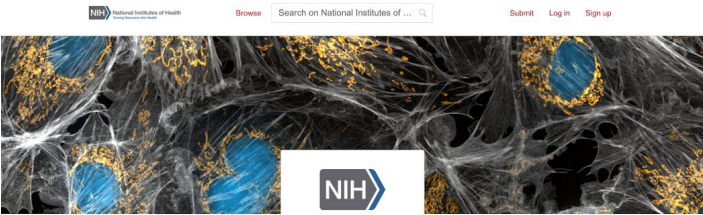


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- Additional file 2: of Simultaneous focal microbial and metabolite prof...
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- Additional file 1: Table S1 of A computational method for genotyp...
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- MOESM3 of Contemporary epidemiological overview of mal...
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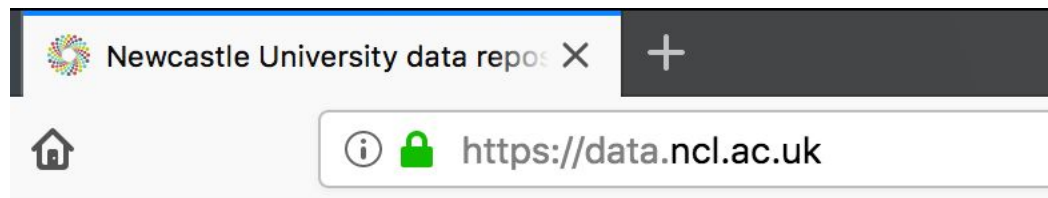
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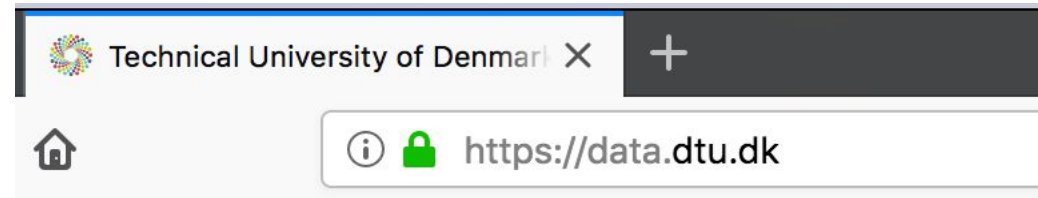
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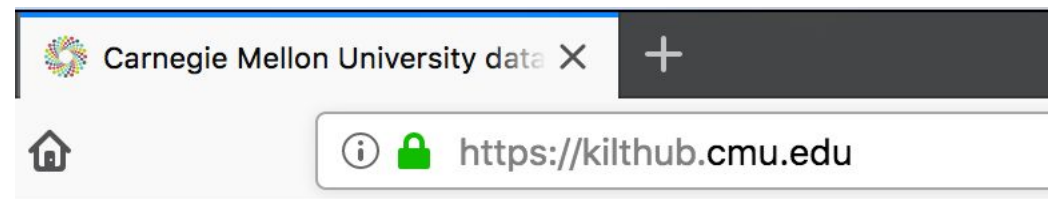
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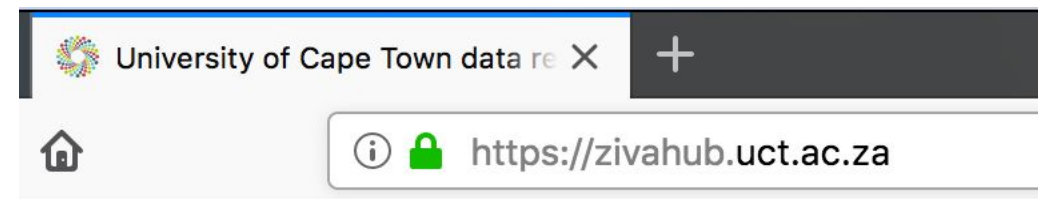
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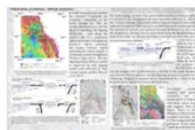
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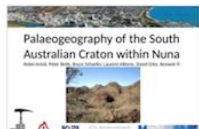
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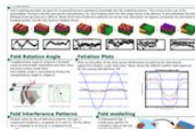
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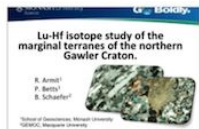
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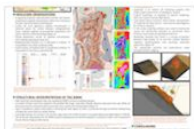
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Example 11.1: Mendu theatre audio-visual excerpts, Natuna, Ria...  
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Appendix 4: 'Biola in the Riau Islands: Reefs, Winds and Sea Cur...  
Karen Kartomi Thomas 12/03/2019



Thamsir Demonstrates Malay Drumbeats  
Geoffrey Benjamin 11/03/2019



Azmi Mahmud, 'Kemarau' (Gawai Seni)  
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Raja Ahmad Helmy, 'Sayang Bini'  
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Raja Ahmad Helmy, 'Sayang Bini' (Gawai Seni)  
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Adi Supriyadi & Ryan Saputra, 'Puanku Bulang Cahaya'  
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Example 11.2: Mendu performance excerpt, 2013  
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Example 6.2 - Bangsawan Syair, Performance 2  
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PosterBIOLAnovember18.pdf  
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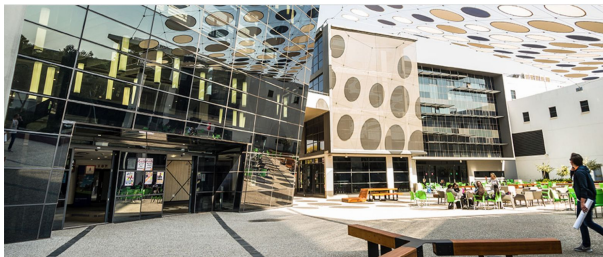



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Updated Feb 22, 2019

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Data set created Feb 22, 2019

Data set updated Feb 22, 2019

Data set published Feb 22, 2019



## FUNDING

### Visualization of Influenza Viral RNA Assembly

National Institute of Allergy and Infectious Diseases

### Visualizing Influenza Viral RNA Packaging

National Institute of Allergy and Infectious Diseases

### The Role of Pathogen-Environment Interactions in the Pandemic Potential of Influenza

National Institute of Allergy and Infectious Diseases



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### Visualization of Influenza Viral RNA Assembly

Funder: [National Institute of Allergy and Infectious Diseases \(NIAID\)](#)

Grant number: [R01AI139063](#)

#### Investigators

[SEEMA S. LAKDAWALA](#) - University of Pittsburgh  
PI

#### Research organization

[University of Pittsburgh](#), United States

#### Abstract

Influenza A viruses (IAV) pose a major public health threat through both seasonal epidemics and sporadic pandemics. The segmented nature of the viral genome promotes reassortment, a process where the genetic material between viruses is exchanged in a co-infected cell. In nature, reassortment leads to increased viral diversity and emergence of pandemic influenza viruses. For example, the 2009 influenza H1N1 (?swine flu?) pandemic virus, emerged from reassortment of two circulating swine viruses. Prediction of future pandemic influenza viruses from circulating zoonotic virus populations is difficult because very little is known about the mechanism of reassortment within a single co-infected cell. To accurately define the process of reassortment, we must first understand the dynamics of intracellular viral RNA (vRNA) assembly. Influenza vRNA replicates in the nucleus and is transported to the plasma membrane for packaging, which requires one copy of all eight segments to assemble within a single virion to produce a fully infectious virus. In this proposal, we will build upon our previous data on influenza assembly and define 1) the assembly dynamics in



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#### Details

Funding amount  
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Funding period  
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## Figshare documentation

The definite guide for figshare and the home of all user documentation.

The sources for these pages are publicly hosted on github at [figshare/user\\_documentation](#) and it's open for contributions. If you feel you can improve anything, fix a mistake, expand on a topic, feel free to open up a pull request.

We are Open API compatible, you can download the Open API Swagger specification [here](#)

### Base URL

All URLs referenced in the documentation have the following base:

```
https://api.figshare.com/v2
```

The Figshare REST API is served over HTTPS. To ensure data privacy, unencrypted HTTP is not supported.

### Authentication

Figshare supports the OAuth 2.0 Authorization Framework. See more about it in the [OAuth](#) section.

## OAuth

Since January 2016 figshare supports the [OAuth 2.0 Authorization Framework](#). If you're new to OAuth make sure you have at least a basic understanding before moving on.

## Quick guide

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SSOLogin Operational

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#### ⊖ Tasks

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featured apps

a collection of apps developed to help with various types of interactions and simplify workflows to make Figshare even easier to work with

Categories

Integrations

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Lab notebooks

Top apps

GitHub: Client for Figshare API

in Applications

This is a simple client for the Figshare API in python. Currently the following actions are implemented: create\_article, update\_article, get\_article\_details, list\_files, and get\_file\_details.

GitHub: Figshare Python Recommender

in Applications

A Python script that ingests Figshare's API data and transforms it into data suitable for loading into a recommendation engine. In our case, we save the recommendation data in Kafka but you can easily change this in ingest.py.

GitHub: Figshare Scala Apache Ignite Recommendation Engine

in Applications

A Scala/Apache Ignite collaborative-filtering based recommendation engine largely stolen from a Spark library but re-written to be a lot faster, flexible and scalable, perfect for Figshare data.

GitHub: Figshare Harvester for OpenVIVO

in Applications

The harvester supports harvesting by tag. Given a tag, the harvester gathers all the content from Figshare with the specified tag, producing RDF for each work. The Harvester uses openVIVO URI conventions for dates and people. Only identified works and identified people are included in the RDF.

GitHub: OmniAuth Strategy

in Applications

An OmniAuth Strategy for the Figshare API. You can use it to authenticate users against the Figshare API in your ruby on rails/another rack-based web application.

GitHub: iRODS

in Applications

Playground for iRODS integration.

labfolder

in Integrations, Lab notebooks

Import your Figshare items into your labfolder account using this integration, documented [here](#).

ORCID

in Integrations

With this integration, push all of your public items from Figshare to ORCID. Instructions for setting up this integration are available [here](#).

GitHub

in Integrations

Import from GitHub from your list of public repositories. Documentation on how to connect Figshare with your GitHub account is available [here](#).

ImpactStory

in Integrations

Link your Figshare and ImpactStory accounts. More information [here](#).

Open Science Framework (OSF)

in Integrations

Connect Figshare to your OSF project. More information available [here](#).

Overleaf

in Integrations

Publish your Overleaf projects directly to Figshare. Click [here](#) for more information.

RSpace

in Integrations, Lab notebooks

Integrate your RSpace Electronic Lab Notebook with your Figshare account. Follow these steps to learn how to enable the integration.

Elsevier Pure

in Integrations

A one-way push of data records from Figshare to an institutional instance of Elsevier Pure, a current research information system (CRIS). More information on this integration can be found [here](#).

Uploader for large files and associated metadata

in Applications

This application enables the bulk upload of files and associated metadata kept in an excel spreadsheet to the Figshare repository. To use the application you will need to log in to Figshare and create a personal token in the Applications section. This will ensure the files and metadata are uploaded to your own account.

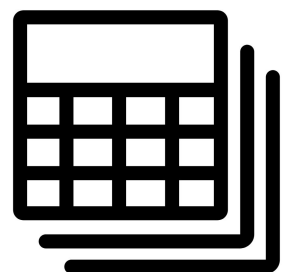
For more information, visit this [page](#) for GitHub references.

Binder

in Integrations

Enter a data or code Figshare DOI to launch a Binder project as a Binder. This will launch an interactive environment based on the content and configuration files in the project. Documentation is available [here](#) and

# The sweet spot



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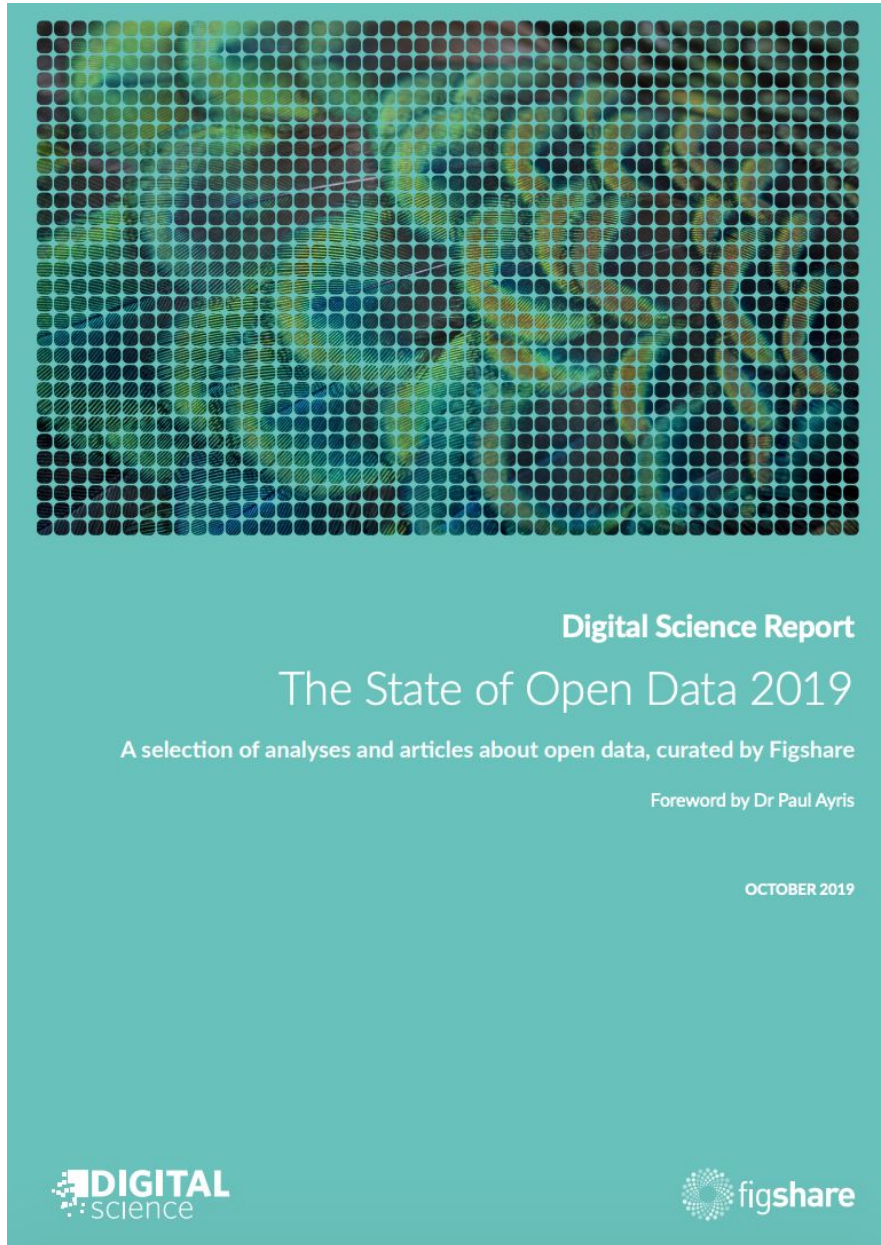
**FAIR**



**FA**







This year's survey received a record number of survey participants with around **8,500 responses** from the research community.

While most trends are encouraging around the adoption and acceptance of open data, the research community is now demanding more enforcement of the mandates that have been adopted by many governments, funders, publishers and institutions around the world.



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