A new approach to evaluate scientific production

Short title

TeamTree analysis

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Abstract

Advances in science and technology depend on the work of research teams and the dissemination of their results through peer-reviewed articles, which constitute a fastly growing socio-economic resource. Current methods to mine publications in a field of interest focus on content, but the workforce credited by authorship remains largely unexplored. This hurdle can be overcome by a new bibliometric approach that visualizes the publication records of authors working in a user-defined field, delineates their genealogic and collaborative connections and provides citation-independent performance measures. This team-centered approach complements existing tools to mine the scientific literature across disciplines.

Keywords

Authorship, citation, collaborations, data science, genealogy, meta research, science of science, scientometrics, informetrics, bibliometrics, team science, TeamTree

Introduction

Progress in science and technology (S&T) depends on research teams working in specific fields of interest and on the publication of their results in peer-reviewed articles. Authorship on these articles credits contributions of individual team members with diverse expertise and skills [1, 2]. The rapidly growing body of scientific information [3] reflects past and current states of the art and represents an invaluable socio-economic resource guiding future research activities, policies and investments [4-9]. Its utility relies on refined methods to search and analyse scientific articles. Nowadays, computational algorithms processing large datasets inform about natural processes, help to formulate new hypotheses or to find new drugs, and

provide new insight in the roles of authors, teams and collaborator networks [10-26]. A typical user interested in a specific topic (e.g. physical phenomenon, chemical compound or human disease) queries a bibliographic database and scrutinizes the list of publications. However, the teams working in the user-defined field remain largely inaccessible. The present work aimed to overcome this hurdle. To this end, a new bibliometric approach and visuals were developed that give users interested in a specific field an instant view on the workforce based on a list of publications. The approach, further referred to as TeamTree analysis (TTA), is introduced here using selected research fields from different scientific disciplines as examples.

Materials and methods

TTA was implemented with the open source software R [27] and selected R packages (data.table [28]; dunn.test [29]; eulerr [30]; ggfortify [31]; ggplot2 [32]; ggrepel [33]; igraph [34]; plot3D [35]). The R script is available upon request to the author and at https://github.com/fw-pfrieger/TeamTree. Publications were obtained by queries of bibliographic databases (Table 1).

Table 1. Selected research fields and authors subjected to TTA.

Field / Discipline	Database	Pubs / Authors / Year
Aplysia	PubMed	4738 / 1624 / 1898
Circadian Clock[1] / Biomedicine	PubMed	17514 / 6759 / 1960
Chirped Laser Pulses[2] / Physics TS=chirped laser pulses	WOS	9021 / 4251 / 1968
Cosmic Inflation[3] / Astronomy	WOS	3311 / 1790 / 1981

TS=("cosmic inflation" OR "inflationary universe")		
CRISPR (clustered regularly interspaced short palindromic repeats OR crispr*)	PubMed	23689 / 12013 / 2002
Ice Core Climate[4] / Geoscience TS=ice core climate	WOS	9723 / 5904 / 1956
Organoids	PubMed	14610 / 10077 / 1946
Quantum Computer[5] / Computer Science TS=("quantum computer" OR "quantum computing")	WOS	28597 / 10390 / 1985
Supramolecular Chemistry[6] / Chemistry TS=supramolecular chemistry	WOS	33642 / 13061 / 1967
Gregory Y. Lip / Selected Team / Biomedicine	PubMed	3017 / 587 / 1991
Hagop Kantarjian / Selected Team / Biomedicine	PubMed	2195 / 366 / 1981
Didier Raoult / Selected Team / Biomedicine	PubMed	3034 / 342 / 1979

Summary of selected fields and authors, their discipline, the query term, the relevant bibliographic database, the number of publications and of authors and the first year of publication. Selected awards: [1]Nobel Prize Physiology/Medicine (2017); [2]Nobel Prize Physics (2018); [3]Kavli Prize (2014); [4]Vetlesen Award (2013); [5]Micius Quantum Prize (2018, 2019); [6]Nobel Prize Chemistry (1987).

TTA extracts a non-redundant list of last authors from articles with at least one additional author. Author names include initials to reduce author ambiguity. Single author articles count towards the publication record of last authors. For simplicity, last authors are further referred to as "authors". TTA assigns a chronologic index with alternating sign (AI; Table 2) to each author according to the year of the first publication as last author. Further, TTA attributes

randomly a color to each author and calculates several parameters summarizing each author's publication record, genealogy and collaborations (Table 2). Genealogic relations are based on offspring - ancestor pairs, where offspring is defined as authors, who appeared initially as first authors on a publication of an ancestor author. Accordingly, TTA calculates the author generation (AG; Table 2). Each offspring (AG = i+1) is assigned to the ancestor (AG = i) with the earliest common publication. A family is defined as progeny of a first ancestor (AG = 1) encompassing all offspring (AG > 1). TTA derives collaborations based on co-authorship [36] separating out- and in-degree connection, where the author lists other authors as co-authors and where the author is listed as co-author, respectively. Statistical analyses were performed using indicated tests. For comparison, citation-based measures of randomly selected authors were obtained manually from the Web of Science database selecting "articles" and excluding self-citations.

Table 2. Summary of TTA-derived parameters.

Parameter	Description
AC	Number of authors per publication
AG	Generation of an author, where AG ancestor = i and AG offspring = i+1
AI	Chronologic index of an author based on the first (last author) publication with alternating sign from one author ($+AI_n$) to the next ($-AI_{n+1}$) enabling a tree-like display of the workforce
CC	Collaboration count of an author: "out", number of co-authors; "in" number of authors that listed the author as co-author
FS	Family size: number of all progeny of a first generation ancestor
OC	Offspring count of an author: number of first authors on an author's publications that subsequently publish as last author
PCannu	Mean annual count of last author publications

PCcol	Number of publications with collaborators: "out", number of articles where the author is last author and a collaborator is listed as co-author; "in", number of papers where the author listed as co-author. Only articles with three authors or more are taken into account.
PCfirst	Number of publications as first author
PClast	Number of publications as last author including single-author articles
PCoff	Number of last author publications with offspring
TTP	TeamTree product: result of PClast × OC × CC (in+out)

Results

The features of TTA are introduced using selected fields of research from distinct disciplines of S&T (Table 1).

Visualizing the workforce driving research fields

TTA introduces a new type of visual, further referred to as TeamTree graph, to display the workforce driving a user-defined research field of interest based on the author lists of scientific articles and their years of publication. To this end, the publication years of each author are plotted against AI creating a tree-like image. To exemplify this feature, TTA was applied to publications related to three fields of biomedical research that were chosen because of their distinct dynamics (Fig 1; Table 1). The corresponding TeamTree graphs reveal the long history and stable workforce of the *Aplysia* field [37], the fastly growing number of teams working on CRISPR-related topics [38] and the peculiar development of the organoid field [39] showing distinct phases of workforce expansion (Fig 1).

Fig 1. TeamTree graphs showing the development of the workforce in selected fields of biomedicine.

TeamTree graphs reveal the distinct duration, size and growth of the three fields shown as examples (Table 1). They are generated by plotting the years of publication of each author against AI. Grey lines connect publication years of each author. Circle area represents PClast per year.

Display and quantitative analysis of publication record, genealogy and collaborations

To further illustrate its features, TTA was applied to publications related to "circadian clock" (Clock), a representative field of biomedical research [40] (Table 1). Figure 2 shows results with respect to the publication records of authors in the field. Individual authors published as many as 115 articles (PClast), but two thirds of the workforce (69%) contributed single articles (Fig 2B) even after exclusion of authors entering during the last two years (67%). The Clock field expanded exponentially within the last decades as indicated by linearly growing annual counts of newly entering authors and of published articles per year, respectively (Fig 2C). Ranking authors by PClast values identified the top contributors to the field with respect to publication record (Fig 2D).

Fig 2. Publication record in the Clock field.

(A) TeamTree graph representing the publication records of authors working in the Clock field. Circle area, PClast per year. (B) Left, publication counts per author separating last and first author articles. Circle area, PCannu. Right, relative frequency distributions of PC values shown on the left. (C) Number of authors entering the field per year (orange) and of articles (black) published per year. (D) Authors with top ten PClast values indicated by circle area.

TTA revealed ancestor–offspring relations in the Clock field based on last author–first author pairs of PubMed articles, respectively (Fig 3). A quarter of authors published previously as first authors thus qualifying as offspring in this field (Fig 2B), whereas 13% of the authors qualified as ancestors. They generated up to 24 offspring and published up to 71 articles with their offspring (Fig 3B). Overall, the Clock field comprised 591 families with a variable number of members spanning up to 8 generations (Fig 3B). For the last two decades offspring authors and publications with offspring represented a small, but constant fraction of the workforce entering the field each year and of the annual scientific production (Fig 3C). Ranking authors by OC values indicated the most prolific authors and their families (Fig 3D).

Fig 3. Genealogic relations in the Clock field.

(A) TeamTree graph showing ancestor-to-offspring connections among authors. Connections of authors with top ten OC values are shown in color (names indicated in panel D). Circle area, OC. AI signs of offspring and of ancestors were adjusted. (B) Left, from top to bottom, OC, PCoff, AG and FS values. Circle area, PCannu. Right, Relative frequency distributions of parameters shown on the left. (C) Fraction of new offspring authors (orange) and of publications with offspring (black) compared to total number per year. (D) Names and family connections of authors with top ten OC values indicated by circle area.

Collaborations in the Clock field were delineated based on co-authorship on PubMed articles (Table 2; Fig 4). In total, 53% of the authors in the Clock field established a variable number of out- and in-degree collaborations and published collaborative papers as last and co-author, respectively (Fig 4B). During the last two decades, collaborators represented half of the new authors entering per year and their contribution remained fairly constant (Fig 4C), whereas

the number of authors per article increased steadily (Fig 4A). Ranking authors based on connection counts revealed the most strongly connected players in the field. They formed a large network with a diameter of 8, a mean distance of 3.82 and an edge density of 0.0117 (Fig 4D).

Fig 4. Collaborations in the Clock field.

(A) TeamTree graph showing collaborations between last authors (out; negative AI) and co-authors (in; positive AI). Connections of authors with top ten CC values (in+out) are shown in color. Circle area, CCout and CCin values of these authors. Inset, mean AC per article published each year. (B) Left, counts of respective collaborators and of resulting articles per author. Circle area, PCannu. Right, relative frequency distributions of parameters shown on the left. (C) Fractions of new collaborating authors (orange) and of collaborative publications (black) compared to total numbers per year. (D) Names of authors with top ten CC values (in+out) and their networks. Circles and squares, offspring and non-offspring authors, respectively. Circle area, CC (in+out) values normalized to the maximum.

Workforce dynamics and field development

TTA was used to explore how the workforce of the Clock field developed over time. Plotting the number of authors entering and exiting the field based on the first and last year of their publications, respectively, revealed a strong growth of the workforce up until three years ago (Fig 5). The publication periods or life-span of authors ranged up to five decades, but the large majority published only during one year and in most cases a single article (Fig 2C; Fig 5A-C). Separating "Newcomers" entering the field per year from "Established" authors revealed that the established workforce consisted mostly of authors with genealogic and

collaborative connections, whereas most newcomers had collaborative connections or no ties at all and contributed single articles (Fig 5D).

Fig 5. Workforce dynamics in the Clock field.

(A) Annual counts of authors entering (green bars) and leaving the field (red bars). Lines show cumulative sums. (B) Publication periods of individual authors in years. (C) Bars and lines showing the relative frequencies of all publication periods and the cumulative relative frequencies of publication periods from indicated categories, respectively. Col, authors with collaborative but no genealogic connections; Off, genealogic but no collaborative connections; Off+Col, both types of connections; Rest, without connections. Statistically significant differences among groups are indicated (Kruskal-Wallis tests chi-squared = 267.1734, df = 3, p = 0. Asterisks: *, $p < 0.05$; **, $p < 0.01$; ***, p = 0; post-hoc Dunn test, Benjamini-Hochberg adjusted; group size = 301; adjusted to minimum by random selection). (D) Annual author (filled) and publication counts (white) of newcomers (left) and established teams (right) from the indicated categories. In each category, authors with single publications are represented by grey bars. Scale bar indicates number of authors or publications.

Author contribution based on publication output, offspring and collaborations

A recurrent goal of bibliometric analyses is to gauge author contributions to a field of research, as this can help to choose referees/experts, recruits and collaborators. TTA delivers three parameters (PC, OC and CC) to estimate the contribution of authors as illustrated in Figs 2-4. Intersection of the top 100 authors for each parameter revealed overlap between PClast-, OC- and CCin+out-based rankings. A core of 35 authors figured among the top in all three categories (Fig 6). Three-dimensional plots of these parameters revealed that authors

occupy distinct volumes (Fig 6B) indicating that the product of the three measures, further referred to as TeamTree product (TTP; Table 2), enables a more differentiated author ranking than each parameter alone (Fig 6C). Notably, TTP values of individual authors correlated significantly with numbers of citing articles (rho = 0.88; $p = 2.2\ 10^{-16}$) and with H indices (rho = 0.94; $p = 2.2\ 10^{-16}$; Spearman's rank correlation; Fig 6D). These findings indicated that TTP can serve as a citation-independent measure of an author's contribution to a field. Teams with highest TTP values included Nobel prize winners (M. Rosbash: 7th, M.W. Young: 18th, J.C. Hall: 41st out of 6759; Table 1; Fig 6C; S1 File).

Fig 6. Introduction of TTP as a new measure of scientific production.

(A) Numbers of intersecting authors ranking among top 100 for each parameter (PClast, OC, CCin+out). (B) Scatterplot of indicated parameters for authors with top ten TTP values. (C) Top, TeamTree graph showing TTP values of authors (circle size) normalized to maximum. Colored circles and names, authors with top ten TTP values. Bottom, log10(TTP) values of authors. (D) Number of citing articles (top) and H index (bottom) of individual authors plotted against their TTP values.

Analysis of distinct scientific disciplines and of authors with exceptional publication records

TTA reveals the workforce driving a field of interest. The choice is not limited to biomedicine. To illustrate this point, TTA was applied to representative fields in other disciplines (Table 1). Combined TeamTree graphs summarizing the publication record, genealogic and collaborative connections and TTP values are shown in Fig 7. In addition, TTA allows to track the activity of single authors, for example those with exceptional publication counts [41], and to separate articles originating from offspring and collaboration.

Thus, TTA can providing a more detailed view on a specific author's publication record (Table 1; Fig 7B-D).

Fig 7. TTA of selected fields in different disciplines and of selected authors with exceptional publication records.

(A) Combined TeamTree graphs summarizing the indicated parameters (PClast, OC, CCin+out, TTP) for selected research fields. Only authors with top ten values for each parameter are shown. Circle areas, relative counts normalized to respective maximum. Names, authors with top ten TTP values. Horizontal and vertical scale bars, number of authors and years, respectively. Stars indicate awardees (Table 1). (B) TeamTree graphs showing publication counts of indicated authors (Table 1). (C) Publication rates per year of the same authors separating articles by contributions (First, first author; Col in, in-degree collaborations; Col out±Off, out-degree collaborations with and without offspring; Off–Col out, offspring without out-degree collaborators; Rest, all other publications). Insets, contributions of indicated categories to total publication record. (D) Mean AC per article published each year.

Discussion

TTA gives users an instant view on the workforce driving a field of interest based on authors and publication years of scientific articles. The new TeamTree graphs depict the origin, size and development of a research field and show the genealogic and collaborative connections among authors. TTA can be performed using a freely available R script. An open source project aims to provide access to a web-based TTA with enhanced functions and visuals.

TTA reveals how the workforce impacts the development of research areas. Only a fraction of authors contributed for more than one year to the Clock field. This supports

previous findings that in many research areas only a small fraction of the workforce publishes during long periods of time [42]. Genealogic and collaborative connections prolonged the life-span of teams within the Clock field. These observations are in line with previous studies highlighting the relevance of training and mentorship [43-45] and the importance of collaborations [5, 46-49]. TTP represents a new measure to estimate the contribution of authors to a specific field. This parameter takes into account the publication record, training/mentorship and cooperation. Stratified publication counts separating last author, first author and co-author contributions provide a detailed view on the publication record. Offspring counts value training and mentoring of junior scientists that continue their career within the field. Collaboration counts signify recognition within the field due to specific expertise and capacities. TTP is citation-independent, but scales with the citation-based H index [50] and thereby complements other bibliometric measures [6, 51-56]. A few caveats should be mentioned. TTP values are field-specific, they scale with the size of research groups and they depend on the life-span of authors in the research field. Therefore, the TTP-based ranking is context-dependent and unsuited for junior scientists [57] and the metric cannot gauge innovative, ground-breaking contributions from small teams or from teams that contribute only briefly to a field. Honorary and ghost authorship will confound results depending on their prevalence in the field of interest [58, 59]. Other limitations may be addressed in future versions. The automatic delineation of family connections from first author-last author pairs provides an alternative to efforts requiring user input [60-62]) (see also Mathematics Genealogy Project: https://www.genealogy.math.ndsu.nodak.edu/; Academic family tree: https://academictree.org/). However, TTA underestimates offspring counts in the case of co-first or co-last authorship, when first authors change the field of interest and in the case of alphabetical author lists or field-specific author ranking [63]. TTA like other name-dependent approaches faces the challenge of author disambiguation. This can

be mitigated by inclusion of initials, author affiliations and advanced computational algorithms [6, 64-67]. An ultimate solution is the assignment of unique and persistent author identifiers such as Orcid iDs [68] and their inclusion in publication records of bibliometric databases. Peer-reviewed articles were used to introduce the features of TTA as this form of publication represents the core of scientific production [69]. In the future, TTA may also be applied to other types such as preprints and patents.

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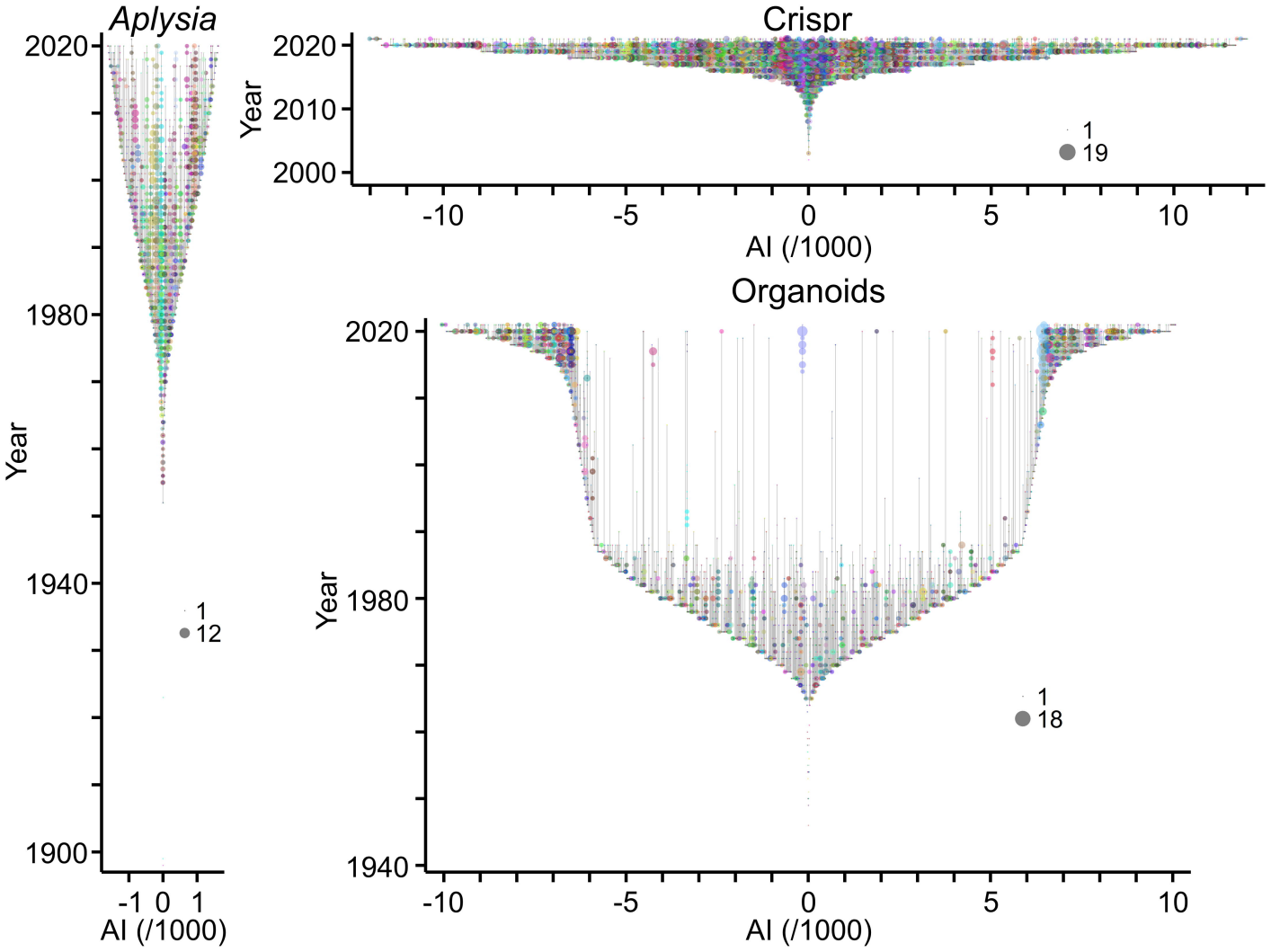
Supporting information

S1 File. TTA-derived results for the Clock field. Csv file summarizing TTA data for the Clock field using PubMed articles related to "circadian clock".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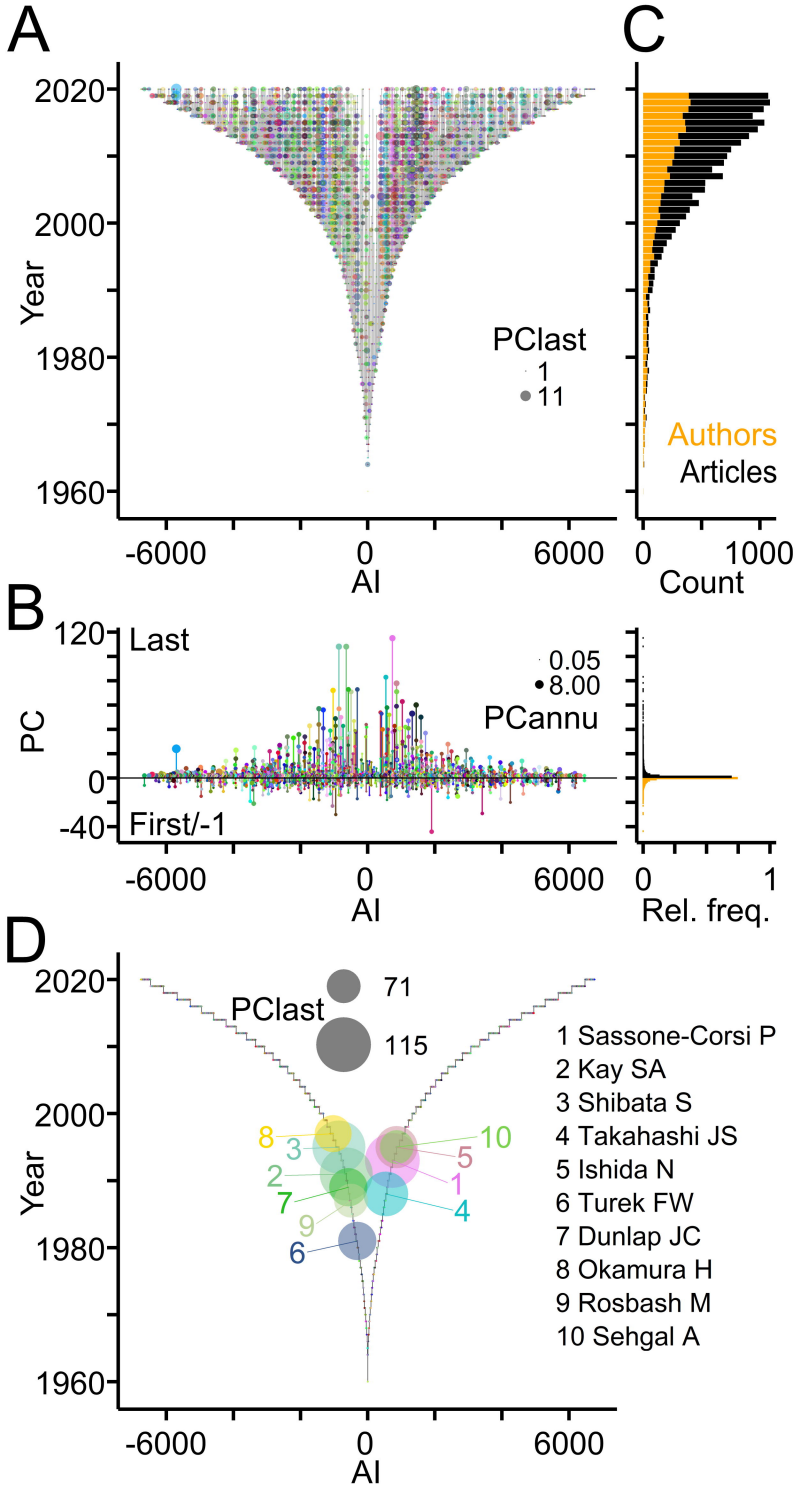
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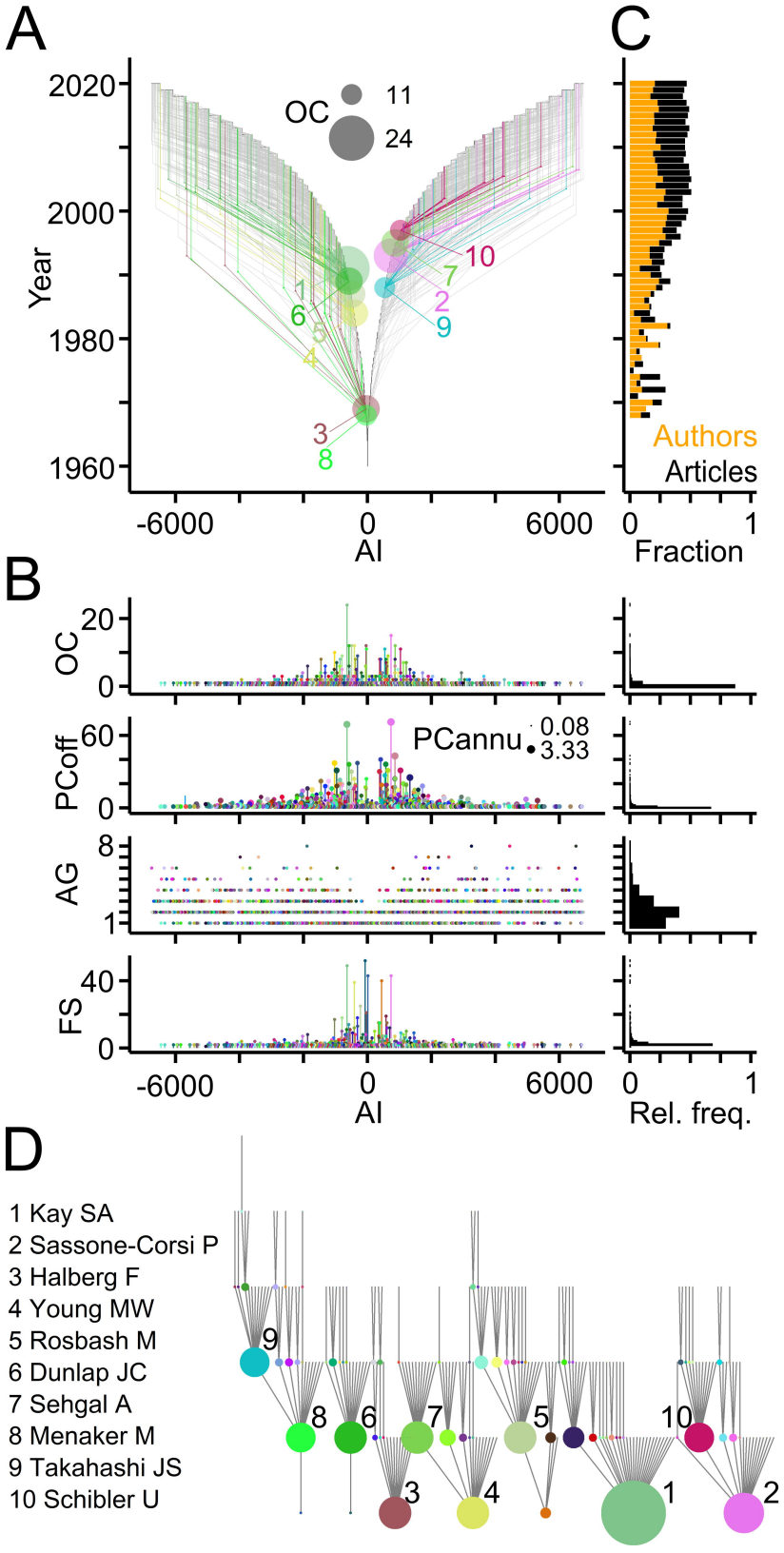
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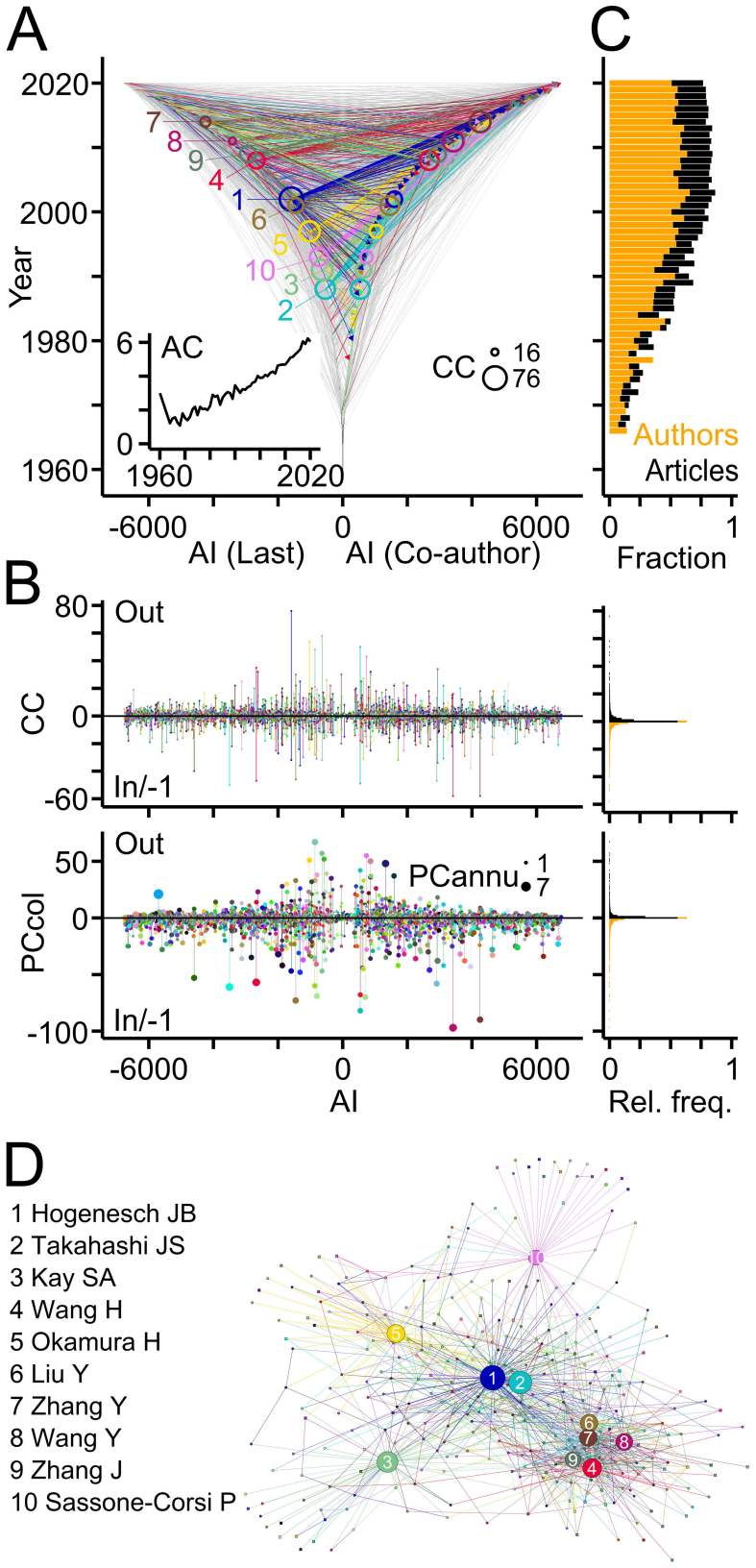
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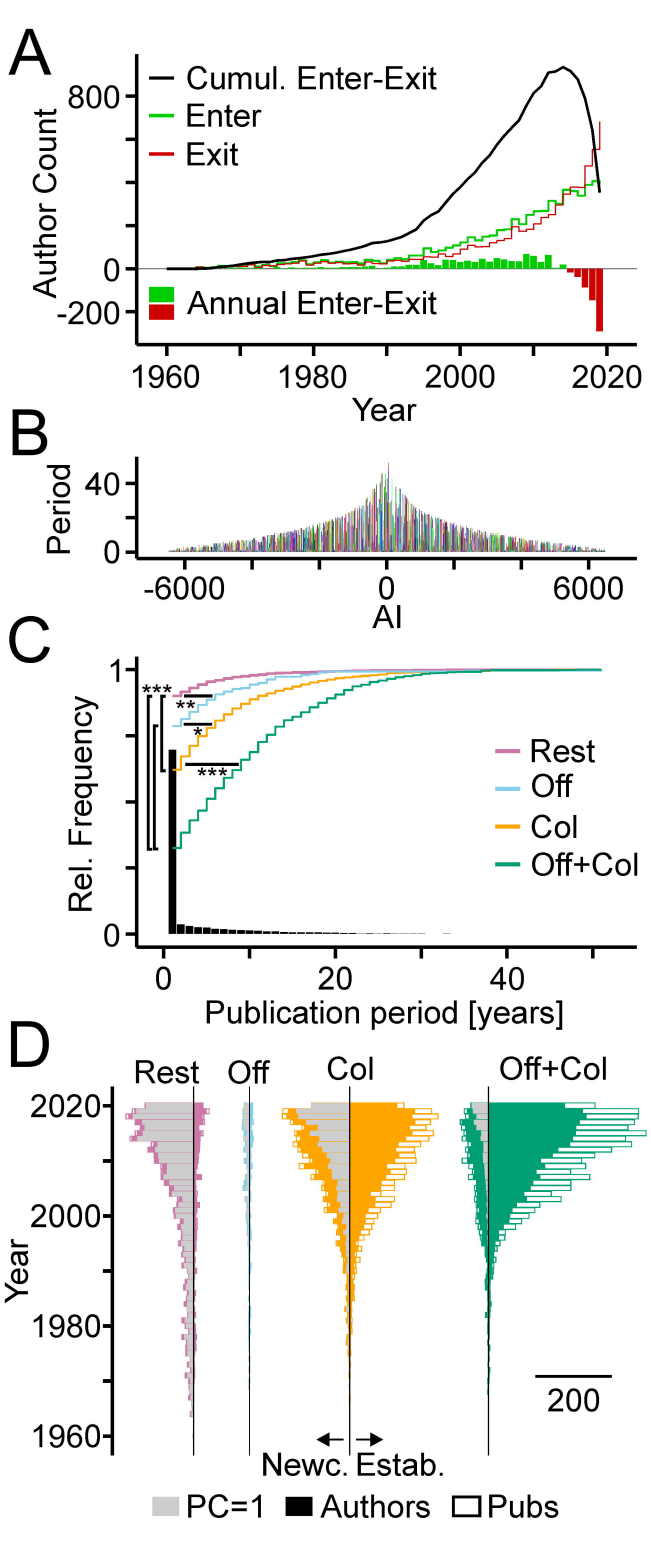
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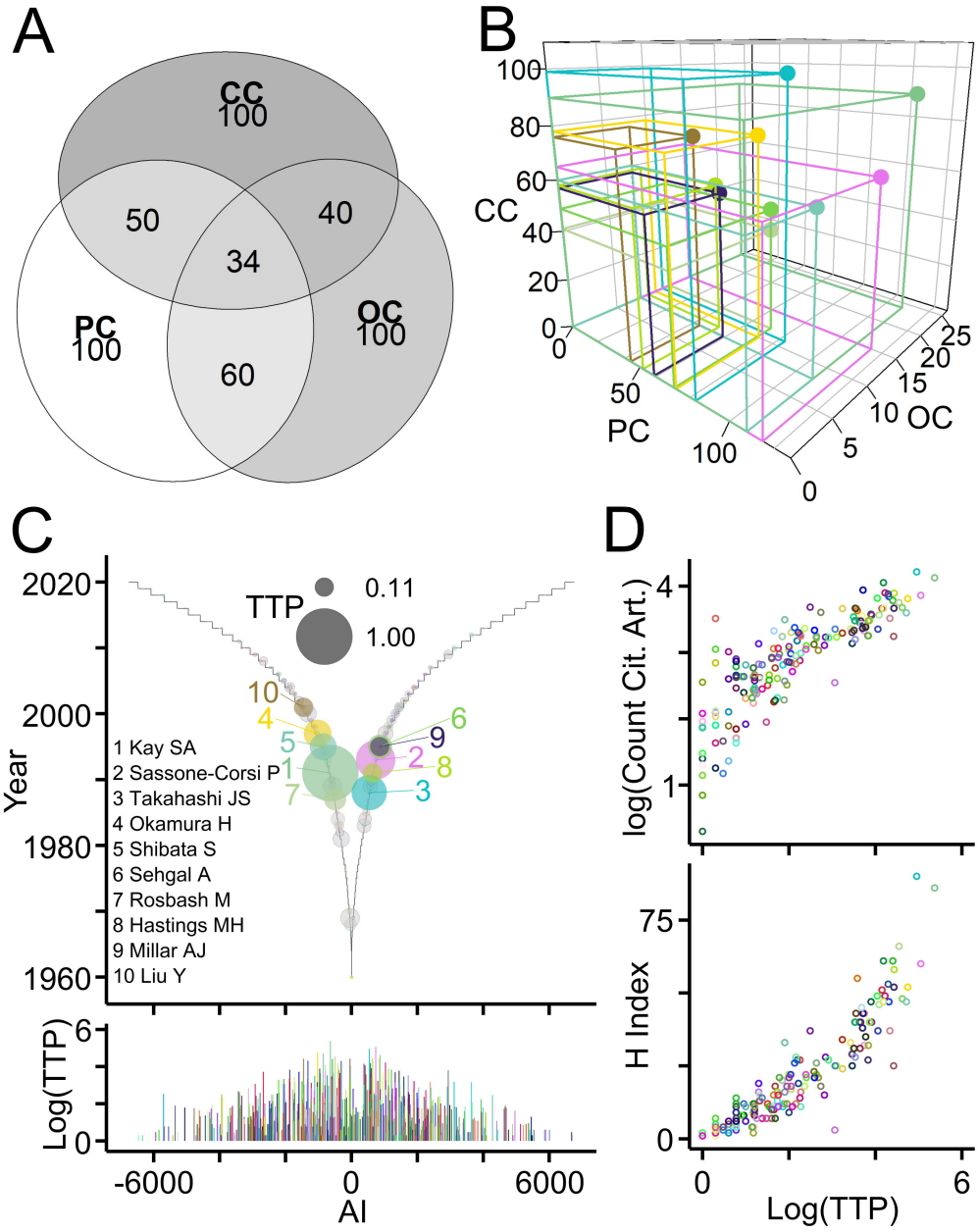
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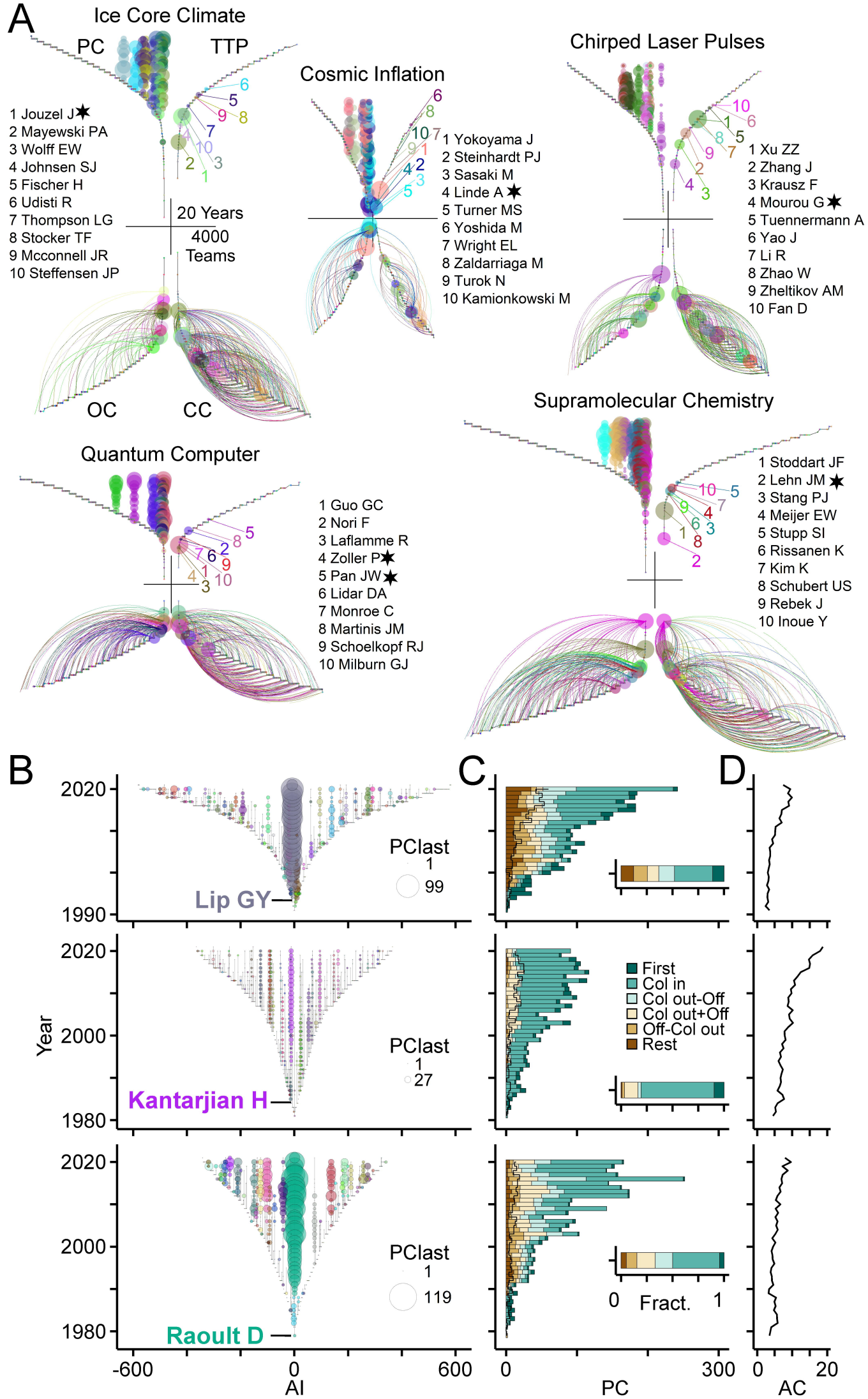
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