Spatio-temporal estimates of apparent tsetse fly density in Uganda: a meta-analysis and meta-regression from 1985-2022

Karla Rascón-García[1], Auther Tamale Wasswa[2], Beatriz Martínez-López[1],

Giuliano Cecchi[3], Albert Mugenyi[4], Enock Matovu[2], Dennis Muhanguzi[2]

[1] Center for Animal Disease Modeling and Surveillance (CADMS), Department of Medicine & Epidemiology, School of Veterinary Medicine, University of California, Davis, USA

[2] Department of Biomedical Laboratory Technology and Molecular Biology, College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Kampala, Uganda

[3] Food and Agriculture Organization of the United Nations, Animal Production and Health Division, Rome, Italy

[4] Ministry of Agriculture, Animal Industry and Fisheries, Kampala, Uganda

MAKERERE UNIVERSITY

College of Veterinary Medicine, Animal Resources and Bio Security (CoVAB)

GloCal Health Fellowship

UNIVERSITY OF CALIFORNIA HEALTH Global Health Institute

CENTER FOR ANIMAL HEALTH AND FOOD SAFETY

UNIVERSITY OF MINNESOTA

UCDAVIS VETERINARY MEDICINE

Center for Animal Disease Modeling and Surveillance

Note:



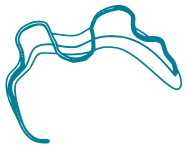
Background

- **Human** and **Animal African Trypanosomiasis**
  - caused by protozoan parasites of the **Trypanosoma** genus
  - primarily transmitted by ***Glossina*** species



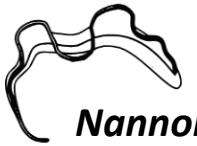
Trypanozoon

T. brucei
T. evansi
T. equiperdum



Duttonella

T. vivax



Nannomonas

T. congolense
T. simiae
T. godfreyi



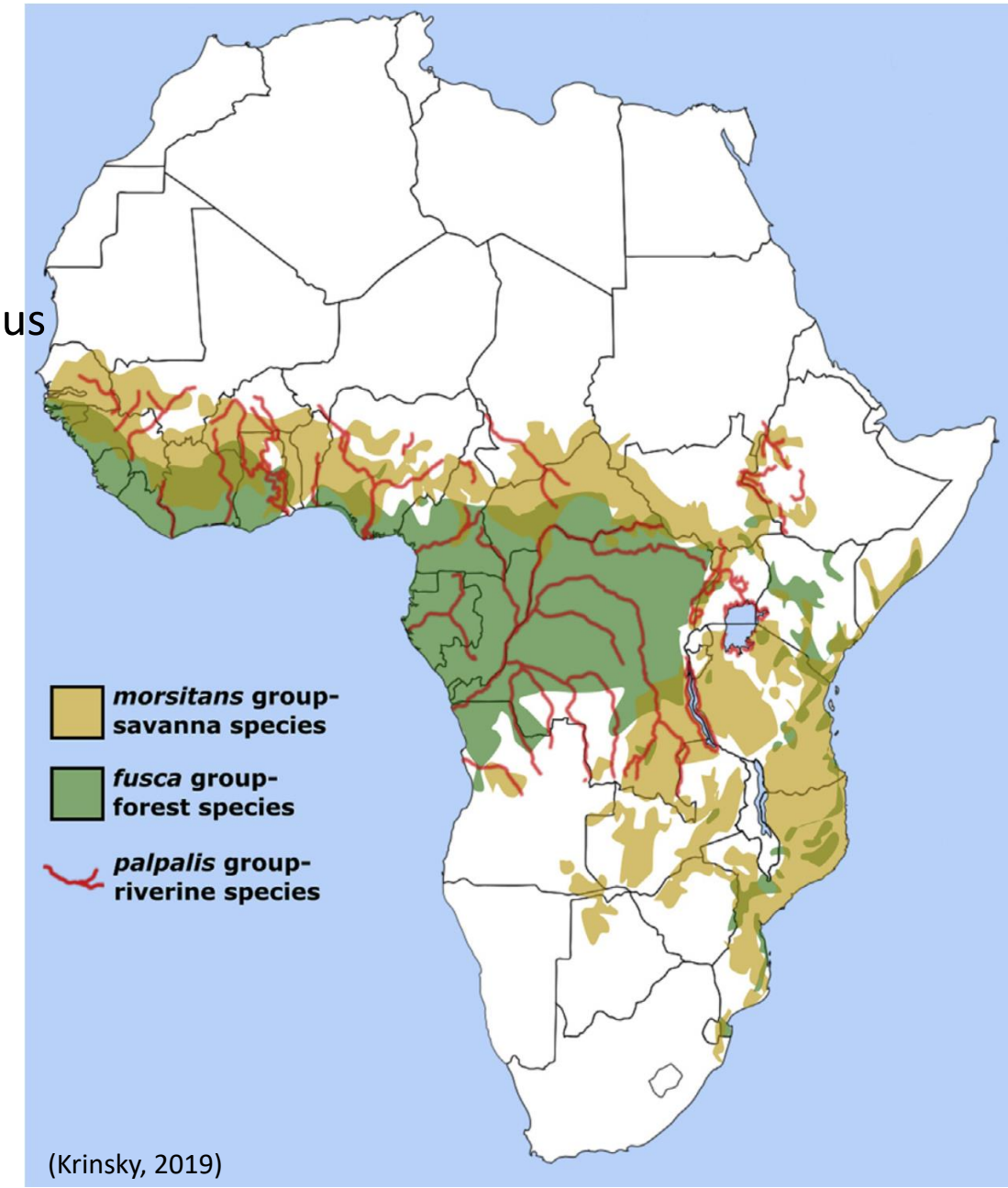
Morsitans Group



Fusca Group



Palpalis Group



(Krinsky, 2019)

Background



Morsitans Group



Fusca Group



Palpalis Group

- **Human** and **Animal African Trypanosomiasis**
  - caused by protozoan parasites of the **Trypanosoma** genus
  - primarily transmitted by ***Glossina*** species

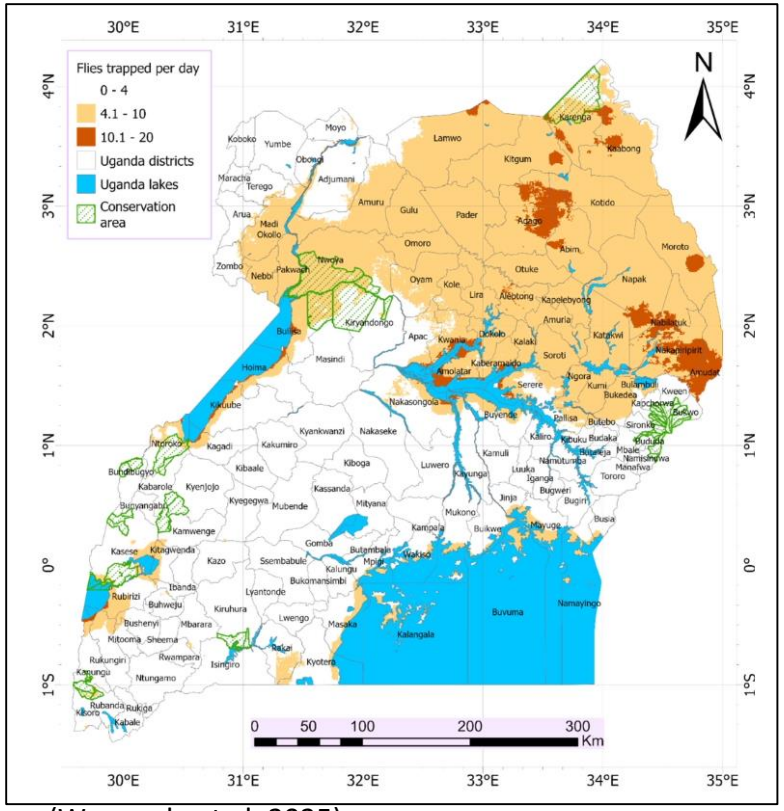
- Tsetse flies (*Glossina* sp.) **infest** an extensive area of approximately **140,000 Km^2 (~58.1%)** out of the total 241,038 Km^2 total land mass (Cecchi et al., 2008)

- ~ **8 million cattle** are estimated to be predisposed to **AAT** (MAAIF, 2014)
- ~ **10 million people** at risk for **HAT** (COCTU, n.d.)

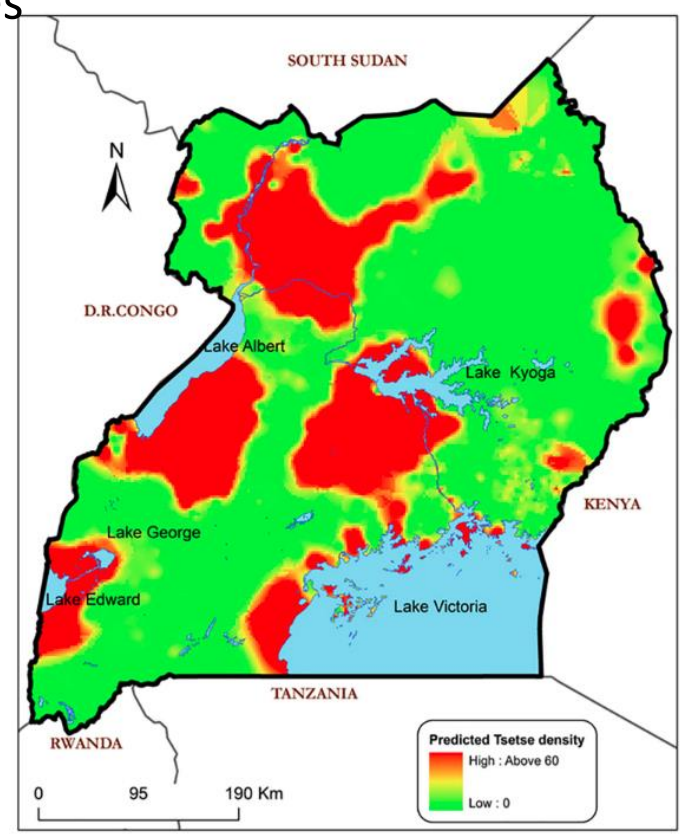
NEED: A granular characterization of tsetse fly distributions in Uganda.

Background

- **Human** and **Animal African Trypanosomiasis**
  - caused by protozoan parasites of the **Trypanosoma** genus
  - primarily transmitted by ***Glossina*** species



(Wangoola et al, 2025)



(Mugenyi et al, 2021)



Morsitans Group



Fusca Group



Palpalis Group

- Different density definitions and different temporal time windows (2014-2024 vs 2008-2018)

Research Objective



Conduct a meta-analysis of the apparent tsetse fly density for Uganda over the past years (1985-2022)

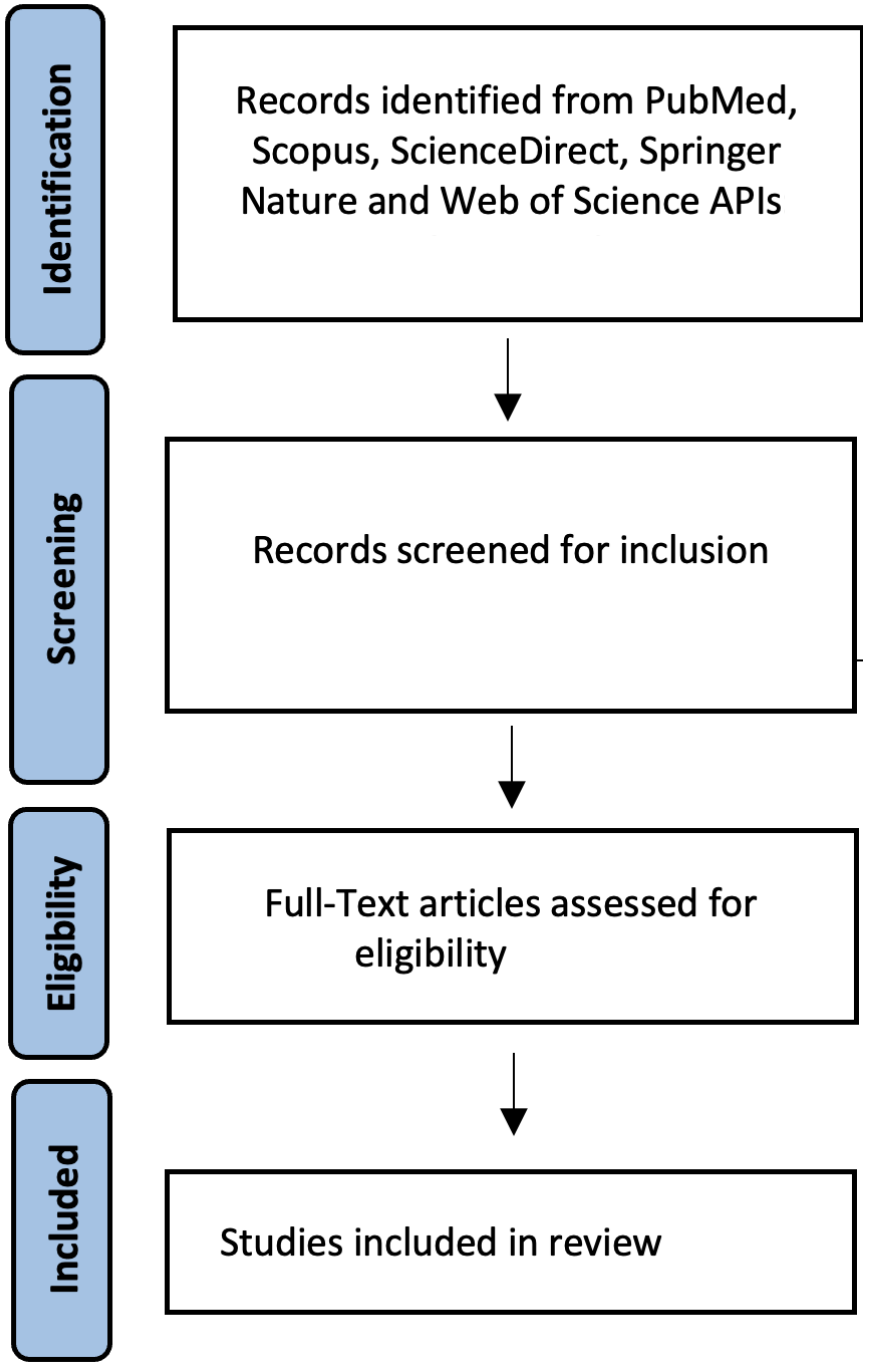




Methods

Methods

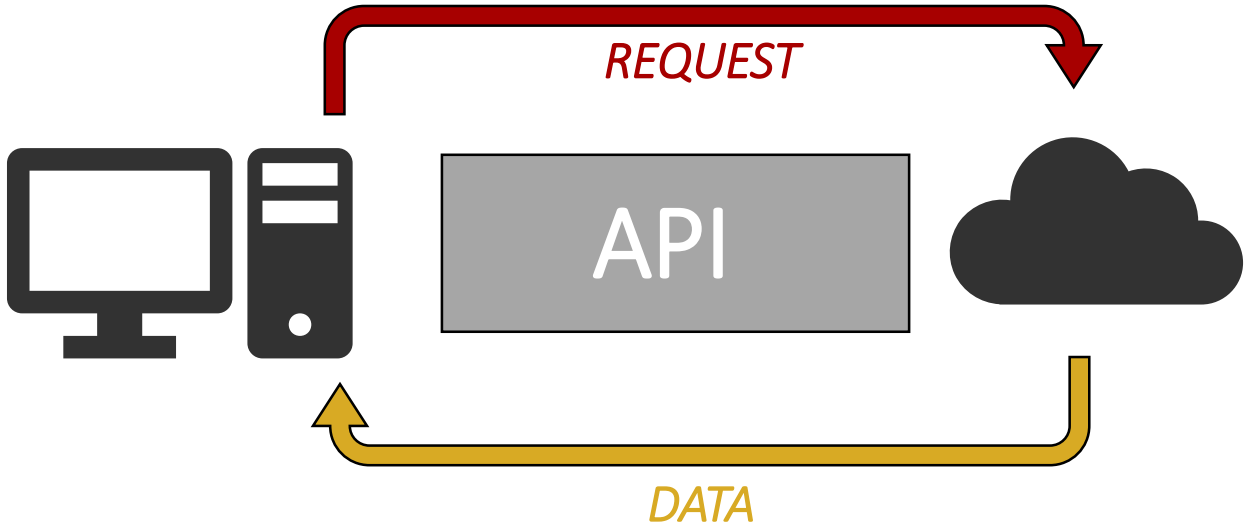
Conducted in accordance with PRISMA guidelines



Methods - *Identification*

Search Strategy and Application Programming Interfaces (APIs)

APIs allow for two-way communication between systems and end-users for the batch retrieval of resources or objects.



PubMed

Scopus

ScienceDirect

Springer Nature

Web of Science

Methods - *Identification*

Search Strategy and Application Programming Interfaces (APIs)

APIs allow for two-way communication between systems and end-users for the batch retrieval of resources or objects.



"trypanosomiasis AND Uganda"

"tsetse trypanosomiasis AND Uganda"

"glossina AND Uganda"

Methods - *Screening*

Inclusion Criteria

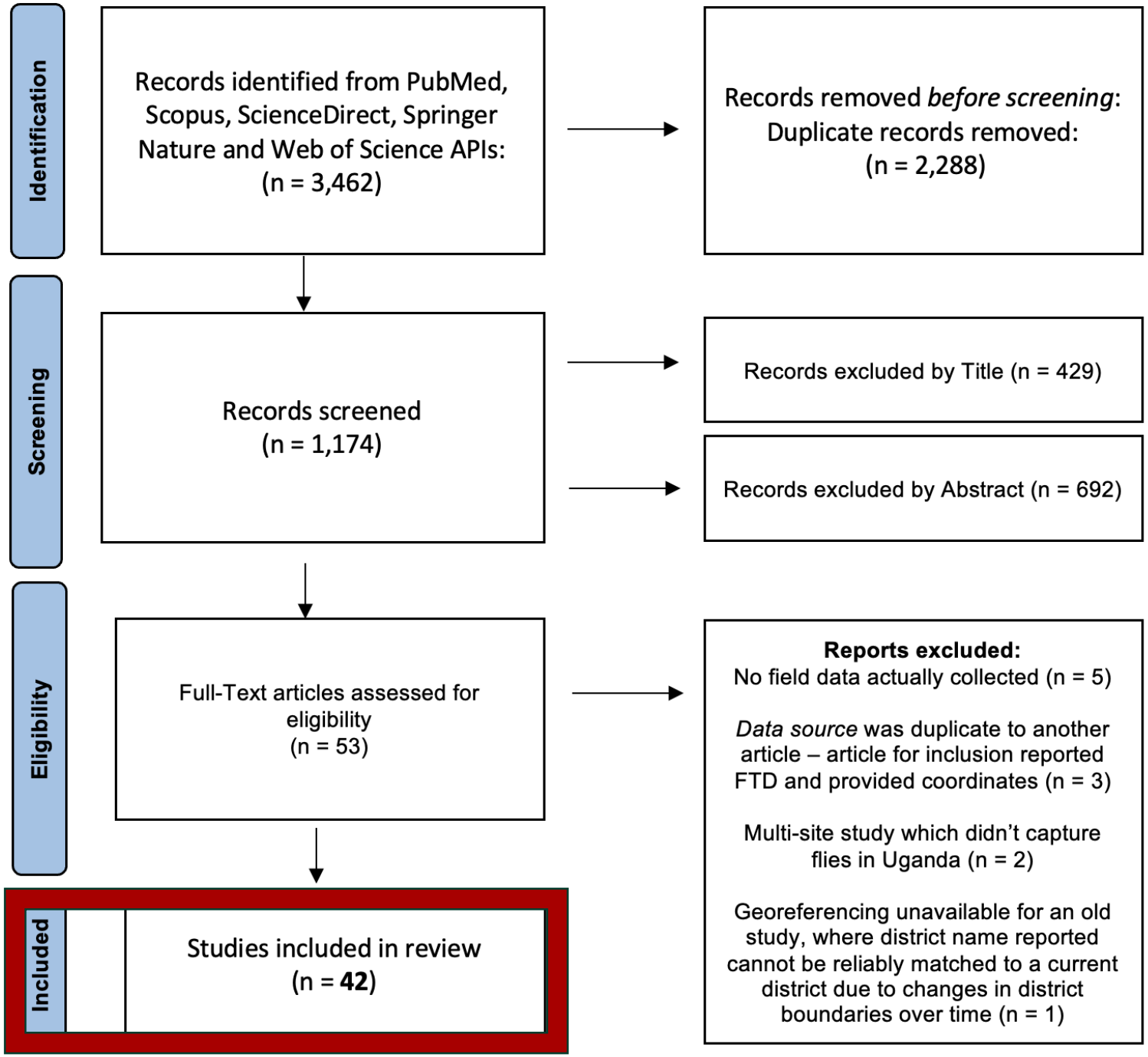
- ✓ Geographic to Uganda
- ✓ Written in English
- ✓ Published between 1980-2022
- ✓ Full-text documents needed to be available
- ✓ Reported the detection of tsetse flies (e.g., total captures, not limited to FTD)
- ✓ If an intervention was involved, only baseline or control data were included

Excluded if…

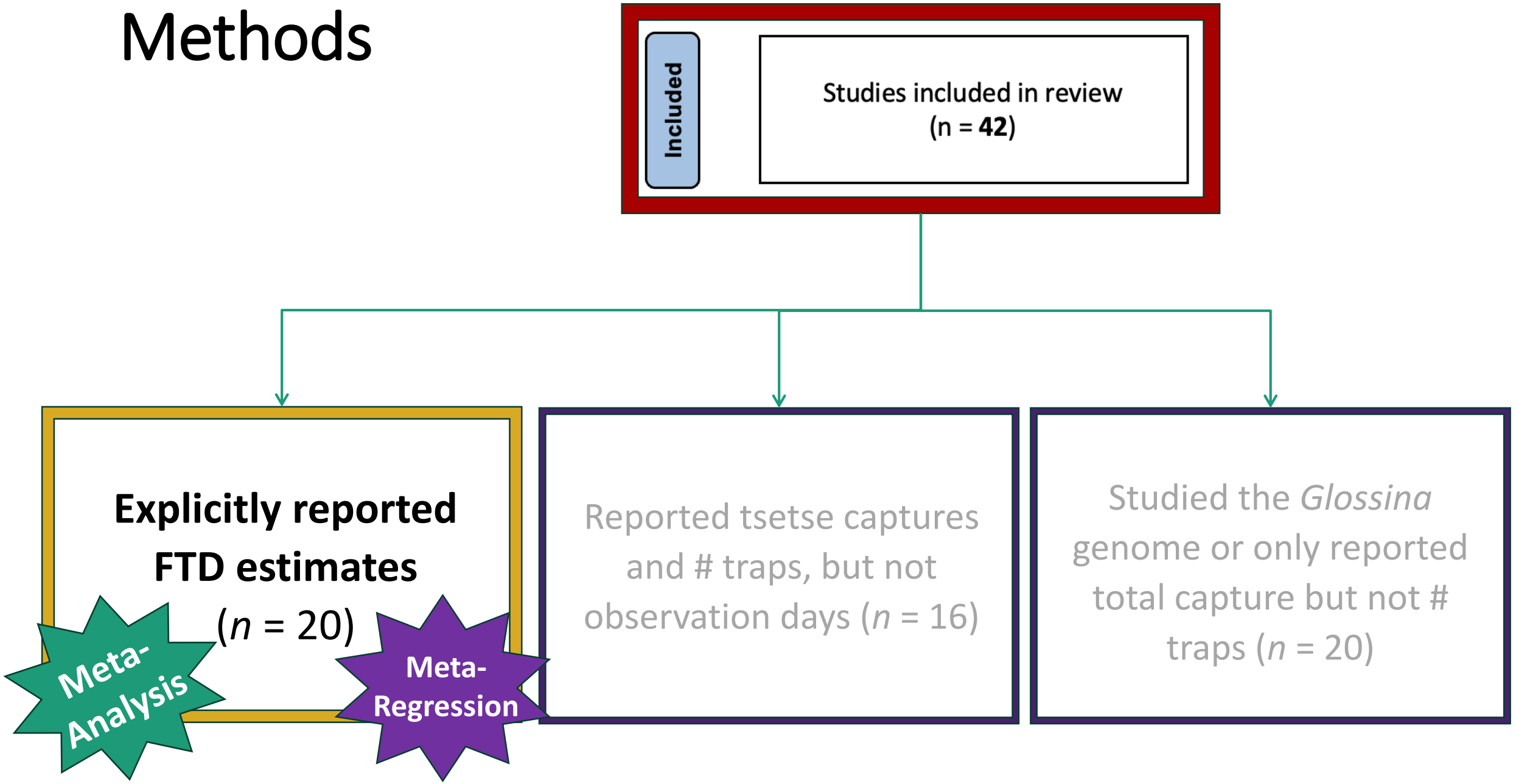
- Study was experimental
- Study was lab-based

Methods

Flowchart



Methods


Included
Studies included in review
(n = 42)
Explicitly reported FTD estimates
(n = 20)
Meta-Analysis
Meta-Regression
Reported tsetse captures and # traps, but not observation days (n = 16)
Studied the Glossina genome or only reported total capture but not # traps (n = 20)

Methods

Meta-Analysis:

- **Heterogeneity** was estimated by a **random-effects model** using a Freeman-Tukey Double arcsine transformation for **estimating *incidence rates***

- **Publication Bias** was assessed through **visual assessment** of funnel plot asymmetry **AND** calculation of the **Luis Furuya-Kanamori (LFK) index**
  - Luis Furuya-Kanamori (LFK) index **values more extreme ±2** indicate "**major asymmetry**" and the presence of publication bias

- **Forest plots** were used to visualize study point estimates

Methods

Meta-Regression:

- **Univariate** and **multivariate** analyses conducted to investigate **sources of heterogeneity**
  - Region
  - District
  - Sub-county
  - Collection period
  - *Glossina* species

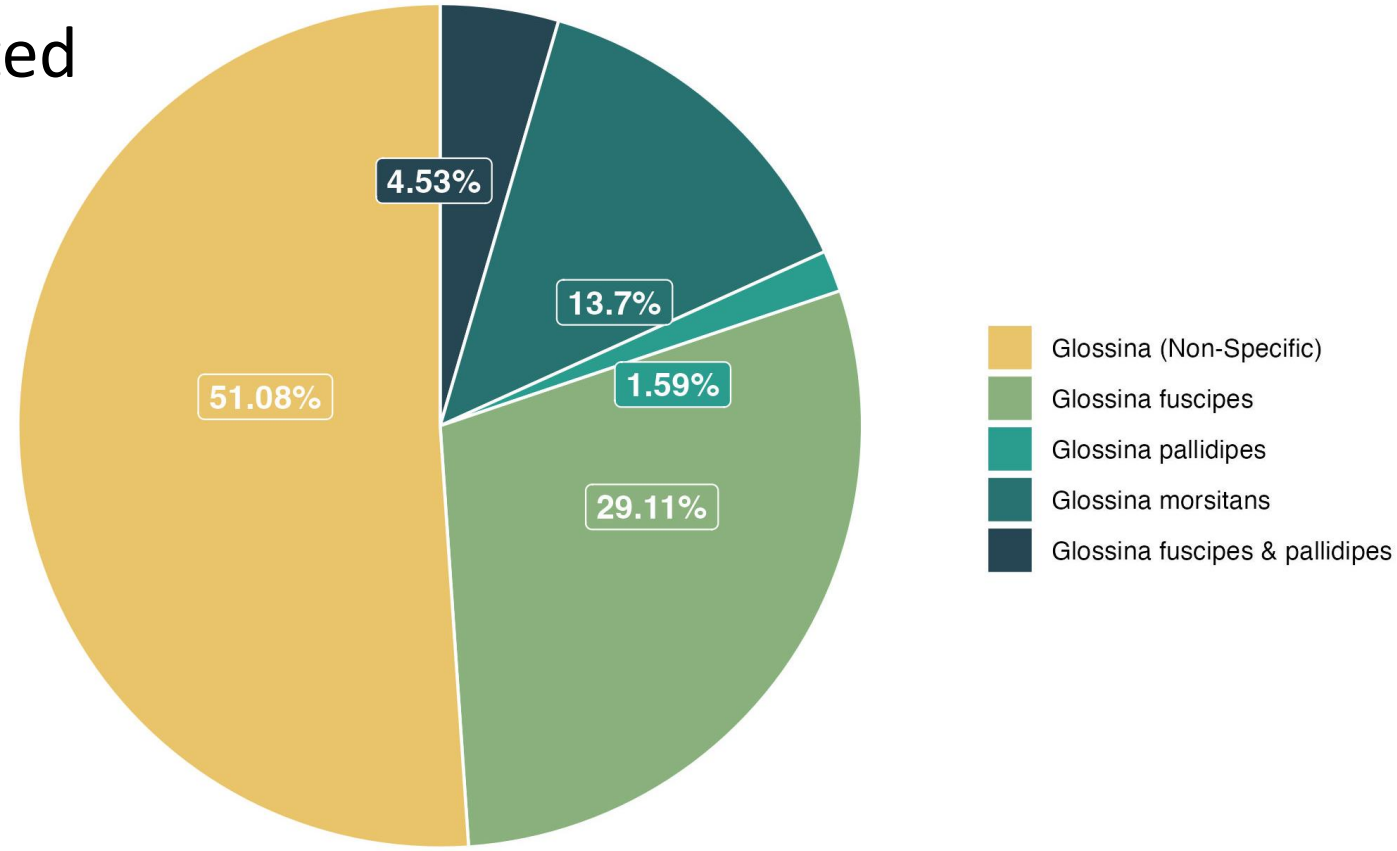
- **Explanatory variables** with a **p-value <0.25** in univariate analyses were included in multivariate models

Results

Results

- **20 articles** included in meta-analysis

- 3 *Glossina* species reported



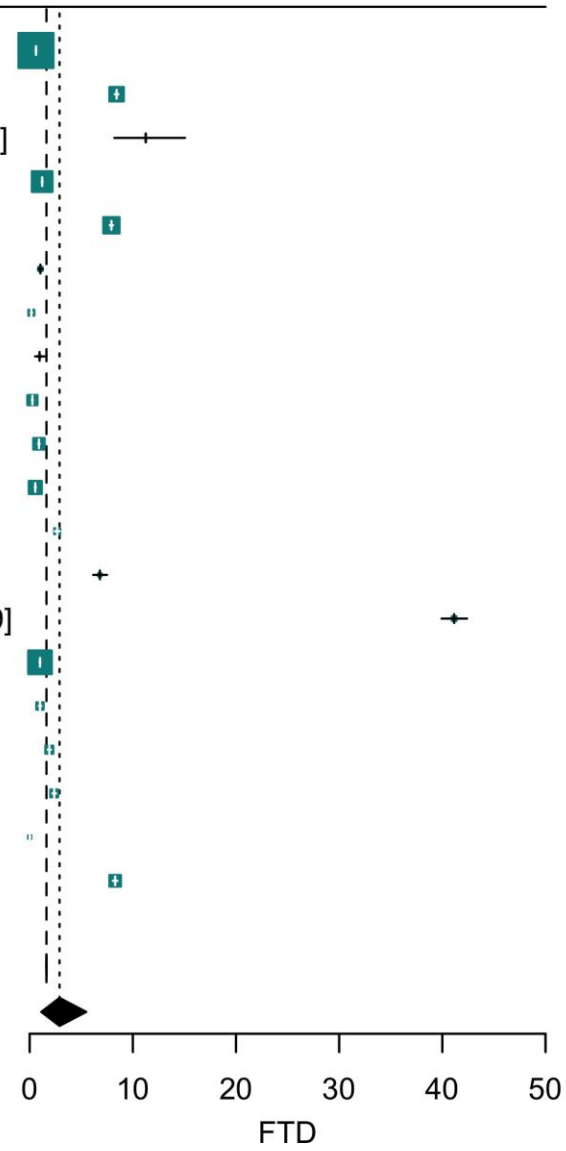
Results

- **20 articles** included in meta-analysis
- 3 *Glossina* species reported
- **44** of 146 **districts** (~ 32%)
- **Biconical** and **Pyramidal** traps reported, 81.0% and 18.7%, respectively

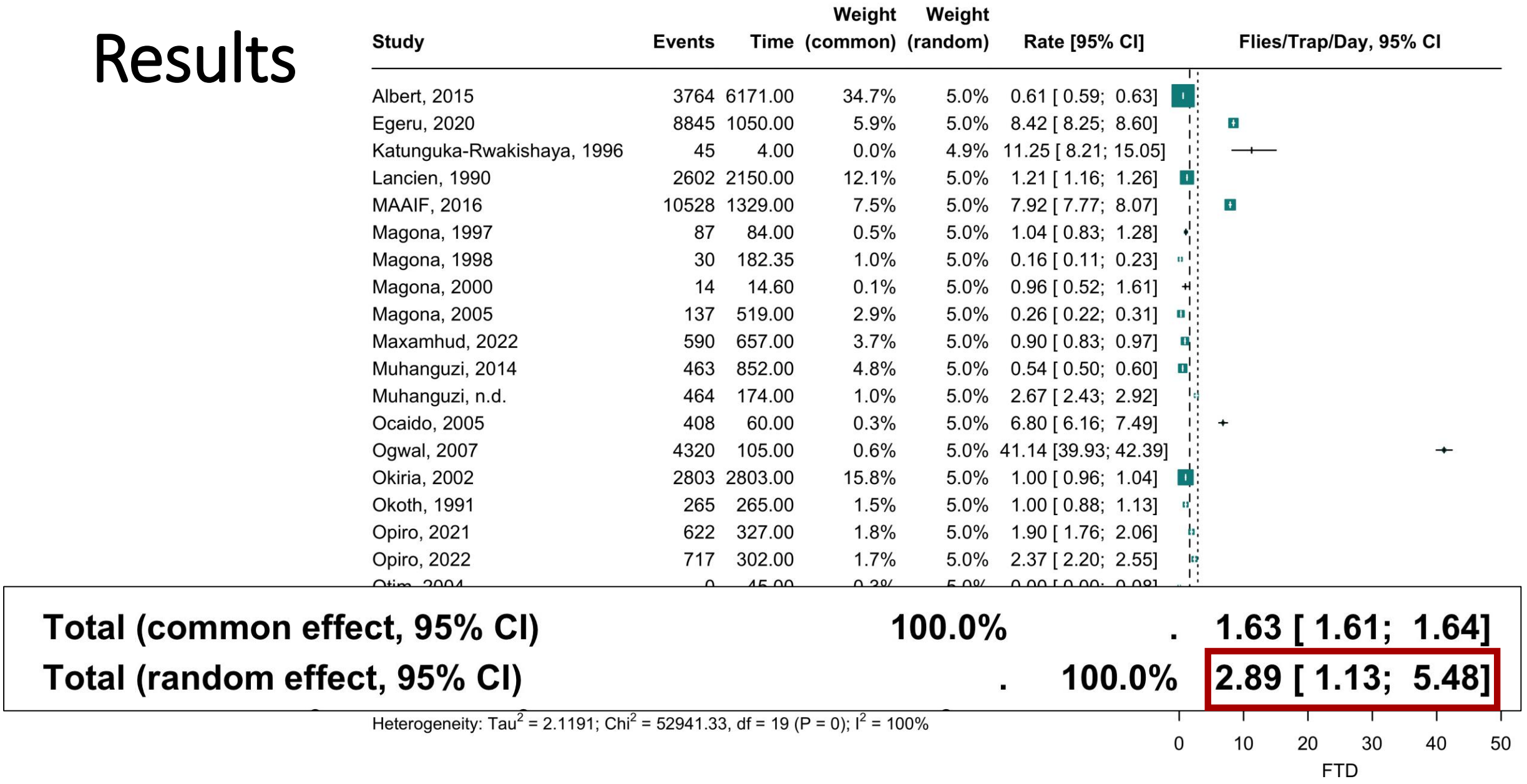
Results

Study	Events	Time	Weight (common)	Weight (random)	Rate [95% CI]
Albert, 2015	3764	6171.00	34.7%	5.0%	0.61 [0.59; 0.63]
Egeru, 2020	8845	1050.00	5.9%	5.0%	8.42 [8.25; 8.60]
Katunguka-Rwakishaya, 1996	45	4.00	0.0%	4.9%	11.25 [8.21; 15.05]
Lancien, 1990	2602	2150.00	12.1%	5.0%	1.21 [1.16; 1.26]
MAAIF, 2016	10528	1329.00	7.5%	5.0%	7.92 [7.77; 8.07]
Magona, 1997	87	84.00	0.5%	5.0%	1.04 [0.83; 1.28]
Magona, 1998	30	182.35	1.0%	5.0%	0.16 [0.11; 0.23]
Magona, 2000	14	14.60	0.1%	5.0%	0.96 [0.52; 1.61]
Magona, 2005	137	519.00	2.9%	5.0%	0.26 [0.22; 0.31]
Maxamhud, 2022	590	657.00	3.7%	5.0%	0.90 [0.83; 0.97]
Muhanguzi, 2014	463	852.00	4.8%	5.0%	0.54 [0.50; 0.60]
Muhanguzi, n.d.	464	174.00	1.0%	5.0%	2.67 [2.43; 2.92]
Ocaido, 2005	408	60.00	0.3%	5.0%	6.80 [6.16; 7.49]
Ogwal, 2007	4320	105.00	0.6%	5.0%	41.14 [39.93; 42.39]
Okiria, 2002	2803	2803.00	15.8%	5.0%	1.00 [0.96; 1.04]
Okoth, 1991	265	265.00	1.5%	5.0%	1.00 [0.88; 1.13]
Opiro, 2021	622	327.00	1.8%	5.0%	1.90 [1.76; 2.06]
Opiro, 2022	717	302.00	1.7%	5.0%	2.37 [2.20; 2.55]
Otim, 2004	0	45.00	0.3%	5.0%	0.00 [0.00; 0.08]
Stanton, 2018	5577	673.00	3.8%	5.0%	8.29 [8.07; 8.51]
Total (common effect, 95% CI)			**100.0%**	**.**	**1.63 [1.61; 1.64]**
Total (random effect, 95% CI)			**.**	**100.0%**	**2.89 [1.13; 5.48]**

Heterogeneity: $Tau^2 = 2.1191$; $Chi^2 = 52941.33$, df = 19 (P = 0); $I^2 = 100\%$



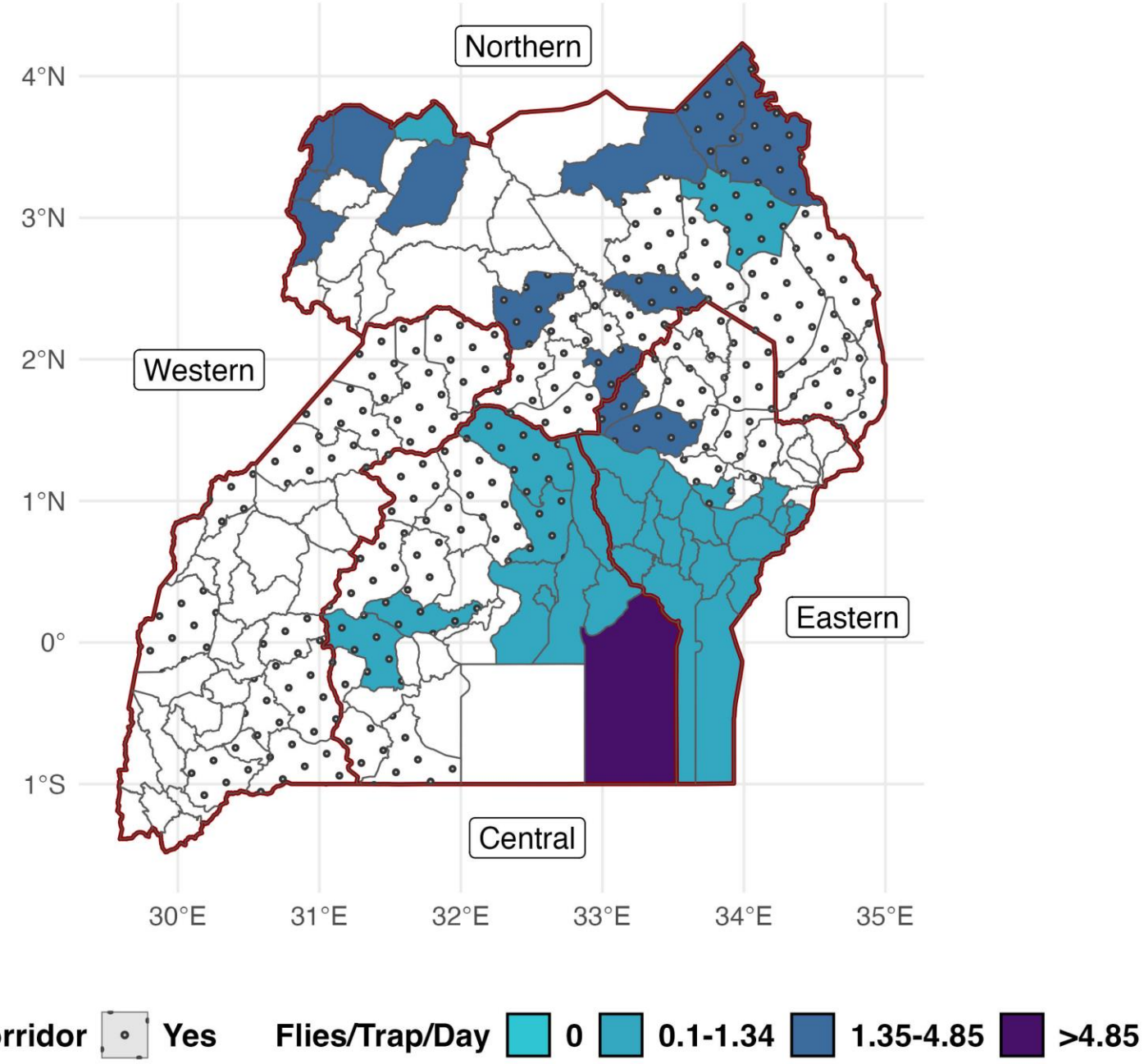
Results


Study
Events
Time
Weight (common)
Weight (random)
Rate [95% CI]
Flies/Trap/Day, 95% CI
Albert, 2015 3764 6171.00 34.7% 5.0% 0.61 [0.59; 0.63]
Egeru, 2020 8845 1050.00 5.9% 5.0% 8.42 [8.25; 8.60]
Katunguka-Rwakishaya, 1996 45 4.00 0.0% 4.9% 11.25 [8.21; 15.05]
Lancien, 1990 2602 2150.00 12.1% 5.0% 1.21 [1.16; 1.26]
MAAIF, 2016 10528 1329.00 7.5% 5.0% 7.92 [7.77; 8.07]
Magona, 1997 87 84.00 0.5% 5.0% 1.04 [0.83; 1.28]
Magona, 1998 30 182.35 1.0% 5.0% 0.16 [0.11; 0.23]
Magona, 2000 14 14.60 0.1% 5.0% 0.96 [0.52; 1.61]
Magona, 2005 137 519.00 2.9% 5.0% 0.26 [0.22; 0.31]
Maxamhud, 2022 590 657.00 3.7% 5.0% 0.90 [0.83; 0.97]
Muhanguzi, 2014 463 852.00 4.8% 5.0% 0.54 [0.50; 0.60]
Muhanguzi, n.d. 464 174.00 1.0% 5.0% 2.67 [2.43; 2.92]
Ocaido, 2005 408 60.00 0.3% 5.0% 6.80 [6.16; 7.49]
Ogwal, 2007 4320 105.00 0.6% 5.0% 41.14 [39.93; 42.39]
Okiria, 2002 2803 2803.00 15.8% 5.0% 1.00 [0.96; 1.04]
Okoth, 1991 265 265.00 1.5% 5.0% 1.00 [0.88; 1.13]
Opiro, 2021 622 327.00 1.8% 5.0% 1.90 [1.76; 2.06]
Opiro, 2022 717 302.00 1.7% 5.0% 2.37 [2.20; 2.55]
Total (common effect, 95% CI) 100.0% . 1.63 [1.61; 1.64]
Total (random effect, 95% CI) . 100.0% 2.89 [1.13; 5.48]
Heterogeneity: Tau² = 2.1191; Chi² = 52941.33, df = 19 (P = 0); I² = 100%
0
10
20
30
40
50
FTD

Results

- Obtained natural breaks using the Jenks algorithm for classifications →

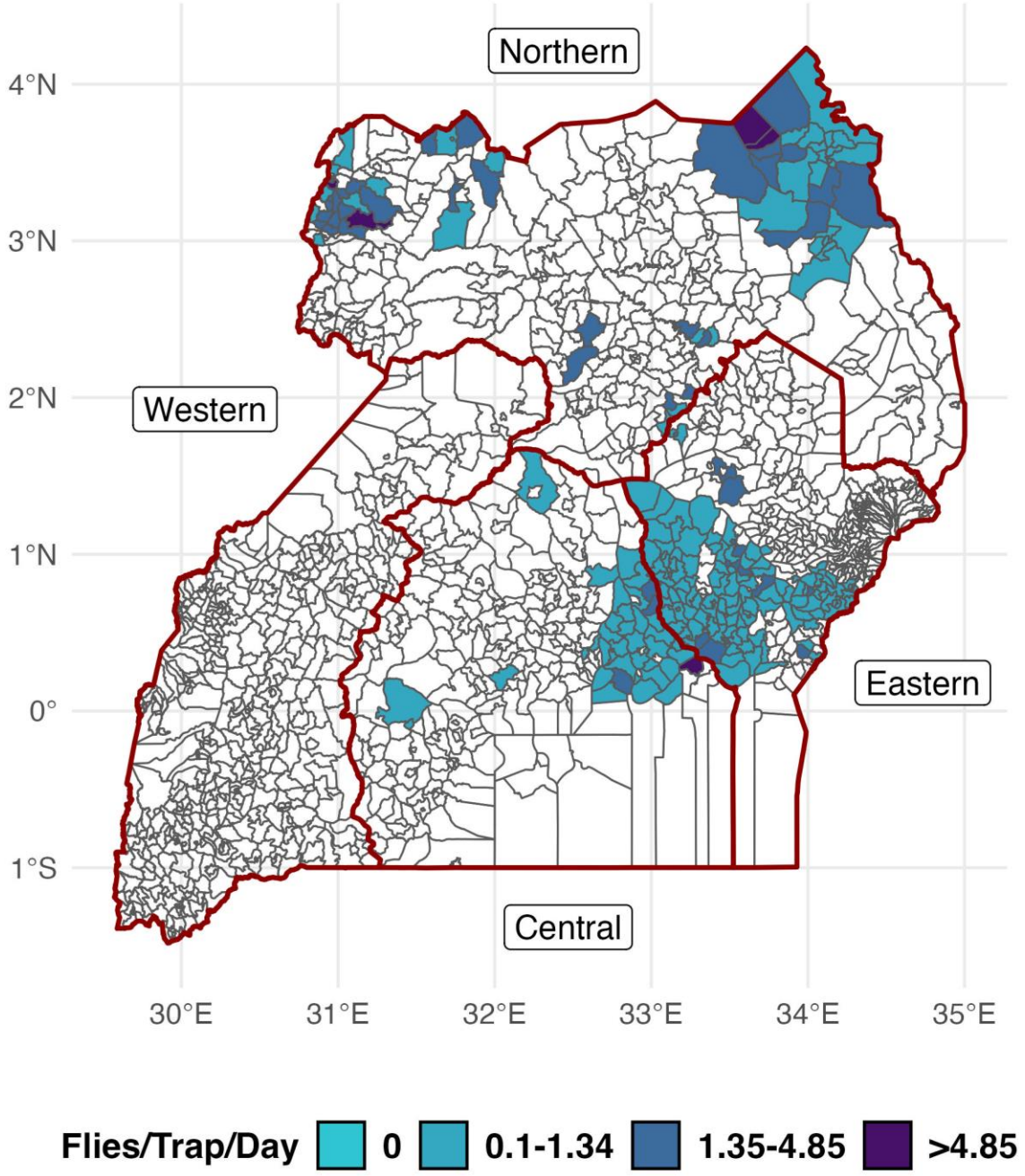




Results

- Obtained natural breaks using the Jenks algorithm for classifications →





Results

- **Meta-Regression** Results

Model	Variable	p-value	R^2
Univariate	Region	<0.0001	8.15
	District	<0.0001	18.58
	Sub-County	0.0878	6.70
	Collection Period	0.0677	1.09
	Glossina Spp	<0.0001	20.46

Results

- **Meta-Regression** Results

Model	Variable	p-value	R^2
Univariate	Region	<0.0001	8.15
	District	<0.0001	18.58
	Sub-County	0.0878	6.70
	Collection Period	0.0677	1.09
	Glossina Spp	<0.0001	20.46
Multivariate	District + Collection Period	<0.0001	21.94
	District + Glossina Spp	<0.0001	32.97
	Collection Period + Glossina Spp	<0.0001	19.96
	Sub-County + Collection Period	0.0004	15.59
	Sub-County + Glossina Spp	<0.0001	56.45
	District * Collection Period	<0.0001	23.02
	District * Glossina Spp	<0.0001	33.73
	Collection Period * Glossina Spp	<0.0001	19.45
	Sub-County * Collection Period	0.0410	8.90
	Sub-County * Glossina Spp	<0.0001	32.83
	District + Collection Period + Glossina Spp	<0.0001	41.02
	District * Collection Period * Glossina Spp	<0.0001	41.66
	Sub-County + Collection Period + Glossina Spp	<0.0001	87.32
	Sub-County * Collection Period * Glossina Spp	<0.0001	41.66

Results

- **Meta-Regression** Results

Model	Variable	p-value	R^2
Univariate	Region	<0.0001	8.15
	District	<0.0001	18.58
	Sub-County	0.0878	6.70
	Collection Period	0.0677	1.09
	Glossina Spp	<0.0001	20.46
Multivariate	District + Collection Period	<0.0001	21.94
	District + Glossina Spp	<0.0001	32.97
	Collection Period + Glossina Spp	<0.0001	19.96
	Sub-County + Collection Period	0.0004	15.59
	Sub-County + Glossina Spp	<0.0001	56.45
	District * Collection Period	<0.0001	23.02
	District * Glossina Spp	<0.0001	33.73
	Collection Period * Glossina Spp	<0.0001	19.45
	Sub-County * Collection Period	0.0410	8.90
	Sub-County * Glossina Spp	<0.0001	32.83
	District + Collection Period + Glossina Spp	<0.0001	41.02
	Sub-County + Collection Period + Glossina Spp	<0.0001	87.32
	Sub-County * Collection Period * Glossina Spp	<0.0001	41.66

Discussion

Discussion

- Of the 42 publications obtained, **only 20 reported FTD**
- Incidence rate meta-analysis results found considerable **gaps in spatial sampling** with **no district from the Western region** reported
- **Eastern Region** has received strong investigative support with **40.9% of records** associated with this region
- Meta-regression results suggest ***Glossina* species, sub-county, and collection period informed** the greatest proportion (R^2 = **87.32**) of **observed variation**. However, we suspect this high R-squared is likely an artifact of underlying data

Discussion

- *Strengths*
  - By leveraging available **APIs**, we were not only able to collect large batches of data rapidly and systematically, but we were able to **search widely** and consider articles that might have otherwise been missed through manual searches
  - We provide updated **FTD estimates for Uganda** from a **larger temporal pool** and have found a strong need to design studies that target sampling from districts homogenously

Discussion

- *Limitations*
  - **Inconsistent FTD reporting** – FTD estimates at times summarized over a rgion but not always reported at the trap-level
  - Most records (**51.08%**) **did not report *Glossina species***, greatly limiting our ability to describe species distributions
  - **Non-uniform spatial sampling** limited our ability to properly characterize tsetse fly distribution at a national level

Thank you!

CENTER FOR ANIMAL HEALTH AND FOOD SAFETY
UNIVERSITY OF MINNESOTA

Contact: rasco011@umn.edu

MAKERERE UNIVERSITY

College of Veterinary Medicine, Animal Resources and Bio Security (CoVAB)

GloCal Health Fellowship

UNIVERSITY OF CALIFORNIA HEALTH

Global Health Institute

UCDAVIS VETERINARY MEDICINE

Center for Animal Disease Modeling and Surveillance