The Elasticity of Science

Online Appendix

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Appendix I Additional NIH Details

A NIH Funding Channels

The application process generates groups of applications in three dimensions, which following Azoulay et al. (2019b), I refer to as Disease (per the Institute the application is submitted to for funding, i.e., National Cancer Institute), Science (per the peer review group charged with evaluating the quality of the application, i.e., Bacterial Pathogenesis) and Time (per the fiscal year the application is submitted). Applications are peer reviewed per their Science-Time group and compete for funding per their Disease-Time group. These Disease-Science-Time (D-S-T) groupings are used to construct counterfactuals in the analysis of Section 4. Importantly, there are no explicit restrictions on the types of science that may be submitted to these competitions, so long as it fits within the NIH's broad objectives. "The NIH's mission is to uncover new knowledge that will lead to better health for everyone. Simply described, the goal of NIH research is to acquire new knowledge to help prevent, detect, diagnose, and treat disease and disability."[1]

Because RFAs are reviewed by a stand-alone peer review group convened just for the RFA, they are technically each unique D-S-T groupings. Thankfully, the NIH Center for Scientific Review (CSR) publishes broader sets of peer review groups, which RFA review groups are assigned to in the administrative data. These "Integrated Review Groups" allow me to match each RFA to a corresponding D-S-T, with the "S" now defined by the Integrated Review Groups. See the CSR for further details.[2] These D-S-Ts are used to define the time-specific research area fixed effects included in the analyses of Section 4.

B RFA Generation and Empirical Relevance

Discussions with the NIH staff responsible for managing RFAs indicated two major forces: political and programmatic. As evidence of the political influence, the NIH's annual Congressional appropriation bills regularly include "soft earmarks," where members request research on specific topics. Hegde and Sampat (2015) find evidence that these diseases referenced by

[1] This is an approximation of the official funding process, which is outlined here: https://goo.gl/blLuuU, accessed July 12, 2017.

[2] https://goo.gl/PmYp2P, accessed July 12, 2017.

Congress often appear as the focus of grants awarded via RFAs.[3] Whether this relationship would lead my elasticity estimates to be over- or underestimates of the population average depends on whether Congressional preferences are correlated with positive or negative features of the science (from scientists perspective). Hegde and Sampat's (2015) findings indicate that disease advocacy lobbying is a key driver of Congressional preferences, and that this lobbying is positively correlated with both disease burden and scientific opportunities, which would suggest a positive correlation between these unobservables, scientists' preferences and RFA generation. However, it is important to note that although Congress may request research on, for example, a specific disease, the nature of RFA mechanisms and their historical use by NIH staff is such that they rarely target a single topic. In effect, this means that Congress's influence will be mixed and muted by the programmatic concerns detailed next. As example, consider the case of the Zika virus outbreak in 2016-17. Unsurprisingly, following this event, the Zika virus appeared in both the Congressional appropriations bill as a requested topic (See: H. Rept. 114-699) and as a part of an RFA (See: https://goo.gl/zQhmN6, accessed July 12, 2017). But notably, the RFA in which a vaccine for Zika is requested is actually a broader request for "Countermeasures Against Select Pathogens," to include a large number of antimicrobial-resistant bacteria or emerging viral pathogens.

On the other hand, the programmatic reasons cited by NIH staff revolve largely around targeting unobservables that are, if anything, likely negatively correlated with scientists' preferences. The staff repeatedly referenced how RFAs are developed to fill "portfolio gaps," or in other words, areas of science where the NIH did not have active grants. These intentions are mirrored in this remark from Thomas Insel, the director of the National Institute of Mental Health (NIMH), who describes the purpose of RFAs as follows[4]:

> "The NIMH uses RFAs to [1] focus on innovation and high-risk science that may suffer in peer review of unsolicited applications ... [2] open up fields that have been relatively neglected ... [3] develop specific, integrated programs that may not be created via unsolicited grants"

Each of these goals revolve around identifying underserved aspects of science, therefore, areas of science relatively less preferred by scientists. This would suggest a negative correlation between any underling trends and the use of RFAs. Whether this correlation is meaningful enough to be empirically relevant is explored throughout the paper.

C Other Relevant NIH Policies

One difference of note regarding RFA and open applications is that after the review and funding decision open applications that fail may be revised and resubmitted again as an open application at a future date. Conversely, the first RFA award decisions are final, so applications may be revised and resubmitted but as an open application. However, because

[3]This channel of influence was confirmed by NIH staff, who noted that these formal requests were often reinforced by direct communications (i.e., phone calls with staffers, on-site visits).

[4]Excerpted from: https://goo.gl/2zfPru, accessed July 12, 2017.

applications initially submitted to RFAs and then resubmitted as an open application are not linked in the NIH data it would be difficult to accurately track such applications. But for the purposes of the following analyses, because this option value of applications is equivalent I only examine outcomes for the first (new) application, and note that whether the option is valued by scientists will not introduce any bias.

Another policy of note is that both successful RFA and open grants may re-apply for continued funding after the initial funding duration expires, but I focus only on first-year direct costs because this feature applies to both mechanisms, and examining the lifetime value of grants potentially introduces selection concerns as more successful projects are more likely to both pursue these continuation grants and receive them.

In addition to RFAs, NIH also releases "Program Announcements" to solicit certain types of science. However, these calls are not accompanied by set-aside funds made specifically available for competition and in practice vary widely in their format. These announcements are used to facilitate efforts beyond traditional research projects such as conferences, training grants, and other integrated efforts.

There is one variant of the program announcements (Program Announcements with Set-aside funds (PASs)) that I include as a part of the RFA set because for all intents and purposes these mechanisms behave exactly the same as RFAs. This fact was confirmed in discussions with NIH staff. I focus my analyses on RFAs (and PASs) because of their well-defined properties both in terms of scientific scope and set-aside funding.

D Example RFA

The following is excerpted from the RFA at the following link: https://goo.gl/peirW6, accessed July 12, 2017. For the list of currently active NIH RFA's and other funding opportunities, visit https://goo.gl/hks3K4.

Figure I.1: Development of New Technologies Needed for Studying the Human Microbiome

Department of Health and Human Services

Participating Organizations
National Institutes of Health (NIH), (http://www.nih.gov)

Components of Participating Organizations
This Funding Opportunity Announcement (FOA) is developed as an NIH Roadmap initiative (http://nihroadmap.nih.gov) through the Office of Strategic Coordination (http://dpcpsi.nih.gov/osc/). All NIH Institutes and Centers participate in Roadmap initiatives. This FOA will be administered by the National Human Genome Research Institute (http://www.nhgri.nih.gov) on behalf of the NIH.

Title: Development of New Technologies Needed for Studying the Human Microbiome (R01)

Announcement Type
This Funding Opportunity Announcement (FOA) is a reissue of RFA-RM-08-026.

Request for Applications (RFA) Number: RFA-RM-09-008

Key Dates
Release/Posted Date: July 16, 2009
Opening Date: August 14, 2009 (Earliest date an application may be submitted to Grants.gov)
Letters of Intent Receipt Date(s): August 17, 2009
NOTE: On-time submission requires that applications be successfully submitted to Grants.gov no later than 5:00 p.m. local time (of the applicant institution/organization).
Application Due Date(s): September 14, 2009
Peer Review Date(s): February-March 2010
Council Review Date(s): May 2010
Earliest Anticipated Start Date(s): July 2010
Additional Information To Be Available Date (Activation Date): Not Applicable
Expiration Date: September 15, 2009

Executive Summary

- **Purpose.** The purpose of this FOA is to solicit applications to develop new and improved technologies for obtaining samples of individual microbial isolates or strains, from the human microbiota, suitable for complete genomic sequence analysis. The goal is to expand the number of "reference" microbial genome sequences, which in turn will aid in the analysis of the complex microbial populations resident in and on the human body.
- **Mechanism of Support.** This FOA will utilize the NIH Research Project Grant (R01) grant mechanism and runs in parallel with a FOA of identical scientific scope, RFA-RM-09-009 that solicits applications under the R21 mechanism.
- **Funds Available and Anticipated Number of Awards.** $2 million is available in FY10 for this FOA and the parallel R21 FOA in combination. It is anticipated that 2-4 R01 grants (of duration up to 3 years) and 2-6 R21 grants will be awarded. . Awards issued under this FOA are contingent upon the availability of funds and the submission of a sufficient number of meritorious applications.
- **Budget and Project Period.** Because the nature and scope of the proposed research will vary from application to application, it is anticipated that the size and duration of each award will also vary. Applicants for R01 grants may request a project period of up to 3 years.

RESEARCH SCOPE: The interpretation of metagenomic sequence data is greatly aided by comparison to the genomic sequence of isolated species and genetically different strains of the same species. Yet, only a small proportion of the microbial species resident in or on the human body has been isolated and sequenced. The purpose of this FOA is to support the development of technologies that will allow the determination of the complete, individual genome sequences of substantial numbers of previously uncharacterized members of the human microbiota, to aid in the interpretation of metagenomic datasets obtained from sampling the human body. The following list, which is certainly incomplete, presents examples of strategies that would be supportable under this FOA:

- Development of methods to isolate single microbial cells. These methods would enable the identification, analysis and isolation of individual cells in the human microbiota that satisfy a specified set of criteria.
- New approaches to obtain pure cultures or simple mixed cultures of small numbers of previously uncultivated species would advance the objective of genomic analysis of the human microbiota. Proposed methods that can be applied to a large number of species rather than to any one particular species will take high priority.
- Development, optimization and validation of methods to isolate, amplify, or clone unamplified or amplified DNA of whole genomes from individual cells at high fidelity (e.g., complete coverage, low bias, low chimerism).
- Development of methods to "normalize" the complexity of the population, at either the cellular or DNA level. Such methods would facilitate either the ability to isolate single cells that are rare within a population, or to perform bioinformatics analysis on metagenomic sequences (e.g., by improving the representation of "rare" members).
- Development of methods to enrich the cells of a given species to essential purity. This is the inverse of reducing redundancy, and might be most effective for species whose abundance is already high. Such methods might substitute, at least for DNA sequencing studies, for the ability to establish pure cultures.
- Development of methods that (as a prelude to isolating single microbial cells, or conducting enrichment or normalization) disaggregate cells from the complex mixtures of microbial cells, human cells, and extracellular materials (e.g., biofilms) that comprise human microbial samples. Methods for cell disaggregation should be developed in conjunction with associated methods such as those described above.

Appendix II Medical Subject Heading Indexing & Data Construction

Medical Subject Heading (MeSH) terms comprise the National Library of Medicine's (NLM) hierarchical dictionary. They provide a useful way to classify "types" of science and generate units of observation fit for econometric analyses (cf. Azoulay et al. 2010). Details on the construction and maintenance of MeSH is available at https://www.nlm.nih.gov/mesh/.

The process by which the NLM assigns MeSH terms to documents includes both machine and human review. The algorithm underling the machine assignment step is publicly available (https://ii.nlm.nih.gov/MTI/), with an interactive version of the software available as well (https://meshb.nlm.nih.gov/MeSHonDemand). This indexer can extract the MeSH terms relevant to a body of biomedical text, effectively classifying each abstract into a set of discrete types of science. Using the RFA announcement from the previous section as example, the MTI identified the following MeSH terms as relevant: "Computational Biology", "Human Body", "Chimerism", "Industrial Development", "Biofilms', "Goals', "Genomics', "Metagenomics', "Sequence Analysis, DNA', "Genome', "DNA', "Cell Separation', "Microbiota', "Bias', and "Complex Mixtures". These terms very intuitively capture the goals of this particular RFA.

The MTI fared well with the abstract of this particular paper. It identifies the following terms as relevant: "National Institutes of Health (U.S.)", "Biomedical Research", "Financial Support", "Financial Management" and "Elasticity". Although the MeSH term for elasticity refers not to the economic concept but the mechanical process of resistance and recovery, illustrating the limitations of generalizing this tool.

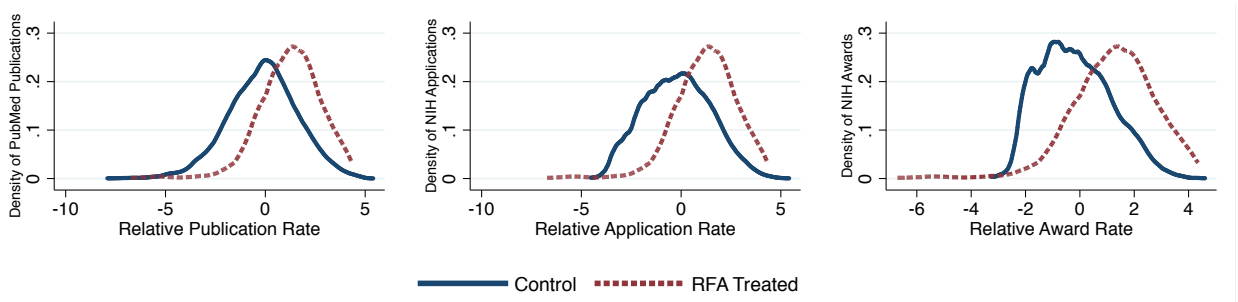
In the analyses using MeSH terms, I control for each MeSH term's position within the MeSH hierarchy using a set of dummy variables that describe each terms' distance (in terms of number of nodes) from its respective top node. Furthermore, I interact this metric with an indicator for each of the seven top nodes to allow this effect to vary within each major set. This eliminates variation that arises simply because certain terms are broader than others (i.e., "Neoplasms," which is 1 nodes from the top node, versus "Large Granular Lymphocytic Leukemia," which is 6 nodes from the top).

For the analyses of Section 2.4, I restrict the sample to include only MeSH terms from the seven major categories that cover purely "scientific" topics: Anatomy; Organisms; Diseases; Chemicals and Drugs; Analytical, Diagnostic and Therapeutic Techniques, and Equipment; Psychiatry and Psychology; Phenomena and Processes.[5] I then include MeSH terms that (1) appear at least once in the NIH application data, (2) occur no more than once in an RFA. Criterion (1) ensures that I examine only MeSH terms at real risk of being pursued by NIH applicants and criterion (2) eliminate any variation in the data that may arise from repeated treatments over the time period I examine.

[5]The other major categories are: Disciplines and Occupations; Anthropology, Education, Sociology, and Social Phenomena; Technology, Industry, and Agriculture; Humanities; Information Science; Named Groups; Health Care; Publication Characteristics; Geographicals.

The cross-sectional distributions of treated and control terms are presented in Figure II.2.

Figure II.2: Distribution of Scientific Subjects, Treated & Control



(a) PubMed Publications **(b)** NIH Applications **(c)** NIH Awards

Plots the average log number of abstracts related to a MeSH term, after controlling for the term's position within the MeSH hierarchy. Abstracts are from the PubMed database of biomedical journal articles (Panel a), all NIH grant applications (Panel b) or successful NIH applications (Panel c).

Appendix III Direction, Similarity & the *pmra* Algorithm

A Choice of Direction & the Role of Similarity

Broadly speaking, there are two main reasons why redirections would be difficult in this setting: they require both tangible (i.e., equipment) and intangible costs (i.e., preferences, cognition). With this in mind, the elasticity I estimate is a *behavioral parameter* in that its magnitude is driven by these tangible and intangible aspects.

In the biomedical sciences, the pecuniary costs of adjustment are substantial; individual pieces of lab equipment routinely cost in excess $100,000. And human capital theory has long appreciated the limitations of specialized knowledge (e.g., Becker 1962), with much emphasis placed on the potential for one's prior endeavors to shape and constrain their search and evaluation of new ideas (Nelson and Winter 1982; Gavetti and Levinthal 2000; Boudreau et al. 2016). Beyond any potential cognitive constraints, scientists have been seen to exhibit preferences over the nature of their work (Stern 2004), and be influenced by social forces (Stuart and Ding 2006; Ding et al. 2006). But notably, many of these studies focus on discrete changes in direction often primarily related to commercialization activities, and not directional adjustments in general. Certainly the commercial transition is one of obvious economic impact, but results on the decisions of direction *before* commercialization or with regards to the *type of science* have been very limited to date. Bhattacharya and Packalen (2011) examine the direction of basic science more broadly using the occurrence of biomedical terms in publications to classify the direction of science as a whole, and find that in the aggregate biomedical scientists do appear to pursue fields related to diseases with higher prevalence as well as those with an increasing underlying fertility.

Two studies that examine the movement of scientists across fields use journal article retractions (Azoulay et al. 2015) and untimely deaths (Azoulay et al. 2019a) as shocks to individuals and fields, respectively. Both papers use the algorithm described below to estimate the degree of scientific redirection, although their implementation relies on publications which means that only successful (per publications) redirection is observed (and the latter is also true of Bhattacharya and Packalen's (2011) analyses). The authors find that following these events, which essentially remove barriers to operating in a particular type of science (e.g., lower competition or fewer "gate-keepers"), scientists from neighboring fields enter. My paper builds on this literature by estimating the costs of scientific redirection in general and before outcomes are realized.

B *pmra* Algorithm Details

Lin and Wilbur (2007) develop a topic-based similarity model based on Bayes' Theorem that estimates the probability that an individual is interested in document a given expressed interest in document b, or in other words, what is the likelihood that a and b are scientifically

similar. They focus on the following relationship:

$$\Pr(a|b) \propto \sum_{j=1}^{N} \Pr(a|s_j) \Pr(b|s_j) \Pr(s_j),$$

where $\{s_1, ..., s_N\}$ denotes the entire set of mutually exclusive topics that could possibly be contained within a, b, or any other document of interest. Lin and Wilbur (2007) then make assumptions about the underlying arrival rates of terms within documents (Poisson) and how likely the occurrence of a term within a document actually reflects the true nature of that document. From these assumptions, the authors arrive at a topic weighting function, $w_{j,x}$, that describes that how important a topic s_j is to any document x, and a document scoring function, $Sim(a, b)$, that quantifies the similarity between a and b, given by:

$$w_{j,x} = \lambda_{j,x} \times \sqrt{\frac{1}{f_j}}$$

$$Sim(a, b) = \sum_{j=1}^{N} w_{j,a} \times w_{j,b},$$

where f_j is the frequency that topic s_j occurs in the universe and $\lambda_{j,x}$ is based on a series of Poisson arrival rate parameters and the number of times that topic s_j occurs in document x. Intuitively, two documents are more likely to be similar when they both use topics that are rare ($1/f_j \uparrow$) many times ($\lambda_{j,x} \uparrow$). The authors estimate, optimize and experimentally confirm parameters within $\lambda_{j,x}$ to align with human assessments. Loosely speaking, this approach is analogous to the cosine similarity approach previously used to estimate scientific similarity (i.e., Boudreau et al. (2016)), here, weighted by the rarity of intersecting topics.

For specific details on the algorithm and how topics are defined, see Lin and Wilbur (2007), and for a broader overview of how this algorithm is implemented at the National Library of Medicine, see https://goo.gl/PbvpvW, accessed July 12, 2017.

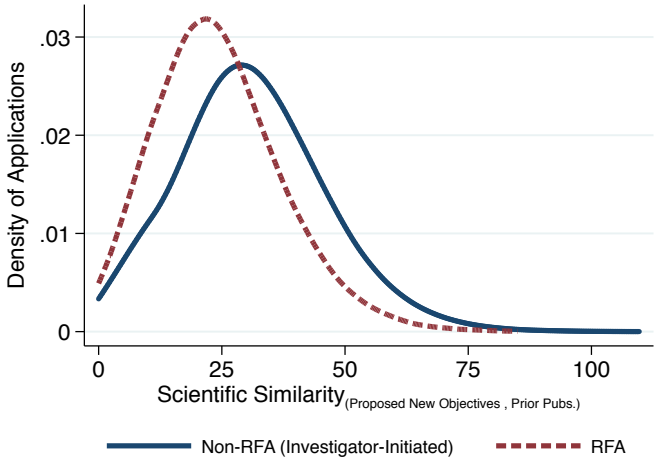
C Full Application Similarity Distribution, RFA v. Open

D Entry Model Similarity Adjustment

Figure III.4 plots the scientist-application similarity as a function of the scientist-RFA similarity. If the first metric (observable for entrants only) is equivalent to the second (observable for all), then there should be a 1:1 relationship between these variables and each data point would lie on the 45 degree line. However, it is clear in Figure III.4 Panel (a) that this is not the case. It appears that relative (percentage) increases in the scientist-RFA similarity implies level (absolute) increases in the scientist-application similarity.

Figure III.4 Panel (b) uses a log-transformation of scientist-RFA metric to explore this log-linear relationship, which fits the data very well. Given the good fit, I predict scientist-application scores using this log-linear model. This predicted value represents, on average,

Figure III.3: Distribution of Application-Scientist Similarity Scores



Includes all new, R01 applications.

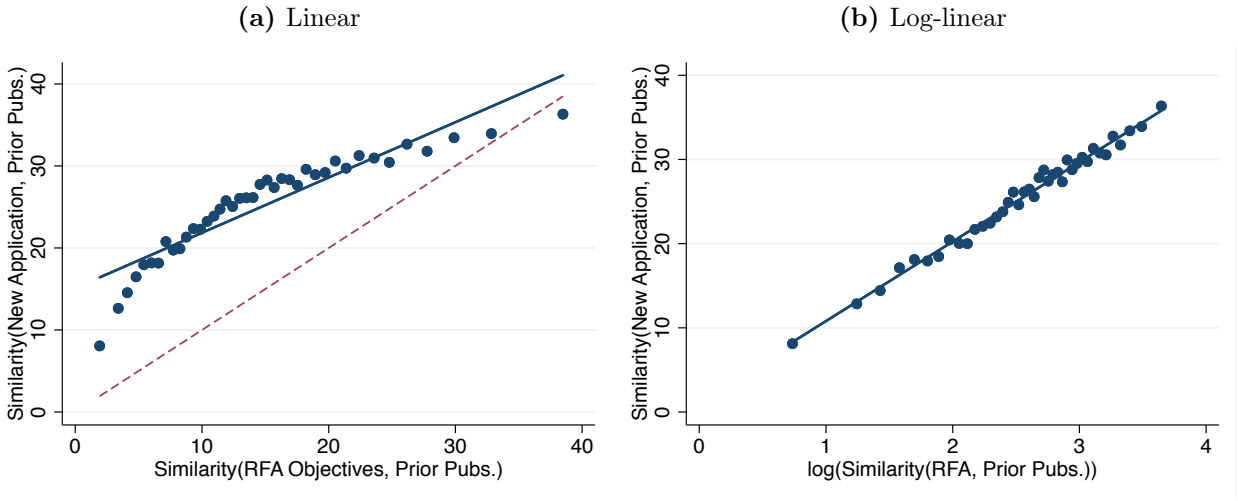
how large of a redirection each scientist would require to enter an RFA given their observed scientist-RFA similarity score. This predicted value represents, on average, how large of a redirection each scientist would require to enter an RFA given their observed scientist-RFA similarity score.

E Qualitative Interpretation

The following two figures (III.5 and III.6) plot the empirical distribution and statistics of *pmra* scores from NIH applications, based on scientists prior publications and their new application. The example figures are generated to consider a publication from the biomedical (III.5) or economics literatures (III.6) as a focal project, e.g., a scientist's most recent work, and ask what would that scientist's next project look like given the NIH sample moments. The focal projects are plotted at the average *pmra* score for documents scored against itself, with three expected "next projects" plotted at the NIH sample mean and a $+/-$ one standard deviation increase (more similar) and decrease (less similar) using those publications approximate *pmra* scores relative to the focal publication.[6] The mean indicates what the average "next project" would look like, and is flanked by projects at $+/-$ 1 standard deviation more/less similar. The figures make clear that virologists developing vaccines for viral diseases and economists studying pharmaceutical R&D tend to keep doing so. Restating the focal result, the analyses suggests that these example scientists (who wrote the "focal" papers) are indifferent between pursuing the mean next-project instead of the + 1 s.d. next-project and a fourfold increase in NIH grant funding (in expectation).

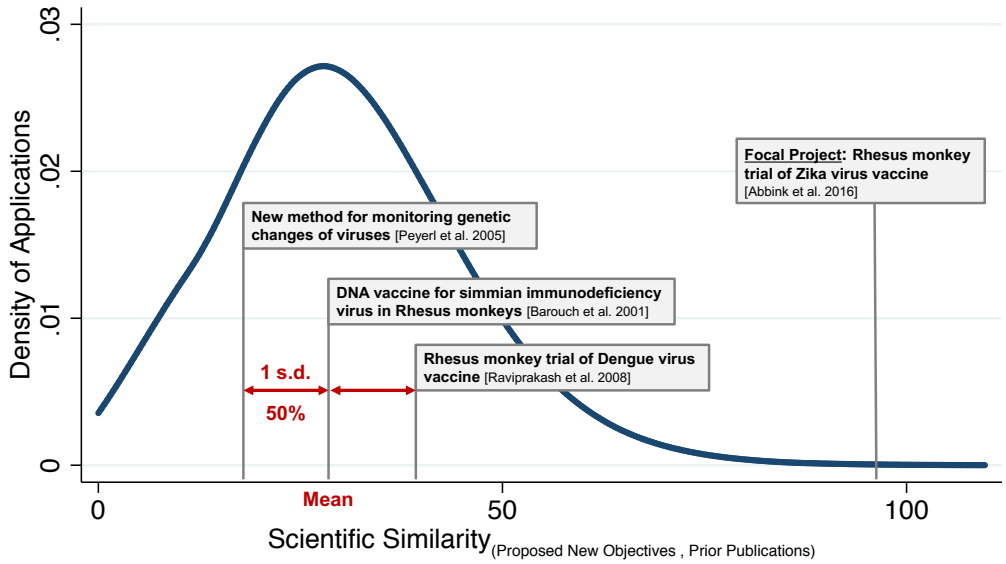
[6]The focal publications are plotted at the average *pmra* score for documents scored against itself, noting that *pmra* scores are likelihoods, not percentages.

Figure III.4: Relationship between Similarity Scores for Entrants



Note: Binned scatterplots ($N_{bins} = 40$) of *pmra*-generated similarity scores for scientists that enter an RFA with fitted lines in solid, and dashed 45°. Plots the "distance-needed" (x-axis) and the "distance-traveled" (y-axis).

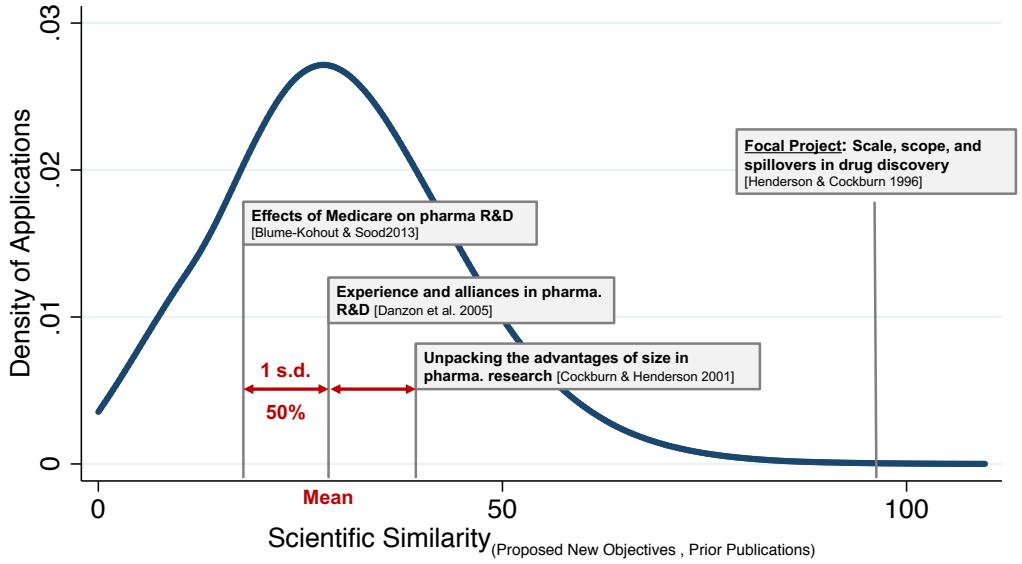
Figure III.5: *pmra* Distribution: Biomedical Examples



Citations:

1. Abbink et al. (2016). Protective Efficacy of Multiple Vaccine Platforms Against Zika Virus Challenge in Rhesus Monkeys. *Science*, 353(6304): 1129?1132.
2. Raviprakash et al. (2008). A tetravalent dengue vaccine based on a complex adenovirus vector provides significant protection in rhesus monkeys against all four serotypes of dengue virus. *Journal of Virology*, 82(14):6927-6934.
3. Barouch et al. (2001). Elicitation of high-frequency cytotoxic T-lymphocyte responses against both dominant and subdominant simian-human immunodeficiency virus epitopes by DNA vaccination of rhesus monkeys. *Journal of Virology*, 75(5):2462-2467.
4. Peyerl et al. (2005). Use of molecular beacons for rapid, real-time, quantitative monitoring of cytotoxic T-lymphocyte epitope mutations in simian immunodeficiency virus. *Journal of Clinical Microbiology*, 43(9):4773-4779.

Figure III.6: *pmra* Distribution: Economics Examples



Citations:

1. Henderson & Cockburn (1996). Scale, scope, and spillovers: the determinants of research productivity in drug discovery. *The RAND Journal of Economics*, 27(1): 32-59.
2. Cockburn & Henderson (2001). Scale and scope in drug development: unpacking the advantages of size in pharmaceutical research. *Journal of Health Economics*, 20(6): 1033-1057.
3. Danzon et al. (2005) Productivity in pharmaceutical-biotechnology R&D: the role of experience and alliances. *Journal of Health Economics*, 24(2): 317-339.
4. Blume-Kohout & Sood (2013). Market size and innovation: Effects of Medicare Part D on pharmaceutical research and development. *Journal of Public Economics*, 97: 327-336.

Appendix IV Controlling for Strategic Interactions

In this setting, scientists observe all RFAs and must incur some costs to enter.[7] These costs are a function of, among other things, the scientific similarity between the individual's prior work and the RFA objectives, s. All potential entrants $i = \{1, 2, ..., N\}$ observe each RFA j, which are characterized by the total amount of funds available (p_j), the expected number of competitors ($\hat{n}_{ij} = \{1, 2, ..., N-1\}$), a vector of observable characteristics ($\mathbf{X}_j$; e.g., year, NIH Institute), and all other characteristics valued by scientists but unobservable to the econometrician (ξ_{ij}). A "revenue" function W and entry cost function C are based on these variables[8], such that each individual's expected payoff from entry is given by:

$$V_{ij} = W(s_{ik}\,,\, p_j\,,\, \hat{n}_{ik}\,,\, \mathbf{X}_k\,,\, \xi_{ik}) - C(\mathbf{X}_k\,,\, s_{ik}\,,\, \xi_{ik}). \tag{1}$$

Assuming that W is linear in its parameters yields the main estimating equation

$$\mathbf{1}\{\text{Entry}_{ij}\} = F(s_{ij}) + G(p_j) + \delta\hat{n}_{ij} + \boldsymbol{\gamma}\mathbf{X}_j + (\xi_{ij} + \mu_{ij}). \tag{2}$$

where μ_{ij} are i.i.d. mean-zero error terms that capture random noise in scientists' decisions. Because each individual is extremely small relative to the full set of potential entrants, I assume that scientists are atomistic in the sense that they are oblivious to any effect their particular decision has on the rest of the sample.[9]

Note that whereas $\mathbf{X}_j$, s_{ij}, and ξ_{ij} enter Equation 1 through both W and C, they enter Equation 2 once and in a separable manner. Therefore, I simply interpret the partial derivatives as encompassing the cumulative costs and benefits of the independent variables.

The elasticity of science with respect to purse size is $\varepsilon \equiv \frac{\partial s_{ij}}{\partial p_j} = \frac{\partial V_{ij}}{\partial p_j} / \frac{\partial V_{ij}}{\partial s_{ij}}$. Scientists trade off the "market size" (p_j) for redirections, holding fixed their competitive expectations.

The difficulty in estimating Eq. 2 is that, instead of competitive expectations ($\hat{n}_{ij}$), only the realized number of entrants (n_{ij}) is observed. Now, if $\mathbb{E}[\xi_{ij} \,|\, p_j, \hat{n}_{ij}, s_{ij}, \mathbf{X}_j] \neq 0$, then each scientist's likelihood of entry will be positively correlated. This will create an endogeneity problem if Equation 2 is estimated with n_{ij} instead of $\hat{n}_{ij}$, where estimates of G will be biased upwards and then, potentially, F downward.[10]

To address this issue, I use the procedure for estimating static strategic interactions outlined by Bajari et al. (2010).[11] $\hat{n}_{ij}$ can be estimated empirically if a variable exists that influences each individual's strategic choice *directly* but only influences others' choices via the *indirect*

[7] Scientists also have the outside options of applying to the default open competitions or not at all. I assume the value of this outside option is fixed conditional on the covariates, which includes time- and individual-fixed effects.

[8] The W function also describes the rules by which the purse is allocated amongst entrants.

[9] That is, there are no general equilibrium effects from any single scientist's decision. This is very reasonable given there are roughly 140,000 potential entrants, and about 16,000 unique individuals apply to the NIH in my data annually.

[10] This will depend on how correlated scientists preferences are for the unobservable features of RFAs (ξ_{ij}). As this correlation increases, so to will the correlation in entry probabilities across the sample, giving rise to a positive correlation between $\Pr(\text{Entry}_{ij})$ and n_{ij}.

[11] While there may certainly be dynamics with respect to each scientist's decision to purse a particular

effect of those strategic choices. One needs a variable that satisfies this "strategic exclusion restriction". In the model outlined above, similarity provides a valid instrument under the assumption that each scientist's similarity to an RFA is exogenous and does not directly influence any other scientists' behaviors.[12]

The underlying information structure assumed in this approach is that scientists know (1) the revenue and cost functions ($W(\cdot)$ and $C(\cdot)$), (2) the features of the RFA (p_j, $\mathbf{X}_j$), and (3) the number of other scientists (N), their similarities (s_{ij}) and the distribution of unobservables (ξ_{ij}). Given this information, they can integrate over the distribution of predicted entry probabilities to form their expectations and then make their entry decisions.[13]

The estimation procedure is a similar process as follows:

1. Regress entry decision ($\text{Entry}_{ij} = \{0, 1\}$) on the vector of exogenous RFA characteristics: p_j , $\mathbf{X}_j$, s_{ij}
2. Predict entry probabilities, $\Pr(\widehat{\text{Entry}}_{ik})$ with parameters from Step 1
3. Sum predicted entry probabilities over each RFA, minus each individual's entry probability to estimate $\hat{n}_{ij}$, given by $\widetilde{n_{ij}} = \sum_{i' \neq i}^{N} \Pr(\widehat{\text{Entry}}_{i'j})$
4. Estimate Eq. 2 using $\widetilde{n_{ij}}$ in place of $\hat{n}_{ij}$

I estimate the regressions in Steps 1 and 4 via OLS. As is common to these estimators, I must assume that a single unique equilibrium is played in the data.[14] Fixed effects at the levels of scientists, years and funding Institutes allows for unobserved heterogeneity across these dimensions.

RFA (e.g., how would moving to topic A effect future research prospects?), the limited recurrence of RFAs and the massive scale of the default open competitions, which present a future option for funding, suggest that *competitive* dynamics are likely not first-order concern. Not at any time in discussions with scientists who have competed in RFAs did the notion of dynamic strategic interactions arise.

[12] One mechanism that may invalidate this assumption is if a scientist's likelihood of communicating with potential entrants is correlated with their similarity to an RFA. Anecdotal discussions with NIH applications who have competed in RFAs did not suggest this is relevant.

[13] These predicted probabilities are often referred to as "conditional choice probabilities". The two steps of these methods involve (1) the estimation of the conditional choice probabilities, and (2) the estimation of the full model including these probabilities. For clarity, I present the approach in four stages.

[14] I am rather restricted from relaxing this assumption because purse size does not vary within each RFA, so G is not identified by within-RFA variation which is the sort of variation necessary for a more lax assumption that a unique equilibrium is played within each RFA.

Appendix V Motivating Theory

To motivate the analyses, consider a world where each scientist $i = \{1, 2, ..., N\}$ can costlessly adjust the trajectories of their research. In this world, they receive the outside option of 0, or can compete for research funding by submitting proposals to one of two competitions $j = \{1, 2\}$, where each a submission's quality is based on scientists' random draws from i.i.d. quality distributions.

In the competitions, funds are allocated based on an award function W, which is well-behaved and maps three variables into awards: (1) each submission's quality q_{ij}; (2) the vector of other submissions $\mathbf{q_j}$, where $n_j \leq (N-1)$ is the number of each submission's competition; (3) the total funds available P_j. Realized awards are then given by $w_{ij} = W(q_{ij}, \mathbf{q_j}, P_j)$. It is assumed that $\frac{\partial W}{\partial q_{ij}} > 0$ and $\frac{\partial W}{\partial N_j} < 0$; higher quality applications in less contested competitions perform better. Furthermore, assume that each individual is extremely small relative to the full set of potential entrants, so although individuals may form strategic expectations about n_j, the general equilibrium effects are negligible; scientists are atomistic.[15]

Let the expected payoff from entry into j simply be $V_{ij} = \mathbb{E}[w_{ij}] - c$, where entry costs c are constant across scientists and competitions. In this case, scientists enter $j = 1$ if three conditions hold: (1) $V_{i1} > 0$, (2) $\mathbb{E}[w_{i1}] > c$, and (3) $\mathbb{E}[w_{i1}] > \mathbb{E}[w_{i2}]$. Clearly, in equilibrium both options, regardless of the amount of funds are made available, should see competition to the point that their expected values are equivalent. If the payoff of entering one of the competitions is larger, then the "free-range" scientists will simply enter and compete down the expected value until it equates with the alternative. This world embodies the zero-profit nature of perfectly competitive markets with free entry.

If the entry costs to one of the competitions is increased, say $c_1 > c_2$, then in equilibrium $\mathbb{E}[w_{i1}] > \mathbb{E}[w_{i2}]$ and most relevant for the analysis, $c_1 - c_2 = \mathbb{E}[w_{i1}] - \mathbb{E}[w_{i2}]$. This implication is a staple of traditional industrial organization models where markets with higher fixed costs also have larger profit margins. And thus, with unbiased estimates of expected payoffs in hand, one can compute the difference in entry costs.

More specifically though, in this setting I am interested in estimating how a certain feature of these competitions - the degree to which they require scientists to adjust their work - might influence entry costs, and therefore, create a wedge in expected payoffs. Rewrite V_{ij} to now be $\mathbb{E}[w_{ij}] - c(s_{ij}, \xi_j)$ with s_{ij} describing the similarity between individual i's scientific expertise and the type of science required for entry into j, and ξ_j capturing the (potentially zero) fixed value all scientists place on j. First, assume that only this similarity factor influence costs and thus, $\xi_j = 0$. Then it follows that on average $c(\widehat{s_{i1}}) - c(\widehat{s_{i2}}) = \widehat{\mathbb{E}[w_{i1}]} - \widehat{\mathbb{E}[w_{i2}]}$, where $\widehat{x}$ denotes the average of variable x across all i. This relationship implies that $\frac{\partial V_j}{\partial \widehat{s_{ij}}} = \frac{\partial V_j}{\partial \widehat{\mathbb{E}[w_{ij}]}}$, providing a way to relate the average marginal gains in expected awards to average marginal differences in similarity - precisely the elasticity of interest: $\frac{\partial \widehat{s_{ij}}}{\partial \widehat{\mathbb{E}[w_{ij}]}}$, or how large of a change in science can be induced by a given change in funds?

[15] In the sample used for this analysis, there are roughly 16,000 unique applicants to the NIH per year.

Taken together, if $\xi_j = 0$, and I can empirically estimate (1) the difference in expected awards between the RFA and open mechanisms that arises from the NIH's exogenous allocation decisions and scientists' endogenous responses ($\widehat{\partial \mathbb{E}[w_{ij}]}$) - the "RFA premium" - as well as (2) the average level of redirection that RFAs induce beyond what is observed in the open applications ($\widehat{\partial s_{ij}}$), then I can identify the elasticity.

However, if $\xi_j \neq 0$, then I will instead be estimating $c(\widehat{s_{i1}}, \xi_1) - c(\widehat{s_{i2}}, \xi_2)$ and conflate the costs of changes in s with some fixed costs (or benefits) captured by ξ_j. In this case I can only clearly estimate the RFA premium ($\widehat{\mathbb{E}[w_{i1}]} - \widehat{\mathbb{E}[w_{i2}]}$), and will overestimate (underestimate) the elasticity if $\xi_j > 0$ ($\xi_j < 0$).

Appendix VI Robustness Tests and Summary Statistics

Table VI.1: Entry Determinants–Robustness Tests

(All coefficients scaled by 10^{-4})

	Entry$_{ij}$					
	(1)	(2)	(3)	(4)	(5)	(6)
Purse$_j$	2.38	4.11	3.73	6.99	2.48	4.73
	(0.555)	(0.500)	(0.00687)	(0.00636)	(0.00629)	(0.00517)
Similarity$_{ij}$	16.2	17.5	9.90	10.9	12.4	15.1
	(0.660)	(0.694)	(3.86)	(4.10)	(0.525)	(0.579)
Competitive		–4.84		–4.34		–5.37
Expectations$_{ij}$		(0.275)		(0.279)		(0.320)
pmra pub. set	≤5 years		≤5 years		all	
pmra score	max		max		median	
Indep. var. transform.	std.		log		std.	

	Entry$_{ij}$			
	(7)	(8)	(9)	(10)
Purse$_j$	2.58	4.81	2.36	4.17
	(0.640)	(0.518)	(0.559)	(0.503)
Similarity$_{ij}$	16.3	20.0	21.1	23.5
	(0.666)	(0.756)	(0.829)	(0.890)
Competitive		–6.03		–4.68
Expectations$_{ij}$		(0.338)		(0.278)
pmra pub. set	all		all	
pmra score	avg.		max	
Indep. var. transform.	std.		std.	

Note: All models include 20,221,541 Scientist-RFA (ij) pair observations, where the mean entry probability is 5.47×10^{-4}. All specifications include the RFA controls and scientist fixed effects.

Table VI.2: RFA versus Open Application Robustness Tests: Award Size

	log(Award Size$_{ijst}$)			
	(1)	(2)	(3)	(4)
$\mathbf{1}\{\text{RFA}_j\}$	0.0824	0.0798	0.199	0.114
	(0.0162)	(0.0161)	(0.0401)	(0.0460)
$N_{applications}$	8,242	8,691	1,123	1,533
$N_{scientists}$	7,445	7,810	529	717
mean(Dep. Var.)	399,237	1,911,925	416,968	2,010,625
Version	1^{st} Year Tot. Costs	All Year Tot. Costs	1^{st} Year Tot. Costs	All Year Tot. Costs
Area-Time F.E.	Y	Y	Y	Y
Scientist F.E.			Y	Y

Note: Standard errors clustered within scientists. Estimates of Equation (5) using alternative specifications and transformations. Total Costs refer to the sum of both Direct and Indirect costs awarded, with All Year costs referring to the total amount of funds awarded over the lifespan of the focal grant award.

Table VI.3: Summary Statistics for Applications Examined in Section 5

	Open	RFA
	(1)	(2)
N apps.	367.3	24.87
in group	(229.4)	(14.96)
N winning apps.	159.1	9.139
in group	(97.37)	(6.027)
Fiscal Year	2004.0	2003.5
	(1.362)	(1.488)
$Requested	1,860,198.8	1,868,188.0
	(1,155,353.7)	(1,282,384.4)
Peer Review Score	198.4	216.6
	(51.38)	(54.84)
Pr(Win)	0.504	0.468
	(0.500)	(0.499)
Study involves	0.506	0.427
animals	(0.500)	(0.495)
Study involves	0.384	0.602
humans	(0.486)	(0.490)
Study involves	0.256	0.401
children	(0.437)	(0.490)
Is "New Investigator"	0.259	0.195
	(0.438)	(0.396)
Has M.D.	0.300	0.378
	(0.458)	(0.485)
Has Ph.D.	0.821	0.750
	(0.383)	(0.433)
Year of First R01	1995.8	1995.9
	(9.215)	(8.839)
Year of First RPG	1995.7	1995.7
	(9.215)	(8.839)
Pre, N F/L Pubs	17.46	17.26
	(16.42)	(16.10)
Pre, Avg. F/L JIF	10.26	8.998
	(23.56)	(20.05)
Pre, Avg. Similarity F/L Pubs		83.11
		(123.3)
Post, N F/L Pubs	9.023	10.31
	(9.402)	(10.35)
Post, Avg. F/L JIF	4.189	4.219
	(11.19)	(10.70)
Post, Avg. Similarity F/L Pubs		59.06
		(100.5)
Obs.	29,488	4,949

Note: Mean, s.d. in parentheses. "F/L" includes only publications where the scientist is the first or last author. "JIF" is Journal Impact Factor.

Table VI.4: Grant Productivity–First Stage

	$\mathbf{1}\{\text{Win}_{jk}\}$				
	(1)	(2)	(3)	(4)	(5)
Panel A: Open Applications					
std(Funding Distance IV_{jk})	–0.245 (0.0119)	–0.246 (0.0119)	–0.249 (0.0117)	–0.241 (0.00964)	–0.267 (0.00917)
F-stat.	226.7	226.7	232.12	138.06	138.06
N Obs.	29,488	29,488	29,488	29,488	29,488
Panel B: RFA Applications					
std(Funding Distance IV_{jk})	–0.166 (0.0130)	–0.166 (0.0130)	–0.168 (0.0129)	–0.188 (0.0153)	–0.207 (0.0149)
F-stat.	51.3	51.3	50.6	57.7	57.7
N Obs.	4,949	4,949	4,949	4,949	4,949
Project **X**		Y			Y
People **X**			Y		Y
Fund. Group F.E.				Y	Y

Notes: This table reports the first stage estimates from for Table 3 columns 2–6, with the estimates in Panel A and B of columns 1 corresponding to the two endogenous variables in Table 3 column 2 (winning an open grant and an RFA grant). All regressions are based on LASSO selection of covariates, and include institute-year fixed effects, except for columns 5 and 6 given the funding group fixed effects which are all within institute-years. Standard errors clustered at funding groups in parentheses.

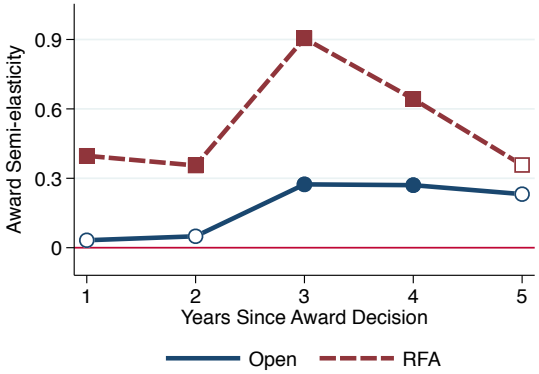
Table VI.5: Grant Productivity–Publication Impact

	IHS(Avg. Pub. JIF_{jk})					
	(1)	(2)	(3)	(4)	(5)	(6)
1{Win, $Open_{jk}$}	0.0341	0.0808	0.0752	0.0742	0.0559	0.0708
	(0.00682)	(0.0322)	(0.0320)	(0.0278)	(0.0271)	(0.0257)
1{Win, RFA_{jk}}	0.0240	0.150	0.168	0.0873	0.0482	0.0709
	(0.0162)	(0.0542)	(0.0553)	(0.0515)	(0.0309)	(0.0299)
Semi-elast. Open	0.035	0.084	0.078	0.077	0.057	0.073
Semi-elast. RFA	0.020	0.160	0.181	0.090	0.049	0.073
p-value diff.	0.56	0.21	0.10	0.80	0.79	0.99
N Obs.	28,527	28,527	28,527	28,527	28,527	28,527
I.V.		Y	Y	Y	Y	Y
F-stat.		289.1	289.1	289.0	4,328.6	7,898.8
Project **X**			Y			Y
People **X**				Y		Y
Fund. Group F.E.					Y	Y
LASSO $Var_{sel/poss}$		5/9	16/31	23/256	5/9	11/354

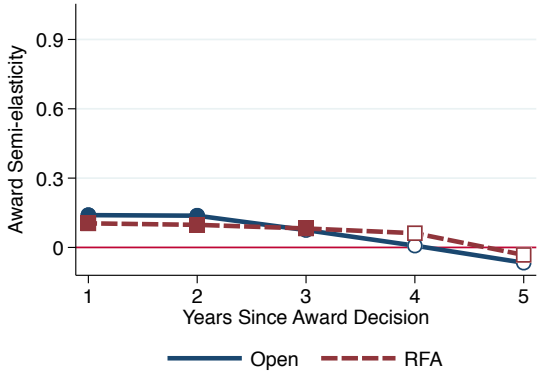
Notes: This table reports 2SLS estimates from Equation 9. The average applicant published articles with JIFs of 0.434 post-decision. Project and People **X** indicates whether covariates specific to the application (i.e., funds requested) and/or the applicant (i.e., publication history) are included. *LASSO* $Var_{sel/poss}$ reports the number of *LASSO* selected and possible covariates. All regressions include institute-year fixed effects, except for columns 5 and 6 given the funding group fixed effects which are all within institute-years. Standard errors clustered at funding groups in parentheses.

Figure VI.7: Grant Productivity–Event Studies

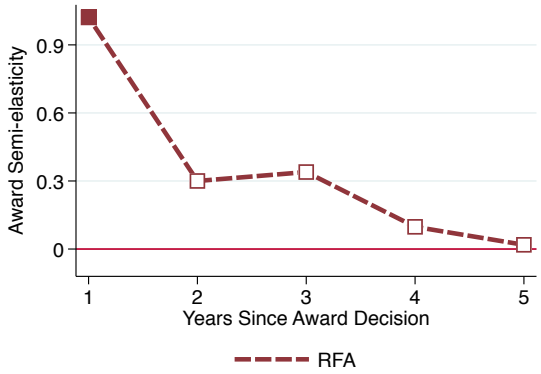
(a) Pub. Count–I.V.



(b) Pub. Count–I.V. and All Controls



(c) Pub. Similarity–I.V. and All Controls



Notes: This figure plots the RFA/open-specific β coefficients from Equation **??**, each relative time period representing a separate regression. Hollow markers indicate that zero is included in 95 percent confidence intervals.

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