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A comment on "Crisis and the Trajectory of Science: Evidence from the 2014 Ebola Outbreak"

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February 20, 2026

Abstract

This report replicates and extends the empirical analysis of Fry (2023), which studies the impact of the 2014 West African Ebola epidemic on the scientific productivity of researchers in Guinea, Liberia, and Sierra Leone. Using the replication package provided by the author, we exactly reproduce all main results, confirming the study's computational reproducibility. We further assess robustness with respect to alternative regression models, sample definitions, and matching procedures. While the main findings are robust across specifications, we find that the estimated effects are largely driven by researchers based in Sierra Leone, highlighting the importance of heterogeneity within the treated group.

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1 Introduction

This report presents a replication and extension of the empirical analysis in Fry (2023), which studies the impact of the 2014 West African Ebola epidemic on the scientific productivity of researchers based in the most affected countries. The original paper focuses on Guinea, Liberia, and Sierra Leone, where the outbreak resulted in more than 11,000 deaths and triggered a sharp increase in global scientific attention and funding, with approximately USD 435 million allocated to Ebola-related research, largely from OECD countries.

Using publication records from the Elsevier Scopus database, Fry (2023) examines how scientists in these endemic countries adjusted their research activity in response to the epidemic. The empirical strategy relies on a difference-in-differences design that compares the publication outcomes of scientists located in Ebola-affected countries before and after the outbreak to those of matched scientists in non-affected West and Central African countries. The final dataset consists of a balanced panel of 589 scientists observed between 2010 and 2019.

The main findings indicate a substantial reallocation of research effort toward Ebola-related topics among scientists in affected countries, accompanied by a pronounced decline in non-Ebola publications. On average, non-Ebola output falls by approximately 49 percent, while Ebola-related publications increase markedly. The paper further documents strong heterogeneity: scientists with prior experience in neglected tropical diseases (NTDs) increase their overall publication output, whereas scientists without such experience a decline in productivity.

Prepared for the Institute for Replication (Brodeur *et* al. 2024), this report pursues three objectives. First, we assess the computational reproducibility of the main results by reproducing the key tables and figures using the author's publicly available data and code. Second, we evaluate the robustness of the findings to alternative matching choices and estimation specifications. Third, we examine the sensitivity of the results to additional data-handling decisions and sample restrictions. Together, these exercises provide a comprehensive assessment of the credibility and stability of the original empirical findings.

2 Computational reproducibility

We use the replication package associated with Fry (2023), provided via the Harvard Dataverse, to assess the computational reproducibility of the study. The replication package contains the final processed and cleaned dataset used for the analysis. The Coarsened Exact Matching (CEM) procedure that matches scientists located in Ebola-affected countries with scientists in non-affected West and Central African countries was carried out prior to the construction of the final dataset and is therefore not included in the provided Stata files.

Using the materials contained in the replication package, we successfully reproduced all tables and figures reported in the original paper and its appendix.[1]

To further assess reproducibility, the Institute for Replication contacted the original author, who provided access to pre-matched and partially pre-cleaned data.

[1] We identified one minor typographical error in column 1b of Table 3: the standard error for `AFTER EPIDEMIC` × `ENDEMIC COUNTRY` × `NTD EXPERIENCE` is reported as 0.57 instead of 0.55. This discrepancy does not affect any of the reported results or conclusions.

Using this intermediate dataset, we successfully reconstructed the final dataset included in the replication package and were thus able to reproduce the study's findings. See Table 1 for details. As the underlying raw data originate from the proprietary Elsevier Scopus publication database, direct access to the raw data was not possible.

3 Robustness

We implement various robustness checks focusing on the main results reported in Table 2 of the original study. These tests concern (i) the choice of the regression model, (ii) the sample selection, and (iii) the matching procedure. First, we employ an alternative regression model using the final dataset included in the replication package. Second, we test the sensitivity of the results to changes in the sample composition. In this test, we exclude researchers from one of the three endemic countries at a time (i.e., Guinea, Sierra Leone, or Liberia). Lastly, we conduct checks on the matching procedure undertaken by Fry (2023) regarding matching quality. We provide alternative matching procedures.

3.1 Alternative regression models

In this subsection, we assess whether the results presented in Table 2 of the original study remain robust when alternative regression models are employed. All estimations are conducted using the final dataset provided in the replication package. Panel A of Table 2 reproduces the original findings based on quasi-maximum likelihood fixed-effects Poisson specifications. Since the dependent variables, the *number of publications* (mean = 0.810, variance = 1.539) and the *number of non-Ebola publications* (mean = 0.776, variance = 1.366), exhibit overdispersion, we additionally estimate fixed-effects negative binomial models in Panel B. The resulting estimates remain qualitatively similar.

Furthermore, we estimate fixed-effects Poisson models in Panel C and linear regressions with multiple fixed effects using the *reghdfe* command in Stata in Panel D. Both alternative approaches yield results that are comparable in sign and magnitude to the baseline estimates, supporting the robustness of the original findings with respect to the choice of regression model.

3.2 Sample selection

In the original study, researchers from the three endemic countries (Guinea, Sierra Leone, and Liberia) are classified as treated. Using the final dataset provided in the replication package, we re-estimate the main specifications reported in Table 2 of Fry (2023), sequentially excluding researchers from one treated country at a time. Panel A of Table 3 reports the original estimates.

Panel B excludes the 26 scientists from Guinea and focuses on the remaining 31 treated scientists from Sierra Leone and Liberia. The results are similar to those reported in the original study: scientists with prior NTD experience in endemic countries produce more publications (column 1b). A positive, though statistically insignificant, effect is also observed for non-Ebola publications (column 2b), consistent with the baseline estimates.

Panel C excludes the 25 scientists from Sierra Leone and retains only researchers from Guinea and Liberia among the treated scientists. In this case, the results change notably, indicating that Sierra Leone plays a central role in driving the main findings. Scientists from Guinea and Liberia with prior NTD experience publish fewer total and non-Ebola publications relative to scientists from non-endemic countries (columns 1b and 2b). Moreover, the interaction term `EBOLA CASES (1,000s)` × `NTD EXPERIENCE` becomes negative and statistically significant (column 4b).

Finally, Panel D excludes the six scientists from Liberia and focuses on Guinea and Sierra Leone. The estimates are again very similar to those reported in Panel A and in Panel B. Taken together, these results suggest that the main findings are largely driven by treated scientists based in Sierra Leone, the country most severely affected by the Ebola epidemic.

3.3 Matching

Fry (2023) exploits a quasi-experimental setting by defining the Ebola outbreak in three West African countries as the treatment, affecting scientists affiliated with institutions located in these countries. To construct a comparison group, the author selects scientists from other West and Central African countries that were not affected by the Ebola outbreak. Given the substantial heterogeneity across scientists and countries, a matching procedure is employed to improve comparability between treatment and control groups prior to estimation.

The matching procedure is implemented using Coarsened Exact Matching (CEM), which allows for inexact matches by grouping continuous variables into discrete categories (Blackwell et al. 2009). In this replication, we examine the sensitivity of the results to the coarsening choices made in the original study and explore alternative matching approaches, assessing how these choices affect covariate balance and subsequent estimation results.

In the original analysis, scientists are grouped into two categories based on a binary indicator for career age, with a cut-off at 21 years.[2] While this threshold is not explicitly discussed in the paper or the replication code, it results in an imbalanced split, with 84% of scientists classified as younger and 16% as older. Figure 1 presents the distribution of career age for each endemic country and for the pooled endemic countries, compared to non-endemic countries. The figure suggests that the cut-off at 21 years (red lines) does not clearly separate the distributions, relative to either the means or medians.

As an alternative, we consider a separation at the median career age of 9 years, or a quantile-based categorization into four groups: 0–6 (25%), 7–9 (50%), 10–17 (75%), and 18–54 (100%) years.

A similar issue arises for GDP per capita, which is grouped into four categories in the original matching procedure: USD 1,000 or less, USD 1,001–2,000, USD 2,001–3,000, and more than USD 3,000. As all three endemic countries fall below USD 1,000, this categorization effectively restricts matching to countries within the lowest income group. Figure 2 illustrates that these cut-offs (red lines) only partially distinguish the country distributions and treat all endemic countries as identical along this dimension, despite observable differences across them.

[2]Career age is defined as the number of years between an author's first publication and the event year 2014, corresponding to the Ebola outbreak.

To address this, we consider alternative GDP per capita groupings based on distributional breakpoints: USD 0–559 (25%), 560–806 (50%), 807–1,462 (75%), and 1,463–10,067 (100%).

Given the central role of matching in this quasi-experimental design, we assess balance between treatment and control groups using the propensity mean squared error (pMSE). Specifically, we regress the binary indicator `ENDEMIC COUNTRY` on the matching variables using a Generalized Linear Model with a binomial link function. We estimate two specifications: one using the coarsened variables employed in the original matching procedure, and one using the corresponding continuous measures. Estimated coefficients for both models are reported in Table 4 (column 1 & 2). If treatment and control groups were identical along a given dimension, the associated coefficient would not be statistically significant at conventional levels.

Consistent with the density plots, the regressions indicate that scientists in endemic countries tend to have higher career ages and are located in countries with slightly lower GDP per capita than their matched counterparts. Differences are also observed in journal impact factor categories and, to a lesser extent, in prior collaborations with OECD-based researchers. In contrast, pre-outbreak publication counts appear similar across groups, suggesting reasonable balance along this dimension.

Using predicted treatment probabilities from the regression models, we compute the pMSE with bounds between $[0, 1]$ as

$$p\text{MSE} = \frac{1}{N} \sum_{i=1}^{N} (\hat{p}_i - c)^2,$$

where $\hat{p}_i$ denotes the predicted probability that unit i belongs to the treatment group, c is the share of treated units, and N is the total number of observations (Snoke et al. 2018). Lower pMSE values indicate greater similarity between treatment and control groups in terms of the matching variables.

Comparing the original matching procedure with alternative specifications, we find that broader categorizations of career age and GDP per capita modestly improve balance, as reflected in lower pMSE values (Table 5). These improvements are primarily driven by adjustments to the GDP per capita groupings. Importantly, however, the estimated treatment effects remain largely unchanged across matching specifications, with neither the direction nor statistical significance of the main coefficients differing meaningfully from the original results. We therefore conclude that the findings in Fry (2023) are robust to reasonable alternative matching variable definitions.

4 Conclusion

This report assessed the computational reproducibility and robustness of the findings in Fry (2023), which examines how the 2014 West African Ebola epidemic affected the scientific productivity of researchers in Guinea, Liberia, and Sierra Leone. Using the author's replication package, we were able to exactly reproduce all main results, confirming the study's computational reproducibility.

We further evaluated the robustness of the findings to alternative estimation strategies and sample definitions. The main results are robust to the use of alternative regression models. However, leave-one-out analyses indicate that the docu-

mented effects are largely driven by researchers based in Sierra Leone, highlighting the importance of heterogeneity within the treated group.

Finally, we examined the sensitivity of the results to the matching procedure used to construct the control group. We find that modest adjustments to the categorical matching variables (particularly GDP per capita and career age) can improve covariate balance. While some coefficient estimates change slightly under alternative matching specifications, the main qualitative findings remain unchanged. These results suggest that, although matching choices matter for balance, the substantive conclusions of the original study are not sensitive to reasonable alternative implementations. The structural differences between the treatment and non-treatment groups in this pseudo-experiment remain an important topic for future research, as the extent to which results based on imperfect blocking, randomisation, or controlling can be generalised is not entirely clear.

Overall, given the underlying experimental design, while some results depend on country composition, the core qualitative conclusions of the original study remain largely robust.

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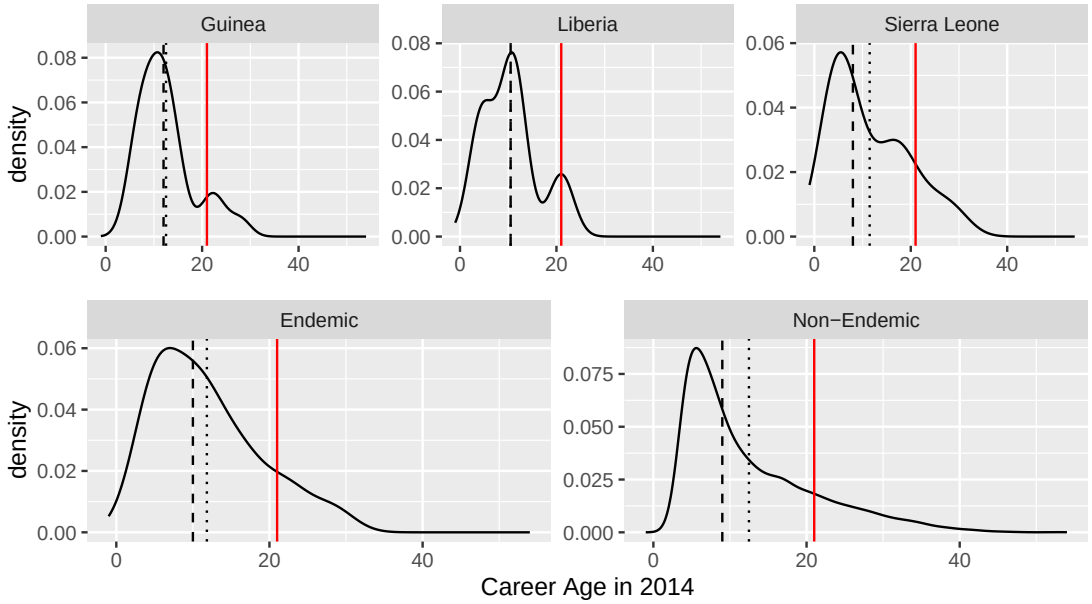
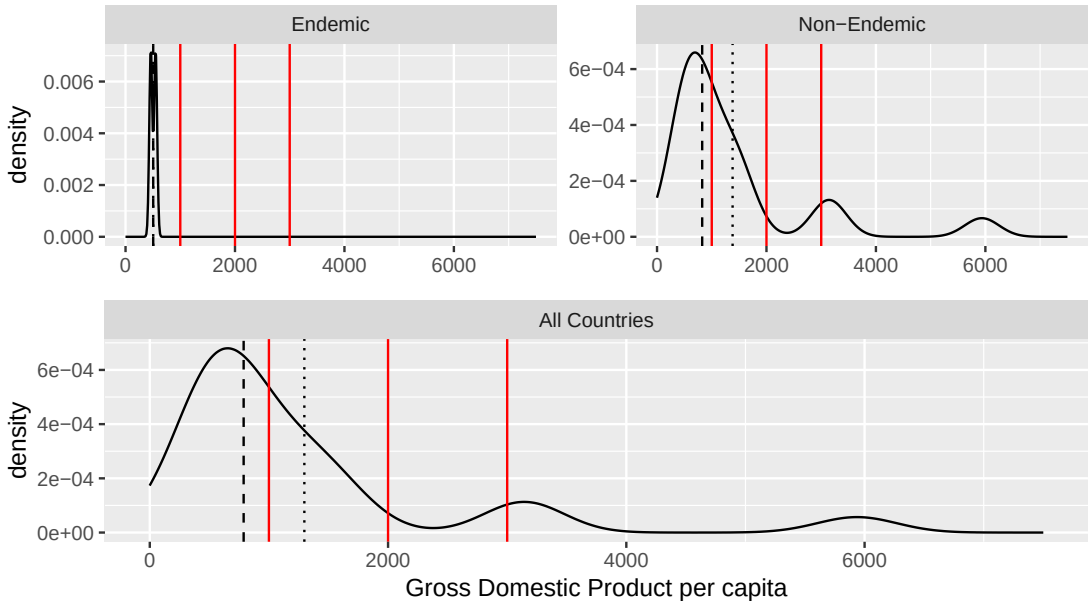
5 Figures



Red line: break point in original study; dashed line: median; dotted line: arithmetic mean

Figure 1: Distribution of career age in endemic and non-endemic countries



Red lines: break points in original study; dashed line: median; dotted line: arithmetic mean

Figure 2: Distribution of GDP per capita in endemic and non-endemic countries

6 Tables

Table 1: Replication Package Contents and Reproducibility

Replication Package Item	**Fully**	**On request**	**No**
Raw data provided			✓
Pre-processed data provided		✓	
Analysis data provided	✓		
Pre-Processing code provided			✓
Cleaning code provided		✓	
Analysis code provided	✓		
Reproducible from pre-processed data	✓		
Reproducible from analysis data	✓		

Notes: This table summarizes the replication package contents contained in Fry (2021).

Table 2: Alternative regression models

	Nb. pubs		Nb. non-Ebola pubs		Nb. pubs		Nb. non-Ebola pubs	
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Panel A: Original estimates using quasi-maximum likelihood fixed effects Poisson specifications								
After epidemic × endemic country	0.156	−0.546**	−0.402**	−0.697**				
	(0.192)	(0.270)	(0.160)	(0.272)				
	[0.419]	[0.043]	[0.012]	[0.010]				
After epidemic × endemic country		0.995***		0.453				
× NTD Experience		(0.337)		(0.319)				
		[0.003]		[0.156]				
Ebola cases (1,000s)					0.024	−0.065***	−0.036**	−0.079***
					(0.019)	(0.020)	(0.016)	(0.019)
					[0.215]	[0.001]	[0.025]	[0.000]
Ebola cases (1,000s)						0.128***		0.070***
× NTD Experience						(0.026)		(0.025)
						[0.000]		[0.005]
Observations	5890	5890	5870	5870	5890	5890	5870	5870
Log likelihood	-6521.57	-6510.99	-6369.29	-6367.40	-6519.29	-6498.00	-6369.89	-6364.82
Panel B: Negative binominal model								
After epidemic × endemic country	0.068	−0.398	−0.318*	−0.548**				
	(0.172)	(0.267)	(0.163)	(0.274)				
	[0.691]	[0.136]	[0.051]	[0.046]				
After epidemic × endemic country		0.727**		0.368				
× NTD Experience		(0.337)		(0.339)				
		[0.031]		[0.277]				
Ebola cases (1,000s)					0.014	−0.050**	−0.030**	−0.064***
					(0.016)	(0.020)	(0.015)	(0.022)
					[0.407]	[0.012]	[0.045]	[0.004]
Ebola cases (1,000s)						0.105***		0.060**
× NTD Experience						(0.024)		(0.030)
						[0.000]		[0.041]
Observations	5890	5890	5870	5870	5890	5890	5870	5870
Log likelihood	-5315.89	-5311.21	-5200.70	-5199.63	-5315.31	-5303.64	-5200.85	-5197.66
Panel C: Fixed-effects poisson model								
After epidemic × endemic country	0.156	−0.546**	−0.402**	−0.697**				
	(0.192)	(0.269)	(0.160)	(0.272)				
	[0.418]	[0.043]	[0.012]	[0.010]				
After epidemic × endemic country		0.995***		0.453				
× NTD Experience		(0.337)		(0.319)				
		[0.003]		[0.155]				
Ebola cases (1,000s)					0.024	−0.065***	−0.036**	−0.079***
					(0.019)	(0.020)	(0.016)	(0.019)
					[0.215]	[0.001]	[0.025]	[0.000]
Ebola cases (1,000s)						0.128***		0.070***
× NTD Experience						(0.026)		(0.025)
						[0.000]		[0.005]
Observations	5890	5890	5870	5870	5890	5890	5870	5870
Log likelihood	-5430.07	-5419.49	-5289.60	-5287.71	-5427.79	-5406.51	-5290.19	-5285.13
Panel D: Linear regressions with multiple fixed effects								
After epidemic × endemic country	0.136	−0.362**	−0.297***	−0.416***				
	(0.183)	(0.143)	(0.098)	(0.132)				
	[0.458]	[0.011]	[0.003]	[0.002]				
After epidemic × endemic country		0.917***		0.219				
× NTD Experience		(0.319)		(0.177)				
		[0.004]		[0.217]				
Ebola cases (1,000s)					0.029	−0.042***	−0.027***	−0.046***
					(0.024)	(0.013)	(0.010)	(0.011)
					[0.229]	[0.001]	[0.010]	[0.000]
Ebola cases (1,000s)						0.145***		0.039**
× NTD Experience						(0.038)		(0.018)
						[0.000]		[0.029]
Observations	5890	5890	5890	5890	5890	5890	5890	5890
Log likelihood	-8662.62	-8649.73	-8361.88	-8361.06	-8658.91	-8626.72	-8362.69	-8360.15

Notes: This table shows results from negative binominal models. Bootstrapped standard errors with 100 repitions are shown in parentheses and p-values in square brackets. All models include year and individual fixed-effects. Significance levels: * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$. Data source: Fry (2021).

Table 3: Leave-one-out analysis

	Nb. pubs		Nb. non-Ebola pubs		Nb. pubs		Nb. non-Ebola pubs	
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Panel A: Original results								
After epidemic × endemic country	0.156	−0.546**	−0.402**	−0.697**				
	(0.192)	(0.270)	(0.160)	(0.272)				
	[0.419]	[0.043]	[0.012]	[0.010]				
After epidemic × endemic country		0.995***		0.453				
× NTD Experience		(0.337)		(0.319)				
		[0.003]		[0.156]				
Ebola cases (1,000s)					0.024	−0.065***	−0.036**	−0.079***
					(0.019)	(0.020)	(0.016)	(0.019)
					[0.215]	[0.001]	[0.025]	[0.000]
Ebola cases (1,000s)						0.128***		0.070***
× NTD Experience						(0.026)		(0.025)
						[0.000]		[0.005]
Observations	5890	5890	5870	5870	5890	5890	5870	5870
Log pseudolikelihood	-6521.571	-6510.992	-6369.294	-6367.401	-6519.286	-6498.006	-6369.887	-6364.820
Panel B: Leaving out Guinea								
After epidemic × endemic country	0.314	−0.892***	−0.419**	−1.076***				
	(0.243)	(0.288)	(0.206)	(0.249)				
	[0.197]	[0.002]	[0.042]	[0.000]				
After epidemic × endemic country		1.783***		1.089***				
× NTD Experience		(0.358)		(0.326)				
		[0.000]		[0.001]				
Ebola cases (1,000s)					0.026	−0.071***	−0.033**	−0.084***
					(0.020)	(0.020)	(0.016)	(0.019)
					[0.187]	[0.001]	[0.040]	[0.000]
Ebola cases (1,000s)						0.141***		0.083***
× NTD Experience						(0.027)		(0.025)
						[0.000]		[0.001]
Observations	5630	5630	5610	5610	5630	5630	5610	5610
Log pseudolikelihood	-6288.929	-6266.170	-6157.493	-6150.559	-6288.296	-6263.810	-6157.142	-6150.315
Panel C: Leaving out Sierra Leone								
After epidemic × endemic country	−0.132	0.304	−0.472**	0.089				
	(0.186)	(0.283)	(0.203)	(0.329)				
	[0.478]	[0.282]	[0.020]	[0.788]				
After epidemic × endemic country		−0.580*		−0.765*				
× NTD Experience		(0.351)		(0.394)				
		[0.098]		[0.052]				
Ebola cases (1,000s)					−0.001	0.055	−0.086***	0.007
					(0.026)	(0.047)	(0.029)	(0.048)
					[0.963]	[0.241]	[0.003]	[0.882]
Ebola cases (1,000s)						−0.074		−0.130**
× NTD Experience						(0.056)		(0.056)
						[0.192]		[0.019]
Observations	5640	5640	5630	5630	5640	5640	5630	5630
Log pseudolikelihood	-6188.454	-6187.054	-6122.299	-6120.088	-6188.826	-6187.987	-6121.868	-6119.701
Panel D: Leaving out Liberia								
After epidemic × endemic country	0.169	−0.632**	−0.353**	−0.736**				
	(0.215)	(0.277)	(0.173)	(0.290)				
	[0.431]	[0.023]	[0.041]	[0.011]				
After epidemic × endemic country		1.149***		0.597*				
× NTD Experience		(0.357)		(0.339)				
		[0.001]		[0.078]				
Ebola cases (1,000s)					0.025	−0.075***	−0.031*	−0.084***
					(0.021)	(0.019)	(0.017)	(0.019)
					[0.234]	[0.000]	[0.069]	[0.000]
Ebola cases (1,000s)						0.147***		0.089***
× NTD Experience						(0.026)		(0.024)
						[0.000]		[0.000]
Observations	5830	5830	5810	5810	5830	5830	5810	5810
Log pseudolikelihood	-6457.504	-6445.002	-6318.702	-6315.751	-6455.267	-6430.544	-6319.182	-6311.880

Notes: This table shows results quasi-maximum likelihood fixed effects Poisson specifications. All models incorporate calendar year and scientist fixed effects and four career age category indicator variables. Heteroskedastic robust standard errors, clustered at the individual scientist level, are shown in parentheses and p-values in square brackets. Significance levels: * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$. Data source: Fry (2021).

Table 4: Regressing Treatment Indicator on Matching Variables

	Endogenous Indicator: Scientist in Endemic Country							
	Original Matching		Ext. GDP Matching		Ext. Age Matching		Ext. GDP+Age Matching	
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
GDP p.c. (binary)	n.A.		−0.682***		n.A.		−0.769***	
			(0.112)				(0.114)	
			[0.000]				[0.000]	
Career Age (binary)	1.095***		1.141***					
	(0.142)		(0.182)					
	[0.000]		[0.000]					
GDP p.c. (metric)		−0.002***		0.002***		−0.002***		0.002***
		(0.000)		(0.000)		(0.000)		(0.000)
		[0.000]		[0.000]		[0.000]		[0.000]
Career Age (metric)		0.035***		0.040***		0.017***		0.040***
		(0.006)		(0.008)		(0.007)		(0.008)
		[0.000]		[0.000]		[0.009]		[0.000]
Career Age (Cat. 2)					−0.390**		−0.673***	
					(0.192)		(0.193)	
					[0.042]		[0.000]	
Career Age (Cat. 3)					0.653***		0.867***	
					(0.130)		(0.133)	
					[0.000]		[0.000]	
Career Age (Cat. 4)					0.599***		0.803***	
					(0.147)		(0.170)	
					[0.000]		[0.000]	
Nb. Publications	0.002	0.043	−0.040	−0.167***	−0.016	0.044	−0.099*	−0.167***
pre Ebola	(0.039)	(0.038)	(0.052)	(0.059)	(0.041)	(0.038)	(0.053)	(0.059)
	[0.951]	[0.257]	[0.449]	[0.004]	[0.700]	[0.244]	[0.061]	[0.004]
Journal Impact	0.592***		0.445***		0.319**		0.327**	
Factors (Cat. 2)	(0.146)		(0.156)		(0.147)		(0.159)	
	[0.000]		[0.004]		[0.030]		[0.040]	
Journal Impact	−0.280*		−0.069		−0.271*		−0.316*	
Factors (Cat. 3)	(0.160)		(0.177)		(0.161)		(0.181)	
	[0.079]		[0.696]		[0.093]		[0.081]	
Journal Impact		−0.070**		−0.007		−0.104***		−0.007
Factors (metric)		(0.030)		(0.045)		(0.034)		(0.045)
		[0.022]		[0.886]		[0.002]		[0.886]
Nb. Co-Authorships	−0.049***	−0.044***	−0.062***	−0.059***	−0.054***	−0.050***	−0.068***	−0.059***
with OECD pre Ebola	(0.011)	(0.011)	(0.014)	(0.014)	(0.012)	(0.012)	(0.014)	(0.014)
	[0.000]	[0.000]	[0.000]	[0.000]	[0.000]	[0.000]	[0.000]	[0.000]
Nb. Publications	0.120***	0.110***	0.129***	0.236***	0.206***	0.230***	0.136***	0.236***
about NTD pre Ebola	(0.036)	(0.037)	(0.044)	(0.044)	(0.038)	(0.040)	(0.044)	(0.044)
	[0.001]	[0.003]	[0.003]	[0.000]	[0.000]	[0.000]	[0.002]	[0.000]
Constant	−2.403***	−1.325***	−0.761***	−3.298***	−2.380***	−0.956***	−0.608**	−3.298***
	(0.163)	(0.252)	(0.243)	(0.301)	(0.172)	(0.270)	(0.257)	(0.301)
	[0.000]	[0.000]	[0.002]	[0.000]	[0.000]	[0.000]	[0.018]	[0.000]
Observations	4,712	4,712	2,880	2,880	3,952	3,952	2,880	2,880
Log Likelihood	−1,436.440	−1,445.435	−1,115.707	−1,125.711	−1,313.959	−1,324.453	−1,082.561	−1,125.711
Akaike Inf. Crit.	2,886.881	2,904.870	2,247.413	2,265.422	2,645.917	2,662.906	2,185.123	2,265.422

Notes: Significance levels: * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$. Data source: Fry (2021).

Table 5: Propensity Score Mean-Squared Error for different matching procedures

***p*MSE Specification**	**Matching Procedures**			
	original	extended (GDP)	extended (Age)	extended (GDP & Age)
Binary	0.6527822	0.5822303	0.6304576	0.5849771
Metric	0.6523423	0.5809416	0.6300302	0.5809416