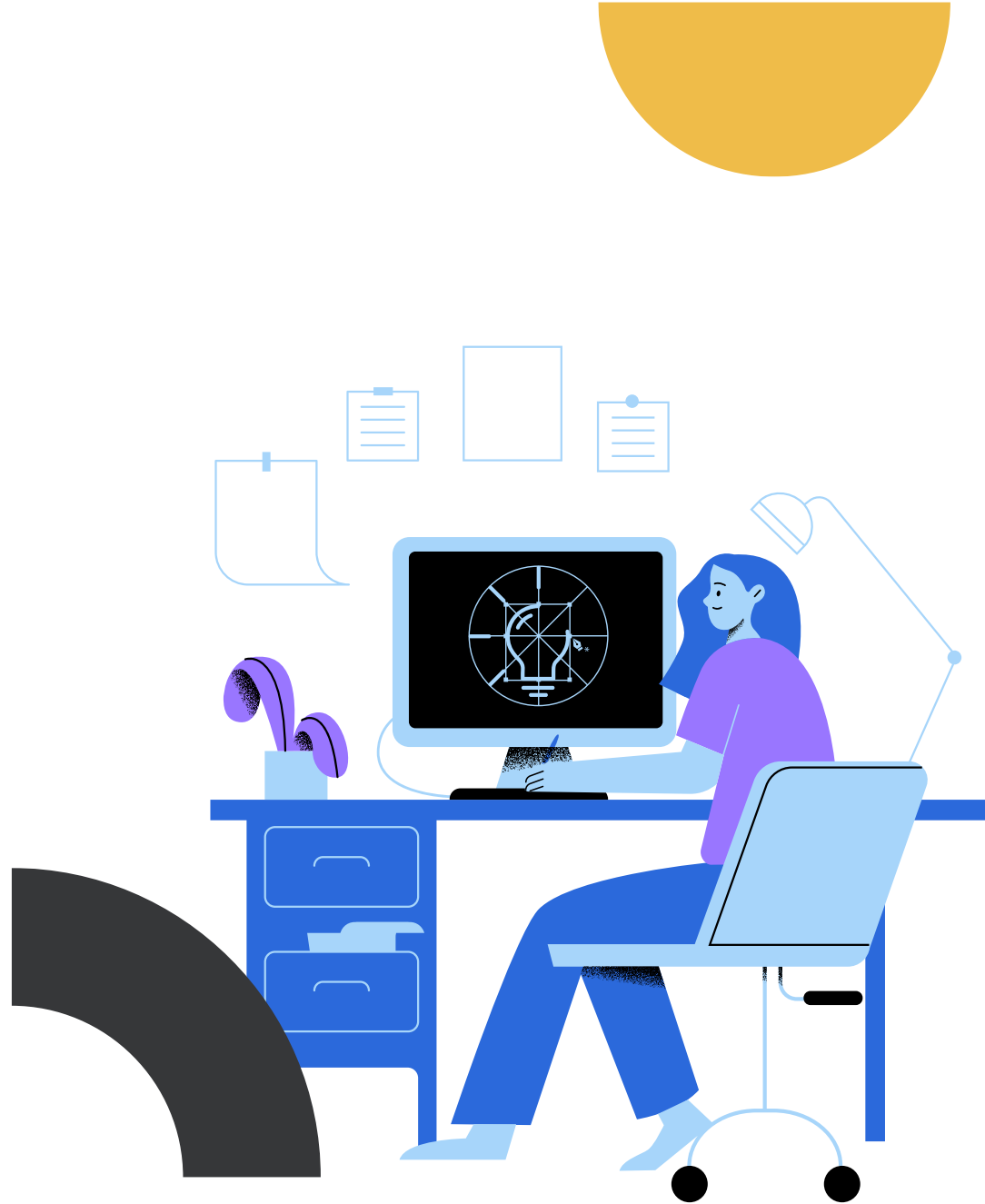




# 從研究流程出發 — 開放時代下的研究支援



徐惠玲  
iesResearch  
iGroup Taiwan



# 研究支援之一一 學術傳播大趨勢



## STM TRENDS 2026

**The Beauty of Open at Scale**  
The next 3 to 5 years will see a sharp rise of Open Access within scholarly communications. In an eco-system that is Open-at-Scale, there will be vast new opportunities for scalable tools for knowledge discovery on massively available content. In our annual STM Trends forecast we foresee a proliferation of platforms offering open access - here depicted as open sunflowers.

Each of them serving certain users:

- Bees:** Authors, Editors, Peers  
We can expect a fierce battle for authors seeking the best and the most convenient publisher platforms. Journal brands will lure them. Institutional platforms may mandate publishing via their home institutes.
- Butterflies:** a new generation of researchers  
A new, younger generation embraces new channels, attracted by preprint platforms and using social media, they go for speed and ease. They seek personal recognition and reward.
- Birds:** new audiences  
Covid and Climate Change have sparked new interest from new audiences in science and research results. They find it on discovery platforms, in social media and on piracy sites.
- Influencers:**  
Influencers and their followers are a here-to-stay phenomenon. Amidst an abundance of information flows, they guide specific target audiences to the information they like.
- Scarecrows:**  
How to secure trust and avoid fake science in this environment of information overflow. Do we need more scarecrows to warn people of untrustworthy information?
- Beehives:**  
Creators of research information seek trusted places where they can be certain of reliable processing. They seek quality, peer review, integrity, trust. They want Trusted Research.

The supportive role of STM publishers in the scholarly comms eco-system is to safeguard quality, integrity and to advance trusted research.  
Find more on [www.stm-assoc.org](http://www.stm-assoc.org)

**STM** Advancing trusted research

**THE BEAUTY of OPEN at SCALE**

**WE HAVE TOOLS THAT SCALE**  
TDR - AI - Data Analysis - New Metrics - Integrity Checks - AND MORE!

**IEEE**



# 研究支援之二 — 研究流程

## 101 INNOVATIONS IN SCHOLARLY COMMUNICATION



Jeroen Bosman @jeroenbosman  
Utrecht University Library

### THE CHANGING RESEARCH WORKFLOW



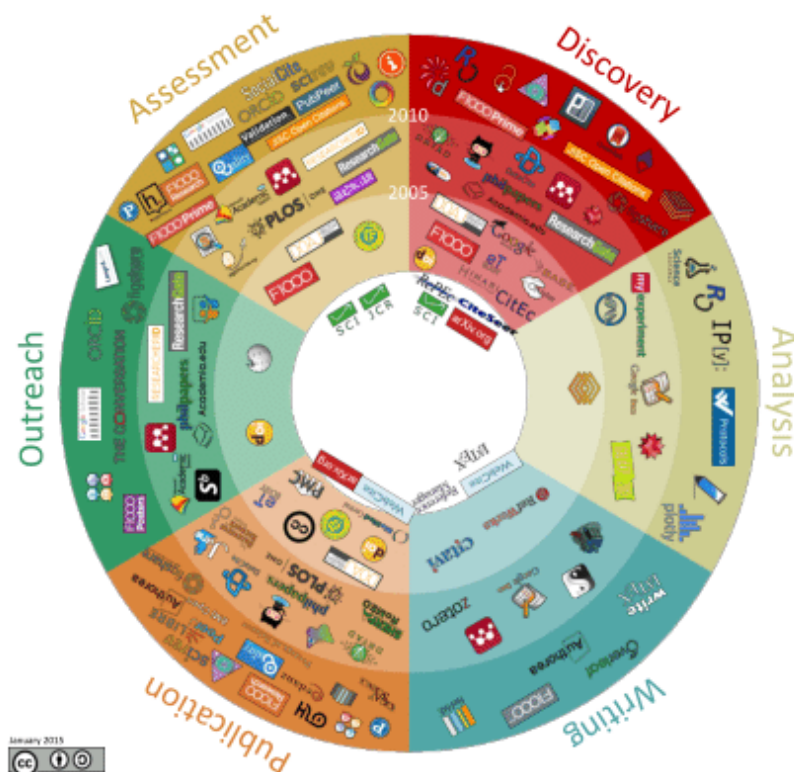
Bianca Kramer @MsPhelps  
Utrecht University Library



Science is in transition. This poster gives an impression of the exploratory phase of a project aiming to chart innovation in scholarly information and communication flows from evolutionary and network perspectives.

We intend to address the questions of what drives innovation and how these innovations change research workflows and may contribute to more open, efficient and good science.

#### 101 Innovative tools and sites in 6 research workflow phases (< 2000 - 2015)

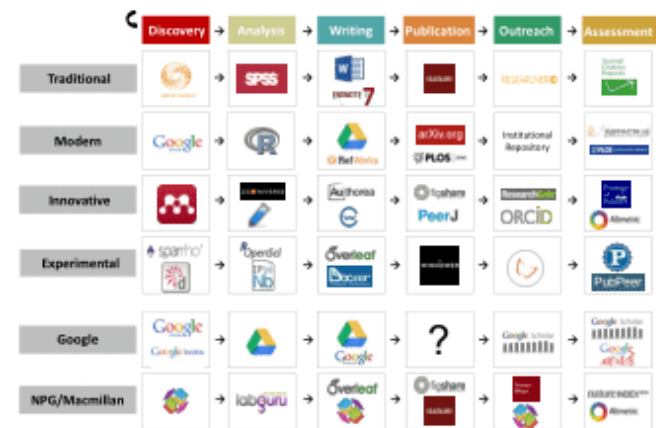


#### Most important developments in 6 research workflow phases

	Discovery	Analysis	Writing	Publication	Outreach	Assessment
<b>Trends</b>	social discovery tools	data-driven & cross-sectional science	collaborative online writing	Open Access & data publication	scholarly social media	article level (alt)metrics
<b>Expectations</b>	growing importance of data discovery	more online analysis tools	more integration with publication & assessment tools	more use of "publish first, judge later"	use of altmetrics for monitoring outreach	more open and post-publication peer review
<b>Uncertainties</b>	support for full-text search and text mining	willingness to share in analysis phase	acceptance of collaborative online writing	effect of journals/publisher status	requirements of funders & institutions	who pays for costly qualitative assessment?
<b>Opportunities</b>	discovery based on aggregated OR full-text	open libraries	semantic tagging while writing/editing	reader-side paper formatting	writing repositories for institutional visibility	using author-, publication- and affiliation IDs
<b>Challenges</b>	real semantic search forecasts & relevance	reproducibility	safety/privacy of online writing	globalisation of publishing/access standards	making outreach a low-way discussion	quality of measuring tools

<b>Most important long-term development</b>	multidisciplinary + citation-enhanced databases	collaboration + distribution	online writing platforms	Open Access	more & better connected research profiles	importance of societal relevance + non-publication contributions
<b>Potentially most disruptive development</b>	semantic/concept search + contextual/social recommendations	open science	collaborative writing + integration with publishing	circumventing traditional publishers	public access to research findings, also for agenda setting	moving away from simple quantitative indicators

#### Typical workflow examples



# 研究支援之二 — 研究流程

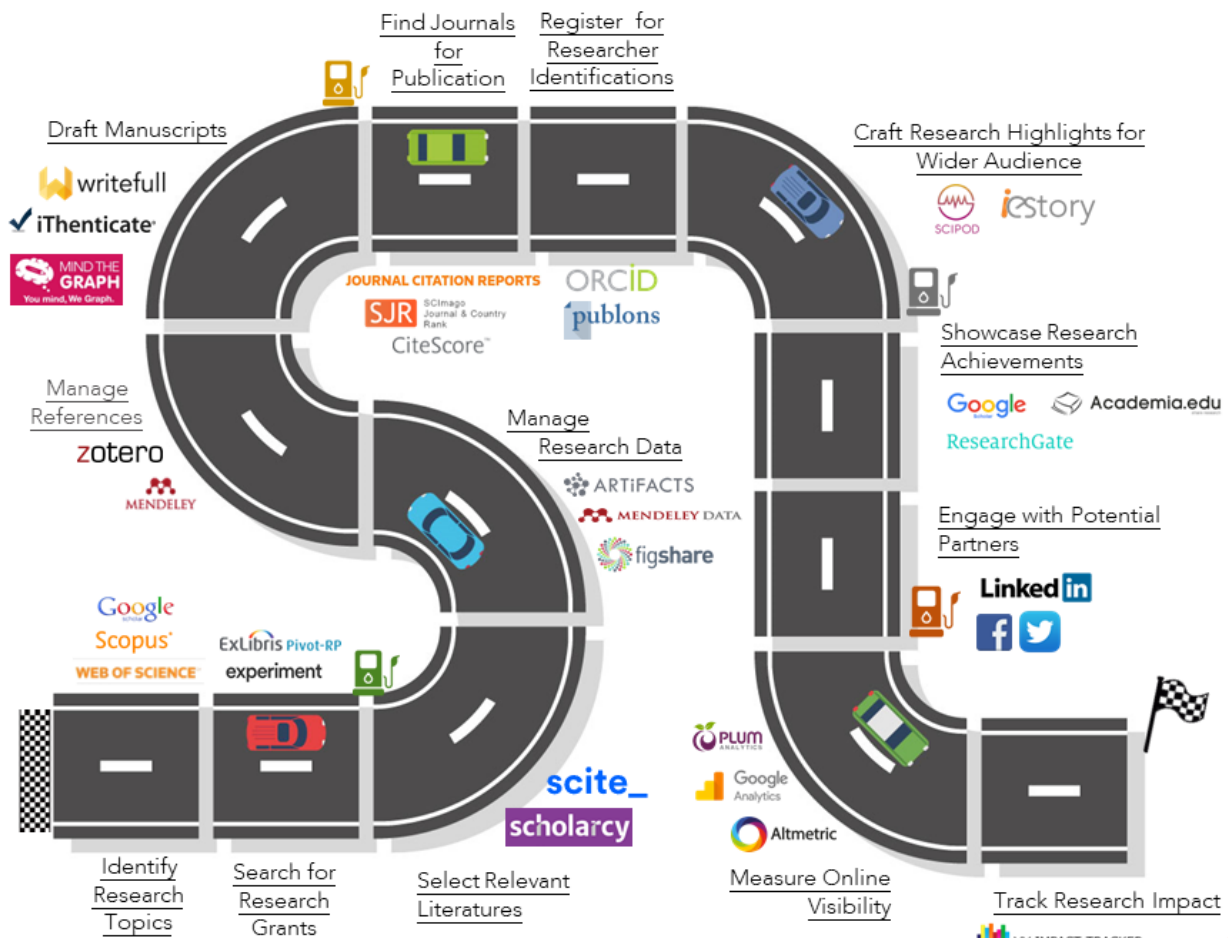


## Accelerate Your Research Journey

With so many tools out there, how do you know when to use what tools in order to improve your research efficiency?

Let's take a tour on the road of research journey, and power you up with the right tools!

Your Journey Begins Here!



Where fund raising might be needed

# 研究支援地圖 – 以研究流程分析支援能量 你開了多少？

## DISCOVERY

### Discovery Tools & Contents

#### Citation Index Database

- Dimensions
- Web of Science
- Scopus

Directional Discovery

### Search

- Science Direct
- ProQuest

### Journals

- IEEE
- Emerald
- Springer Nature
- JSTOR

Specific Discovery

### Other Contents

### Recommended OA (including in-house)

## AUTHORING & PUBLISHING

### Reviewing Tools

### Editing Tools

- iThenticate

### Reference Management Tools

- Endnote
- Mendeley

### Journal Selection Guides

- JCR
- CiteScore

## ASSESSMENT & ENGAGEMENT

### Platforms

- IR
- CRIS

### Engagement & Impact Quantification

### Evaluation Tools

- Web of Science
- Scopus
- Altmetrics

# 研究支援地圖 – 以研究流程分析支援能量

## 以 Open Access 服務自動升級

### DISCOVERY

#### Discovery Tools & Contents

##### Citation Index Database

- Dimensions
- Web of Science
- Scopus
- Google Scholar

Directional Discovery

#### Search

- Science Direct
- ProQuest

#### Journals

- IEEE
- Emerald
- Springer Nature
- JSTOR

Specific Discovery

#### Other Contents

#### Recommended OA (including in-house)

- DOAJ

### AUTHORING & PUBLISHING

#### Reviewing Tools

#### Editing Tools

- iThenticate

#### Reference Management Tools

- Endnote
- Mendeley
- CiteReady
- Zotero

#### Journal Selection Guides

- JCR
- CiteScore
- Scimago
- DOAJ
- RetractionWatch

### ASSESSMENT & ENGAGEMENT

#### Platforms

- IR
- CRIS
- ORCID
- ResearchGate

#### Engagement & Impact Quantification

#### Evaluation Tools

- Web of Science
- Scopus
- Altmetrics
- Google Scholar

# 研究支援地圖 – 以研究流程分析支援能量

## 引進工具, 加速支援力道

### DISCOVERY

#### Discovery Tools & Contents

##### Citation Index Database

- Dimensions
- Web of Science
- Scopus
- Google Scholar

Directional Discovery

#### Search

- Science Direct
- ProQuest

#### Journals

- IEEE
- Emerald
- Springer Nature
- JSTOR

Specific Discovery

#### Other Contents

#### Recommended OA (including in-house)

- DOAJ

### AUTHORING & PUBLISHING

#### Reviewing Tools

- Scholarcy
- Scite

#### Editing Tools

- iThenticate
- WriteFull
- MindTheGraph

#### Reference Management Tools

- Endnote
- Mendeley
- CiteReady
- Zotero

#### Journal Selection Guides

- JCR
- CiteScore
- Scimago
- DOAJ
- RetractionWatch

### ASSESSMENT & ENGAGEMENT

#### Platforms

- IR
- CRIS
- ORCID
- ResearchGate

#### Engagement & Impact Quantification

- ChronosHub
- Impact Tracker
- ieSTORY

#### Evaluation Tools

- Web of Science
- Scopus
- Altmetrics
- Google Scholar



# A.I. 技術已成為學術傳播中的重要一環



Multi-disciplinary  
Discovery

A.I. accelerate the process of recognizing the relationship between contents, across disciplines

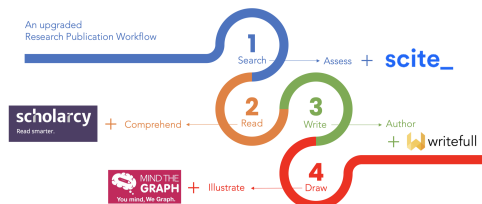
Plagiarism  
& Data  
Fabrication

A.I. processes a large volume of text and data to look for the similarity or the "unusual patterns"

Content  
Review &  
Checking

A.I. resolves the semantic complexity at high speed for researchers to better understand the contents, for publishers to fasten the speed of peer review

# 以 A.I. 支援研究流程



## Accelerate Your Research Journey

With so many tools out there, how do you know when to use what tools in order to improve your research efficiency?

Let's take a tour on the road of research journey, and power you up with the right tools!

Your Journey Begins Here!



Where fund raising might be needed

# 以 A.I. 支援研究流程

An upgraded  
Research Publication Workflow



+ Comprehend



+ Illustrate

**1**  
Search

Assess

+ **scite\_**

**2**  
Read

**3**  
Write

Author

+ **writefull**

**4**  
Draw

Accelerate Your  
Research  
Journey

With so many tools out there, how do you know when to use what tools in order to improve your research efficiency?  
Let's take a tour on the road of research journey, and power you up with the right tools!



Where fundraising might be needed

# A.I. 支援研究流程 - 工具實例

scite\_

SEARCH: Literature Discovery  
ASSESS: Literature Review

## Lysyl Oxidase Is Essential for Hypoxia-Induced Metastasis [🔗](#)

Janine T. Erler<sup>1</sup>, Kevin L. Bennewith<sup>2</sup>, Monica Nicolau<sup>3</sup>, Nadja Dornhöfer<sup>4</sup>, Christina S. Kong<sup>5</sup>, Quynh-Thu Le<sup>6</sup>, Jen-Tsan Ashley Chi<sup>7</sup>, Stefanie S. Jeffrey<sup>8</sup>, Amato J. Giaccia<sup>9</sup>

**Abstract:** Metastasis is a multistep process responsible for most cancer deaths, and it can be influenced by both the immediate microenvironment (cell-cell or cell-matrix interactions) and the extended tumour microenvironment (for example vascularization). Hypoxia (low oxygen) is clinically associated with metastasis and poor patient outcome, although the underlying processes remain unclear. Microarray studies have shown the expression of lysyl oxidase (LOX) to be elevated in hypoxic human tumour cells. Paradoxically, LOX...

Expand abstract [▼](#)  
Editorial notices [▼](#)

Search citation statements

Context, author(s), titl... 🔍

Order By: Relevance [▼](#)

Paper Sections [🕒](#)

<input checked="" type="checkbox"/>	Intro	208
<input checked="" type="checkbox"/>	Methods	26
<input checked="" type="checkbox"/>	Results	93
<input checked="" type="checkbox"/>	Discussion	292
<input checked="" type="checkbox"/>	Other sections	498

Citation Types [🕒](#)

<input checked="" type="checkbox"/>	Supporting	<input checked="" type="checkbox"/>	46
<input checked="" type="checkbox"/>	Mentioning	<input checked="" type="checkbox"/>	1,131
<input checked="" type="checkbox"/>	Contrasting	<input type="checkbox"/>	10
<input checked="" type="checkbox"/>	Unclassified	<input type="checkbox"/>	17

Year Published

**Cited by 1,136 publications** (1,204 citation statements)

**References 27 publications**

**Paper Section:** Results

"...Treatment of established tumors with  $\beta$ APN (100 mg/kg/BW ip qd) reduced significant collagen cross-linking in the tumor ECM (Supplementary Figure S2). In contrast to previous studies that reported a solid reduction of growth in various tumor models [ 22 - 25 ], treatment with  $\beta$ APN reduced tumor growth only in the 4T1 model, while three models (MT6, EMT6, and E0771) did not respond with a change in growth rate and growth of LLC tumors was even strongly increased (Fig. 3a )...."

[🔍](#) contrasting (Confidence: 99%) [flag classification](#)

**Paper Section:** Discussion

"...Previous studies have reported a solid and consistent anti-tumor effect of LOX(L) inhibition in a variety of different tumor models [ 23 - 25 ]. Baker et al have demonstrated that the proliferative effect of lysyl oxidases is caused by increased tissue stiffness and subsequently enhanced FAK signaling [ 28 ]..."

[🔍](#) mentioning (Confidence: 90%) [flag classification](#)

**LOX-catalyzed Collagen Stabilization Is a Proximal Cause for Intrinsic Resistance to Chemotherapy**

Rossow, Veitl, Vorlová et al, 2018  
*Oncogene*

[📄](#) 33 [👍](#) 0 [👎](#) 38 [🔍](#) 0

[View full text](#) [Add to dashboard](#)

**Paper Section:** Discussion

"...Opposite to all other survival analyses, this effect was predominately due to ER positive cases, with only a weak trend in ER negative patients. In contrast to a previous report, LOX expression was not significantly associated with the overall survival, which may, at least in part, be due to the smaller number of patients in the present study [ 3 ]. The prognostic power of LOX expression was more pronounced with respect to metastasis-free survival than overall survival also in that previous study [ 3 ]..."

[🔍](#) contrasting (Confidence: 99%) [flag classification](#)

**Paper Section:** Discussion

"...In contrast to a previous report, LOX expression was not significantly associated with the overall survival, which may, at least in part, be due to the smaller number of patients in the present study [ 3 ]. The prognostic power of LOX expression was more pronounced with respect to metastasis-free survival than overall survival also in that previous study [ 3 ]. Finally, in multivariable Cox proportional hazards regression analyses of the DFS and MFS of the variables LOX expression, G473A genotype and ER status, LOX expression was a potent independent prognostic parameter (Table S3 and S4; see below)..."

# 研究支援 – DISCOVERY & ACCESS

*Citation Analysis by Scite*

Find if research has been supported or contrasted

Find appropriate references and data when writing papers

Find highly supported researchers

Find Key Opinion Leaders

The screenshot shows a web browser displaying an eLife research article. The article title is "Chromosome mis-segregation and cytokinesis failure in trisomic human cells". The authors listed are Joshua M Nicholson, Joana C Macedo, Aaron J Mattingly, Darawalee Wangsa, Jordi Camps, Vera Lima, Ana M Gomes, Sofia Dória, and Thomas Ried. The article is dated May 5, 2015. A video player is overlaid on the bottom left, showing a video titled "Abstract" with a duration of 0:00. The video player includes a play button, a progress bar, and a volume icon. The article content is partially visible, showing the beginning of the abstract: "Cancer cells display aneuploid karyotypes and typically mis-segregate...". On the right side of the article, there are options to "Download", "Cite", and "Comment". Below these options, there are social media sharing icons for Twitter, Facebook, LinkedIn, and YouTube. The article has 11,726 views and 65 citations. A "scite\_" widget is visible on the right, showing 74 items, 4 supported, 73 contrasted, and 0 unknown. The browser's address bar shows the URL "elifesciences.org/articles/05068".

Watch the video online [here](#)

# A.I. 支援研究流程 - 工具實例

scite\_

圖書館可利用 scite badge 提升 IR 文獻能見度


The screenshot shows a DSpace repository page for a research article. The header includes the Hacettepe University logo and 'HACETTEPE ÜNİVERSİTESİ Açık Erişim Sistemi'. The article title is 'Voomdda: Discovery Of Diagnostic Biomarkers And Classification Of Rna-Seq Data'. The abstract discusses RNA-Seq technology and the development of voomDDA classifiers. The author list includes Zararsiz, Gokmen, Goksuluk, Dincer, Klaus, Bernd, Korkmaz, Selcuk, Eldem, Vahap, Karabulut, Erdem, and Ozturk, Ahmet. The page also features a Scite badge showing 13 publications, 0 supporting, 10 mentioning, and 0 contrasting. A blue arrow points to the 'Mentioning' count. On the right, there is a 'Validated' badge by OpenAIRE and a contact form for 'Çevrimiçi Danışma'.

HACETTEPE ÜNİVERSİTESİ  
Açık Erişim Sistemi

English Login

DSpace Home Tıp Fakültesi Temel Tıp Bilimleri Bölümü Temel Tıp Bilimleri Bölümü Makale Koleksiyonu View Item

### Voomdda: Discovery Of Diagnostic Biomarkers And Classification Of Rna-Seq Data




View/Open

- licence.txt (265bytes)
- 6385.pdf (2.951Mb)

Date  
2017

Author  
Zararsiz, Gokmen  
Goksuluk, Dincer  
Klaus, Bernd  
Korkmaz, Selcuk  
Eldem, Vahap  
Karabulut, Erdem  
Ozturk, Ahmet



scite\_

Publications	13
Supporting	0
Mentioning	10
Contrasting	0

RNA-Seq is a recent and efficient technique that uses the capabilities of next-generation sequencing technology for characterizing and quantifying transcriptomes. One important task using gene-expression data is to identify a small subset of genes that can be used to build diagnostic classifiers particularly for cancer diseases. Microarray based classifiers are not directly applicable to RNA-Seq data due to its discrete nature. Overdispersion is another problem that requires careful modeling of mean and variance relationship of the RNA-Seq data. In this study, we present voomDDA classifiers: variance modeling at the observational level (voom) extensions of the nearest shrunken centroids (NSC) and the diagonal discriminant classifiers. VoomNSC is one of these classifiers and brings voom and NSC approaches together for the purpose of gene-expression based classification. For this purpose, we propose weighted statistics and put these weighted statistics into the NSC algorithm. The VoomNSC is a sparse classifier that models the mean-variance relationship using the voom method and incorporates voom's precision weights into the NSC classifier via weighted statistics. A comprehensive simulation study was designed and four real datasets are used for performance assessment. The overall results indicate that voomNSC performs as the sparsest classifier. It also provides the most accurate results together with power-transformed Poisson linear discriminant analysis, rlog transformed support vector machines and random forests algorithms. In addition to prediction purposes, the voomNSC classifier can be used to identify the potential diagnostic biomarkers for a condition of interest. Through this work, statistical learning methods proposed for microarrays can be reused for RNA-Seq data. An interactive web application is freely available at <http://www.biosoft.hacettepe.edu.tr/voomDDA/>.

URI  
<https://doi.org/10.7717/peerj.3890>  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5633036/>  
<http://hdl.handle.net/11655/16413>

xmlui.mirage2.itemSummaryView.Collections  
Temel Tıp Bilimleri Bölümü Makale Koleksiyonu [459]

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by OpenAIRE

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Çevrimiçi Danışma

Şu anda online operatör yok, lütfen mesaj bırakın

İsim\* E-posta\*

Adınızı girin E-postanızı gir

Sorunuz\*

Mesajınızı girin

Mesaj bırak

# A.I. 支援研究流程 - 工具實例

scholarcy

READ: Literature Review  
WRITE: Manuscript Writing  
PROMOTE: Research Outreach

## Key concepts

culturomics rdna sequencing rRNA B. timonensis massiliensis C. saudii culturomics study MALDI-TOF laser  
Assistance Publique des Hôpitaux de Marseille P. massiliensis spectrometry desorption ionization Institut de Recherche po  
Institut Hospitalo-Universitaire microorganisms carbapenemase-producing Enterobacteriaceae maldi tof mass spectrometry  
commensal bacteria flight mass spectrometry microbiology bacterial species rDNA infectious disease C. difficile  
Anaerosalibacter massiliensis bacterial repertoire new bacterial species clinical microbiology bacteria ionization time  
Pseudomonas massiliensis P. grossensis

## Abstract

Culturomics has permitted discovery of hundreds of new bacterial species isolated from the human microbiome. Profiles generated by desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry have been added to the mass spectrometer database used in clinical microbiology. We retrospectively collected raw data from MALDI-TOF mass spectrometry used routinely in our laboratory in Marseille, France, during the study period and analyzed 16S rDNA sequencing results from misidentified strains. During the study period, 744 species were identified from clinical specimens that were species first isolated from culturomics. This collection involved 105 clinical specimens, accounting for 98 patients. In 64 cases, isolates were considered clinically relevant. MALDI-TOF mass spectrometry was able to identify the species in 95.2% of the 105 specimens. While only a subset of the bacterial repertoire associated with humans, culturomics studies also enlarge the spectrum of prokaryotes involved in infectious diseases.

## Scholarcy highlights

- Culturomics has permitted discovery of hundreds of new bacterial species isolated from the human microbiome
- The creation of new spectra enabled us to increment our MALDI-TOF mass spectrometry database used for clinical microbiology of bacterial species first isolated as a part of culturomics studies and improving the accuracy of diagnosis of infectious diseases
- We identified 744 unique bacterial species correctly using MALDI-TOF mass spectrometry
- Routine Identification of Species Isolated as Part of Culturomics Studies Among the 351,937 bacterial identifications performed during the study period, we identified species first isolated from culturomics studies in 105 clinical specimens, accounting for 98 patients
- This work constitutes the proof of concept that exploration of the repertoire of commensal bacteria enables identification of bacterial species in clinical microbiology
- Identification of 9 strains using 16S rDNA sequencing, accounting for 5 species, confirmed the initial recognition by MALDI-TOF (Table 2). These results strengthen our belief that identifying commensal microbes provides a valuable contribution to clinical microbiology by the decrease in the number of unidentified colonies by MALDI-TOF mass spectrometry over time (Figure)

# 研究支援 – READ, WRITE, PROMOTE

*Structured text extraction by Scholarcy*



Identifies and explains key concepts



Highlights most important points



Creates a cited summary



Finds and links to all cited sources



Extracts figures, tables & references

From Culturomics to Clinical Microbiology and Forward

Notes

Export 1

DOC

10.3201/eid2409.170995 (10 citations)

Exploration of the repertoire of commensal bacteria enables identification of

Tweet

massiliensis C. saudii culturomics study MALDI-TOF laser desorption clostridium

spectrometry desorption ionization Institut de Recherche pour le Développement

Institut Hospitalo-Universitaire microorganisms carbapenemase-producing Enterobacteriaceae maldi tof mass spectrometry gene sequencing

ry bacterial species rDNA infectious disease C. difficile Bacteroides timonensis

bacterial species clinical microbiology bacteria ionization time clinical specimen

Abstract

terial species isolated from the human microbiome. Profiles generated by using matrix-assisted laser  
ometry have been added to the mass spectrometer database used in clinical microbiology laboratories  
spectrometry used routinely in our laboratory in Marseille, France, during January 2012–March 2018  
strains. During the study period, 744 species were identified from clinical specimens, of which 21  
olved 105 clinical specimens, accounting for 98 patients. In 64 cases, isolation of the bacteria was  
considered clinically relevant. MALDI-TOF mass spectrometry was able to identify the species in 95.2% of the 105 specimens. While contributing to the extension  
of the bacterial repertoire associated with humans, culturomics studies also enlarge the spectrum of prokaryotes involved in infectious diseases.

Scholarcy highlights



# A.I. 支援研究流程 - 工具實例



A screenshot of the Microsoft Word interface with the Writefull AI proofreading tool integrated into the right-hand sidebar. The document title is "Fire Effects on Forest Composition: A Case Study of California". The sidebar shows a list of 16 remaining issues, with two examples highlighted. The first example shows the sentence "Forest sampling was carried out in central California, which has seen a great quantity of wildfires over the last years." with "great quantity" and "over the last years" highlighted in black. The second example shows "Forest sampling was carried out in central California, which has seen a large number of wildfires in recent years." with "large number" highlighted in yellow. Below each example are "ACCEPT" and "DISMISS" buttons. The bottom status bar of Word shows "第 1 頁, 共 1 頁 377 個字 英文(美國) 協助工具: 一切準備就緒" and a zoom level of 80%.

WRITE: Manuscript Proofreading

# 研究支援 – WRITE

*Manuscript Proofreading by Writefull*

Proofreading the manuscript

Academic writing guidance

One-click language checks



Automate your scientific writing.

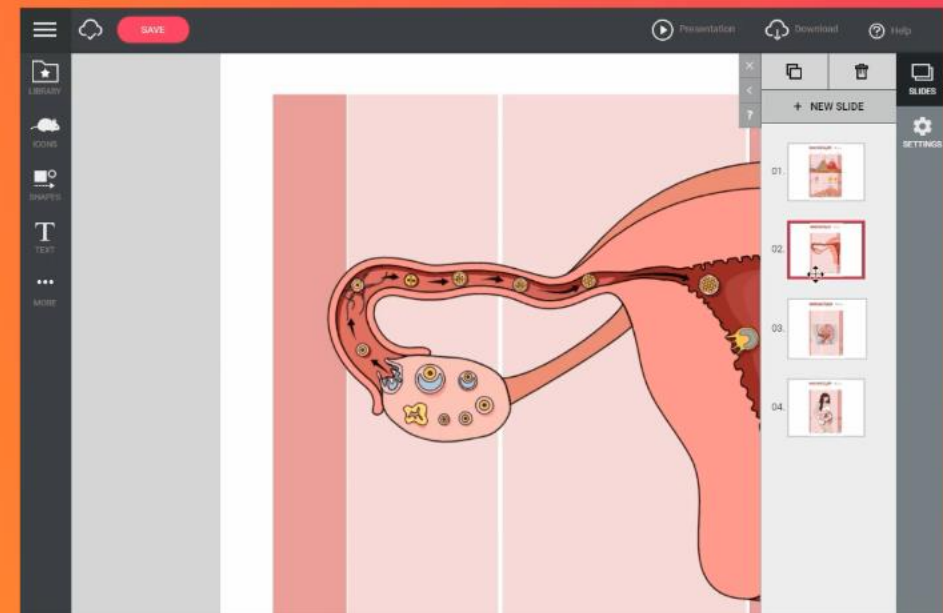
Watch the video online [here](#)

## A.I. 支援研究流程 - 工具實例



WRITE: Graphical Abstract  
PROMOTE: Research Outreach

# A free infographic maker for medical doctors and scientists.



# 研究支援 – DRAW and PROMOTE

## Graphical Abstract and Poster Preparation by MindtheGraph

### Pathophysiology, prognosis, and treatment of tardive dyskinesia

#### Context

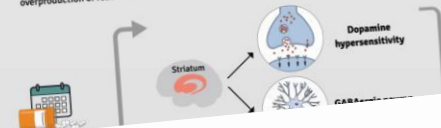
Knowledge of tardive dyskinesia (TD) may be lacking among physicians in Japan.

Accurate and timely diagnosis is challenging.

Effective treatment options are limited.

#### Pathophysiology

The pathophysiology of drug-induced TD is not fully understood. It has been suggested that dopamine hypersensitivity, dysfunction of gamma-aminobutyric acid (GABA)-ergic neurons in the striatum, and overproduction of reactive oxygen species may all contribute.



#### Complications and prognosis

-Patients with TD have a poorer prognosis and higher risk of mortality compared with patients without TD. Severe TD may be life-threatening.

-TD can profoundly affect a patient's ability to care for themselves and perform activities necessary for daily living.

-Patients may have difficulty maintaining employment and socialising.



#### Conclusions

Prevention should be prioritised, and the development of effective treatment options is essential.

### Predicting outcomes with machine learning: a study of patients with castration-resistant prostate cancer

March 2021

#### Study summary

Machine learning is a powerful tool that can help predict clinical outcomes in a range of diseases. This study used machine learning to identify factors that could predict clinical outcomes in patients with castration-resistant prostate cancer being treated with cabazitaxel.

Better outcomes were associated with neutropenia and treatment duration.

#### Why was this study conducted?

A wide range of factors can contribute to outcomes of an illness or treatment. Identifying these factors, termed prognostic factors, can improve our understanding of a disease, and can contribute to the optimization of treatment strategies for an individual patient.

While statistical modelling is commonly used to identify prognostic factors, machine learning algorithms may lead to better identification of prognostic factors through increased flexibility and enhanced performance.

Previous studies have identified several factors that may predict clinical outcomes in patients with CRPC, including neutropenia. Higher doses of taxane, such as cabazitaxel, have been shown to improve survival, but may also lead to more cases of neutropenia. It is therefore unclear whether the dose of cabazitaxel or the development of neutropenia is the key to predicting survival.

#### What was the aim of the study?

The aim of this study was to use machine learning to identify the key factors that may predict clinical outcomes in patients with CRPC being treated with cabazitaxel.

#### How was the study conducted?

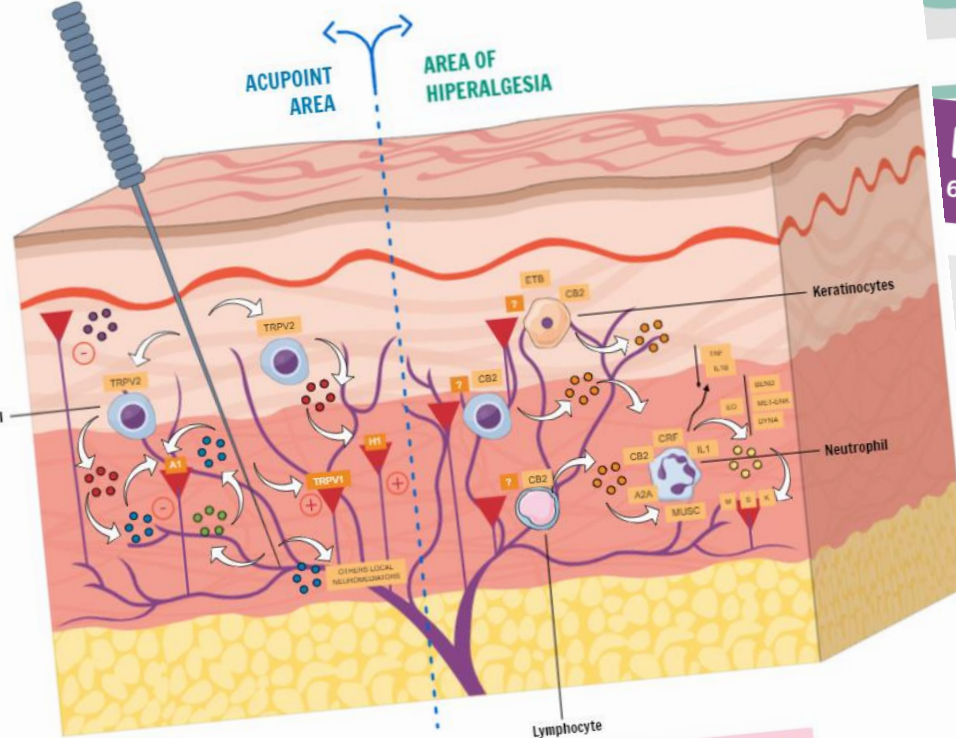
This study used machine learning to analyze data from a previously published study of 660 adult male patients with CRPC who were previously treated with docetaxel. Two types of analyses, graphical Markov model-based simulations and network clustering in 'R' packages, were conducted to identify relationships between the following potential patient factors and clinical outcomes:

- Patient factors: These included patient demographics, clinical features at baseline, performance status (which describes a patient's level of functioning), treatment histories, and side effects.
- Clinical outcomes: These included overall survival, the time-to-treatment failure, and the time to next treatment (which describes a patient's level of functioning).

#### Q&A

**What is castration-resistant prostate cancer?**  
The disease is characterized by a lower level of testosterone, which occurs in castration-resistant prostate cancer. The disease responds to treatment.

**What is a Mast cell?**  
Mast cells are a type of white blood cell that is involved in allergic reactions and tissue repair. They release histamine and other chemicals that cause inflammation.



### Effects of Lifestyle on Cognition

#### 6-Month Lifestyle Coaching Intervention on Cognition on Older Adults

6 months healthy lifestyle coaching intervention

to improve their brain health

#### Average Changes in Cognition After 6 Months of Lifestyle Psychoeducation

Spatial Planning	99.5
Verbal Reasoning	109.8
Episodic Memory	96.5
Attention	105.7
	100.8
	102.8
	103.3
	102.2

#### Exercise

#### Lifestyle/ Nutrition

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## Accelerate Your Research Journey

With so many tools out there, how do you know when to use what tools in order to improve your research efficiency?

Let's take a tour on the road of research journey, and power you up with the right tools!



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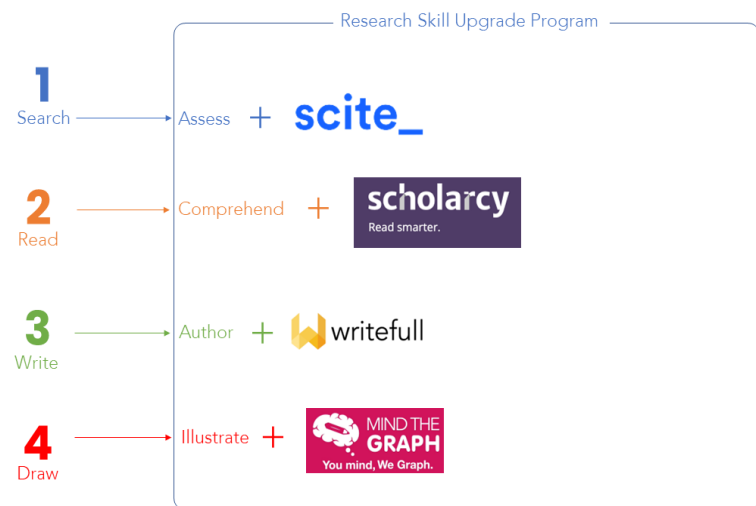
### Accelerate Your Research Journey

With so many tools out there, how do you know when to use what tools in order to improve your research efficiency?

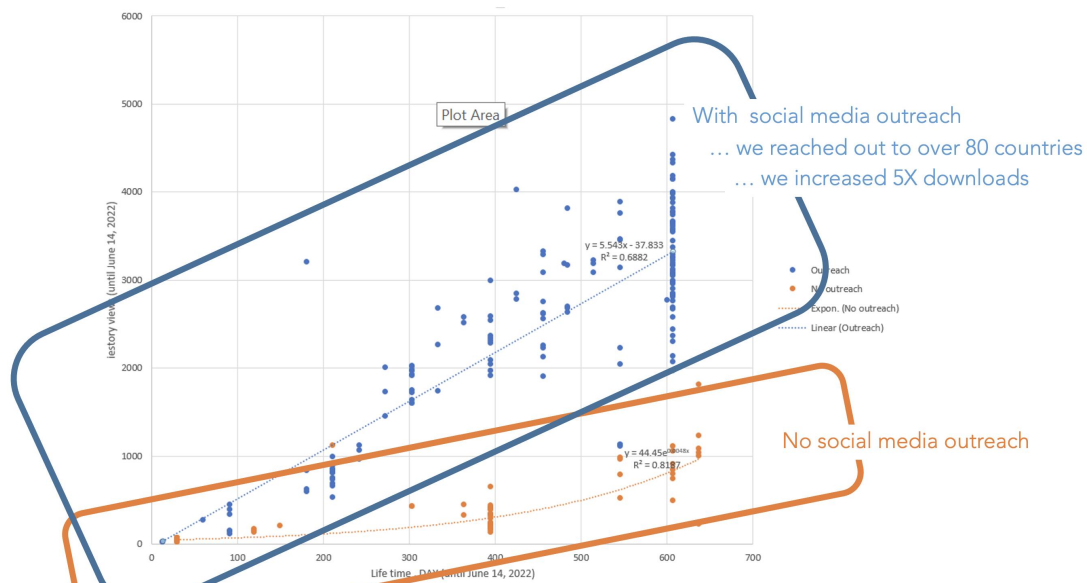
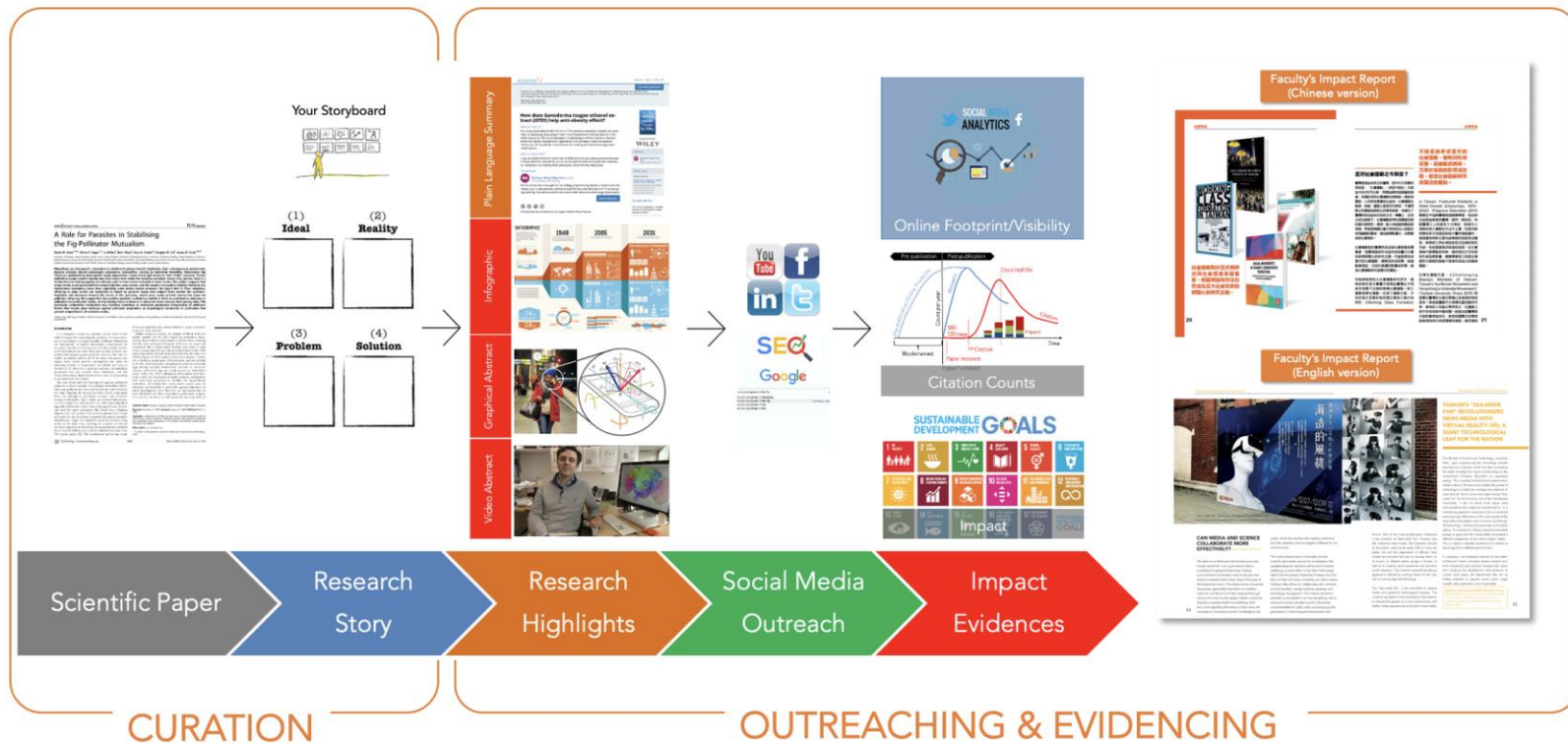
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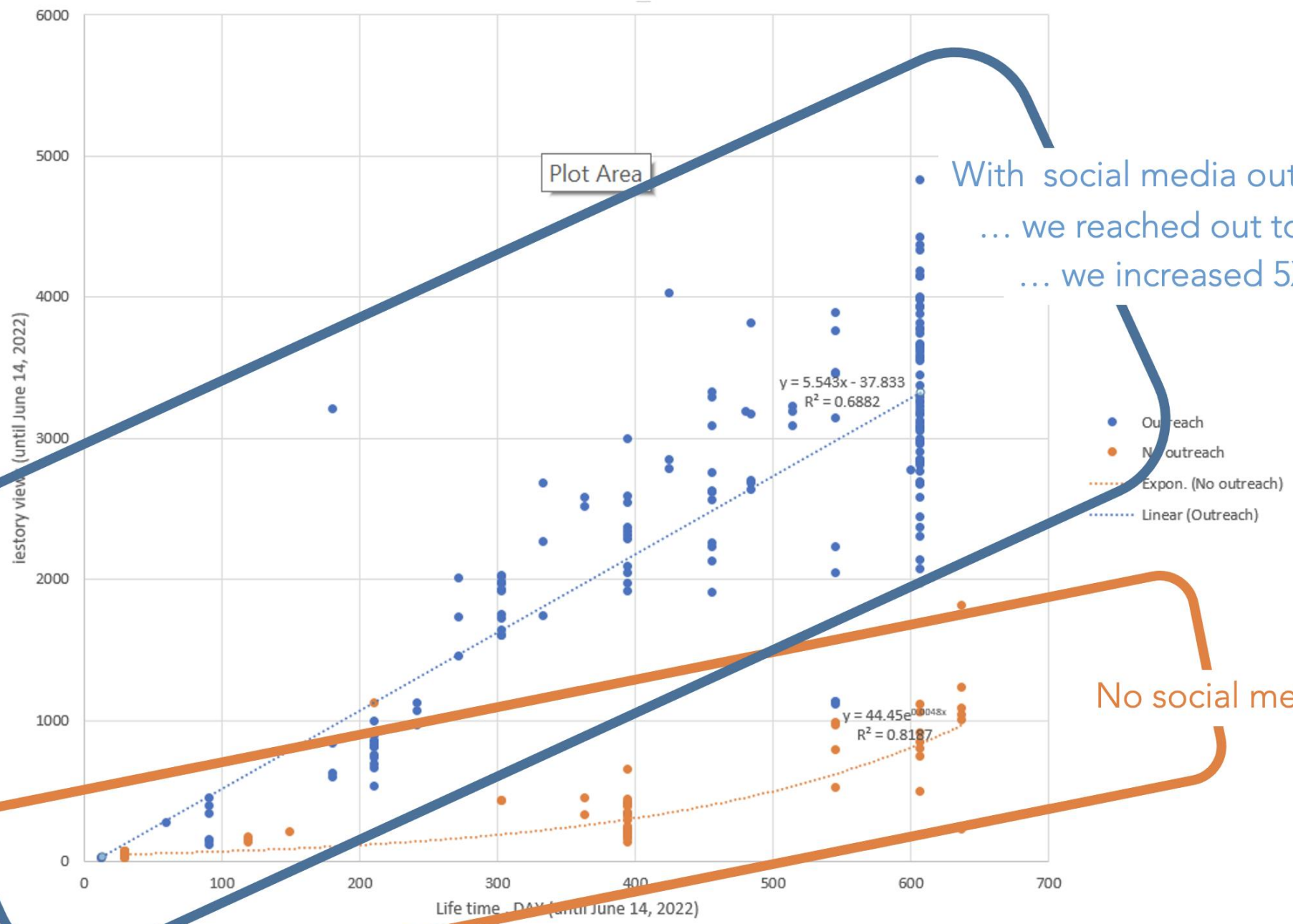
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• With social media outreach  
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 ... we increased 5X downloads

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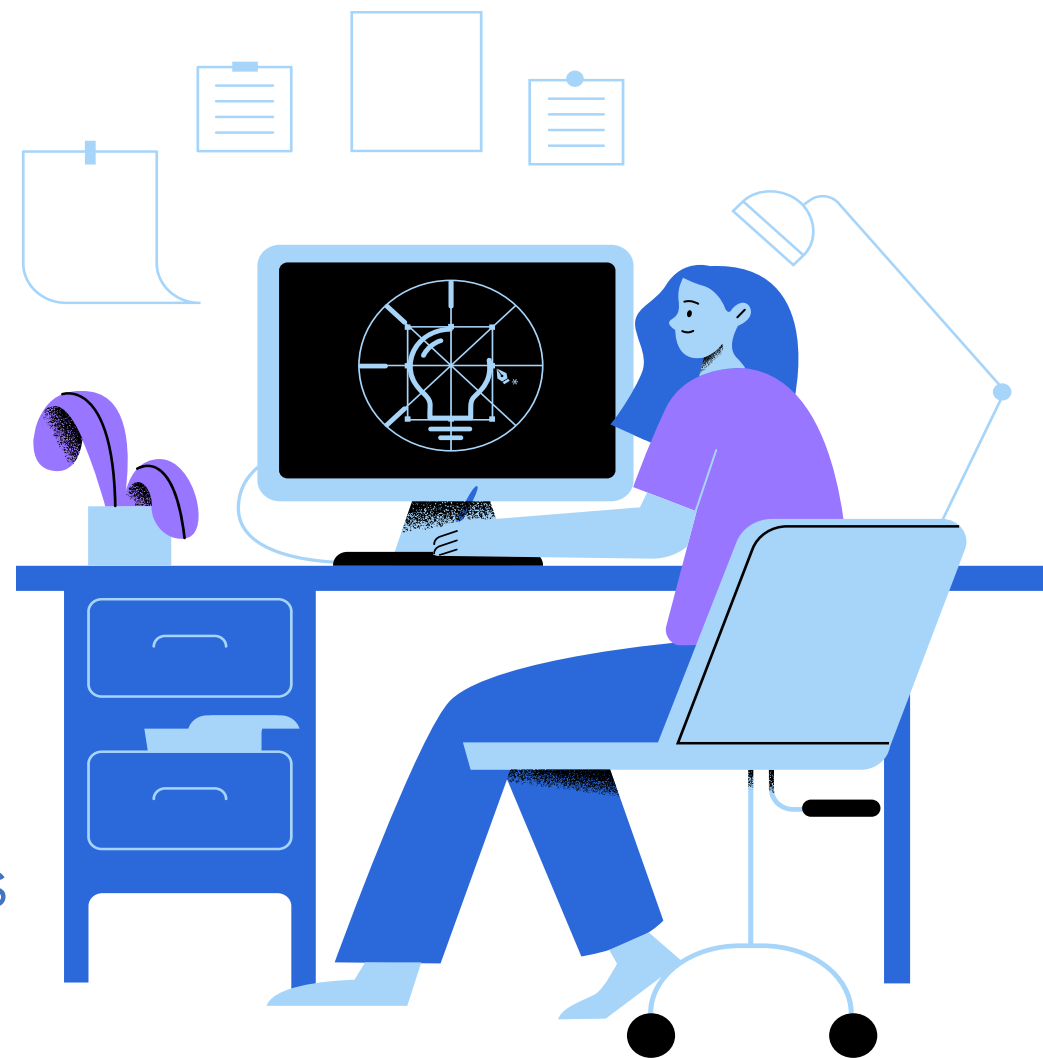
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