# **Social network analysis and zoonotic gastrointestinal parasites in urban macaques:** The role of social centrality and synanthropy in infection rates

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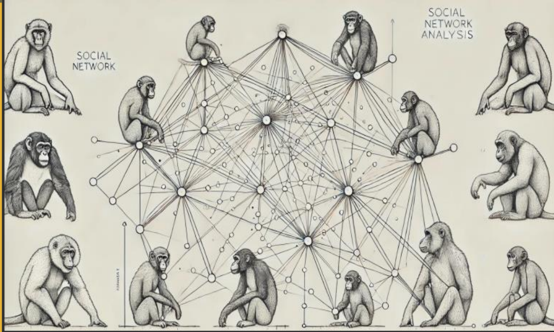
monkey forest UBUD




**Encroachment of human activities** into natural habitats

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**Contacts** between **humans and wildlife**

**Encroachment of human activities** into natural habitats

**Zoonotic diseases** transmission

**Contacts** between **humans and wildlife**


**Human-animal interfaces**
=
crucial for **understanding** and **controlling** the **emergence of zoonoses**

- **Zoonotic disease outbreaks** = challenge to **global health**
- **60%** of infectious diseases in humans

**Human-NHPs interfaces** = **hotspots** for zoonotic pathogen transmission

**Genetic similarity** to humans, **sensitive** to identical pathogens

Malaria (*Plasmodium knowlesi*)

*Strongyloides sp*

Bali, Indonesia

**Commensal** long-tailed macaques (*Macaca fascicularis*)

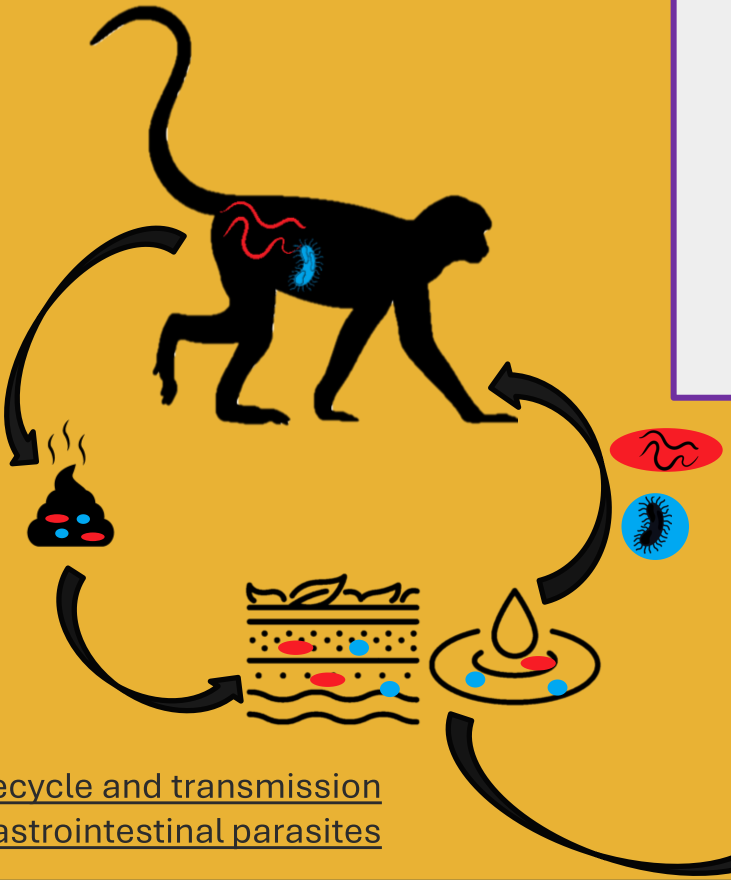
**Highly touristic** area, **share space** with human population, frequent and close **direct contacts** between macaques and humans

**Gastrointestinal parasites**

***Helminths*** *(Cestoda, Nematoda, Trematoda)*

***Protozoa***

**Fecal-oral** transmission, **most common zoonotic agent** shared between humans and primates



Direct lifecycle and transmission of gastrointestinal parasites

**Risk factors of infection :**

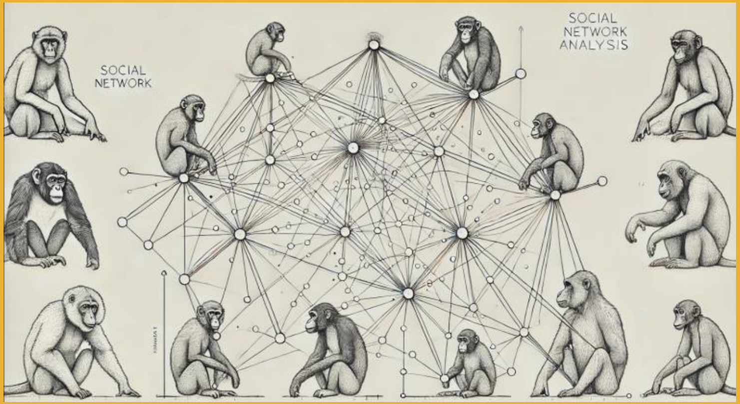
Food access

**Contact with other species**

**Social environment**

**Host biological parameters**

**Social Network Analysis (SNA):** quantitative tool → study **infection dynamics**, predict **the risk of infection** at the **individual and group level**




Partially explored **BUT** → **contrasting** results, often focus on a **single aspect**

**Need to consider multiple factors**


Evaluate the role of :

- **Social centrality**
- **Host characteristics**
- **Human-macaque interactions**

on zoonotic GI parasites

**Understand how social position and individual relationships influence disease transmission**

# Material and Methods

Ubud Monkey forest

monkey forest UBUD

**Touristic site in Bali, Indonesia**

Temples, close contacts with macaques, 3000 tourists/day

**Urban sanctuary**

Forest fragment (20 ha) in the city

**Long-tailed macaques (*Macaca fascicularis*)**

~ 900 free ranging macaques (in 2022) divided into 10 groups: overpopulation

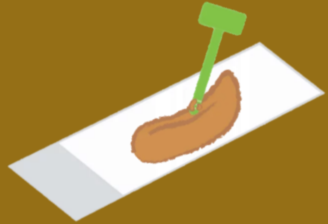
**Study group**

Michelin group, 161 individuals, 53 adults (males and females) identified as focal subjects

All data were collected between **February to November 2022** (1 observer) and **March to August 2023** (3 observers)

## Parasitological analysis:

**Non-invasive** and **opportunistic** fecal sample collection



**Direct smear**

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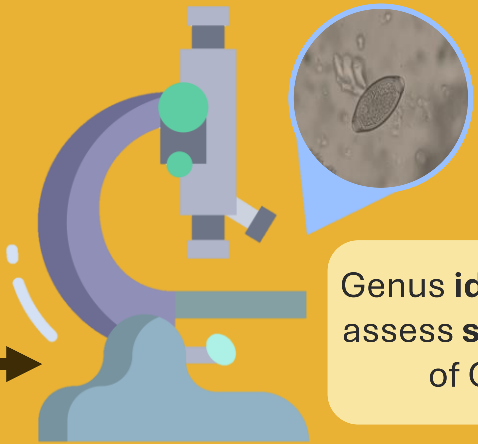
**Fecal flotation**



Genus **identification** and assess **species richness** of GI parasites

+

**Quantification of parasitic load** with MacMaster slide (EPG-P and EPG-H)

All data were collected between **February to November 2022** (1 observer) and **March to August 2023** (3 observers)

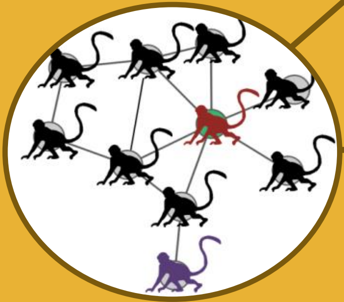
## Behavioral analysis:

Agonistic

Interactions with humans (HM)

Affiliative

53 adults as focal subjects, 15 min focal sampling, **social behaviors** and **HM interactions**



Centrality measures
- Strength
- Eigenvector

Hierarchy
- David's score

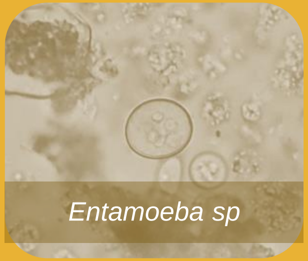
- **Clustering analysis** → identify social clusters
- **K-test analysis** → GI parasite infections follow grooming network pathways
- **GLMMs** → effects of risk factors on host's **GI parasites species richness/presence**

# Results

## Parasitology:

2022 : **68** fecal samples ; 2023 : **73** fecal samples

**141** samples : 105 positive (**74 %**)







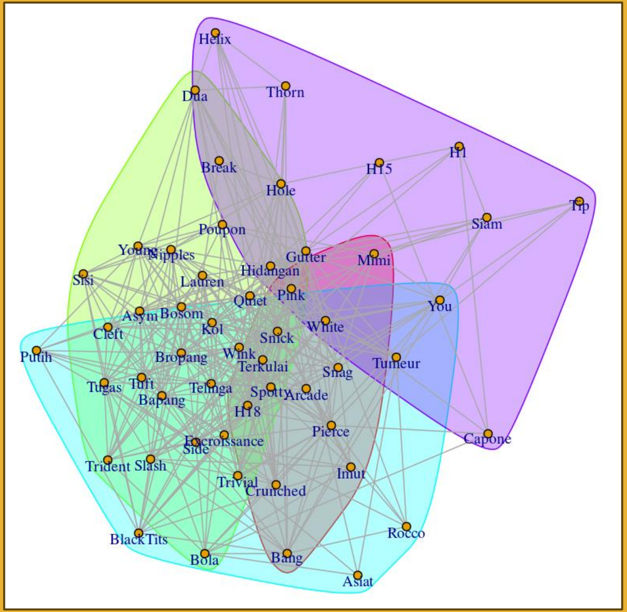



| Protozoa: | 2022 | 2023 |
|---|---|---|
| ***Entamoeba sp*** | **0.62** | **0.79** |
| ***Iodamoeba sp*** | 0.15 | 0.25 |
| ***Balantiodes sp*** | 0.02 | 0.35 |

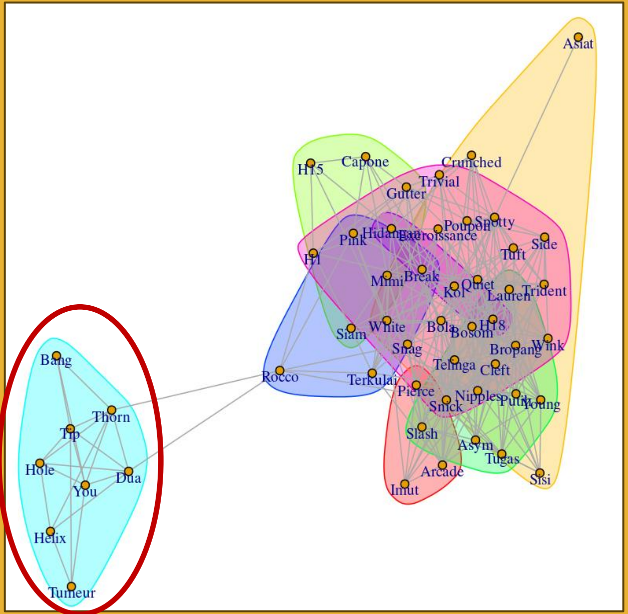
| Helminths: | 2022 | 2023 |
|---|---|---|
| ***Strongyloides sp*** | 0.00 | 0.04 |
| **Hookworm** | **0.43** | **0.40** |
| ***Oesophagostomum sp*** | 0.26 | 0.15 |
| ***Trichuris sp*** | 0.08 | 0.07 |

**Each focal individual sampled** was assigned a **specific richness value** for GI parasites

Clustering analysis: **Community detection** in **grooming** networks




**Grooming** network in **2022**




**Grooming** network in **2023**

**2023 :** isolated subgroup
"Peripheral group "
→ Grooming network **divided** into **two** sub-networks **for SNA analysis**

K-test analysis: GI parasite infections follow **grooming network pathways?**

K-test analysis for **each genus of GI parasites**

K-statistic (p-value) : NS

| | 2022 | 2023 |
|---|---|---|
| ***Entamoeba sp*** | 0.98 | 0.45 |
| ***Iodamoeba sp*** | 0.77 | 0.65 |
| ***Balantiodes sp*** | NA | 0.48 |
| ***Strongyloides sp*** | NA | NA |
| **Hookworm** | 0.99 | 0.76 |
| ***Oesophagostomum sp*** | 0.95 | 0.87 |
| ***Trichuris sp*** | 0.27 | 1 |

**K-statistic**: How many infected individuals are in direct contact with other infected individuals

**Observed** k-statistic → compared to a **permuted distribution** of k-statistics

**K-test** → determine whether individuals near an infected case in network had a **higher likelihood** of being infected

Individuals neighboring an infected case **DO NOT HAVE** a higher likelihood of being infected

## K-test analysis:

GI parasite infections follow **grooming network pathways?**

K-test analysis for **each genus of GI parasites**

| Average pathway distance (p-value) : NS | 2022 | 2023 |
|---|---|---|
| ***Entamoeba sp*** | 0.89 | 1 |
| ***Iodamoeba sp*** | 0.92 | 0.73 |
| ***Balantiodes sp*** | NA | 0.90 |
| ***Strongyloides sp*** | NA | NA |
| **Hookworm** | 0.77 | 0.93 |
| ***Oesophagostomum sp*** | 0.70 | 0.71 |
| ***Trichuris sp*** | 0.70 | 0.95 |

**Pathways analysis** → measure the **average distance** between two infected individuals

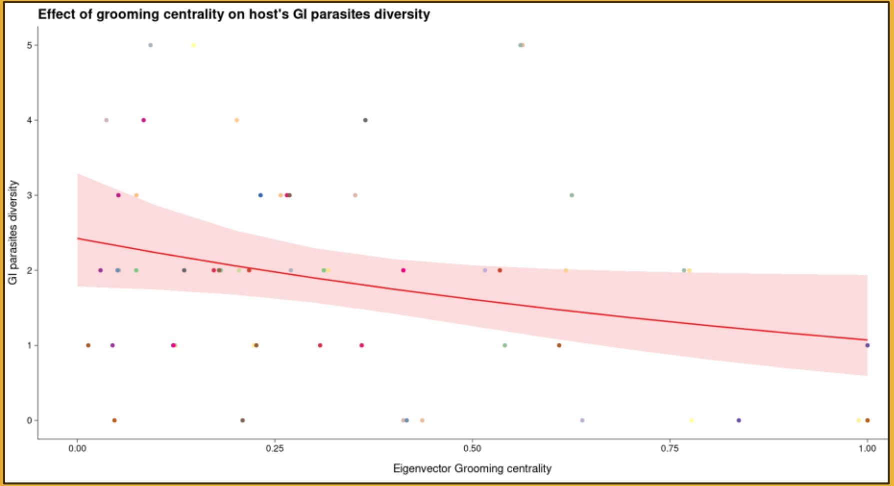
Average pathway distance between **2 infected individuals** ≮ Average distance observed between **2 random individuals**

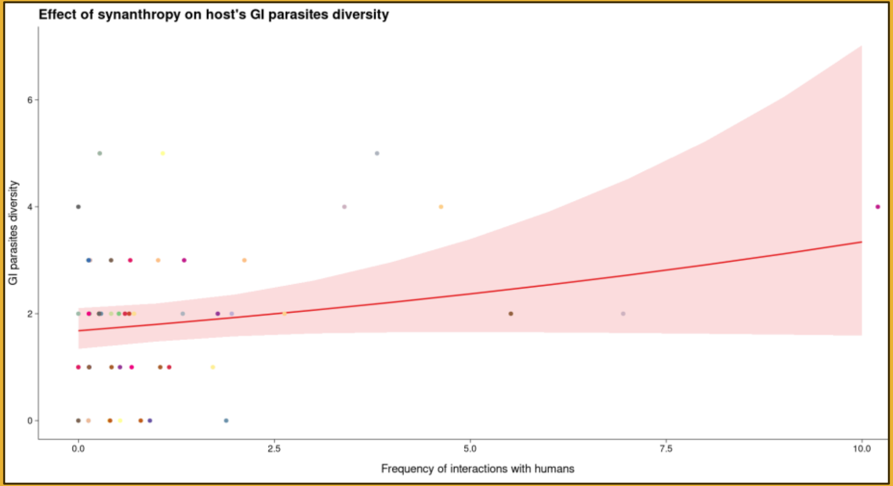
Results indicate that **grooming interactions ALONE** are **not sufficient** to explain the transmission patterns of GI parasites.

GLMMs:

Effects of **grooming network centrality**, **HM interactions**, and **host parameters** on host's **GI parasites species richness**

Best model: **GI parasites species richness**~ grooming_eigenvector + HM_interactions + (1|ID), family = Poisson



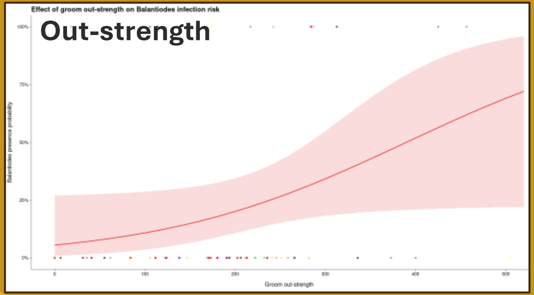



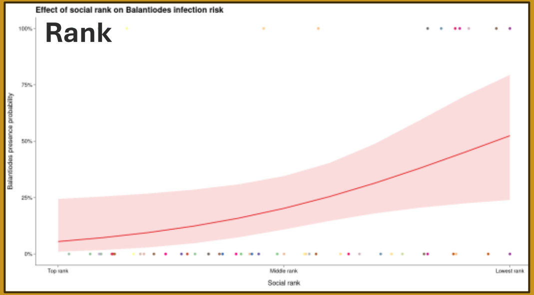

**↗ Eigenvector centrality → ↘ GI parasite species richness**

**↗ HM interactions → ↗ GI parasite species richness**

## GLMMs: Effects of **grooming network centrality**, **HM interactions**, and **host parameters** on **GI parasites taxon presence**

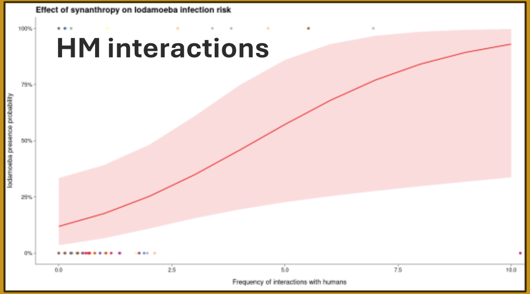
Best model: **GI parasites taxon presence**~ grooming network centrality + HM_interactions + **host parameters** + (1|ID), family = binomial

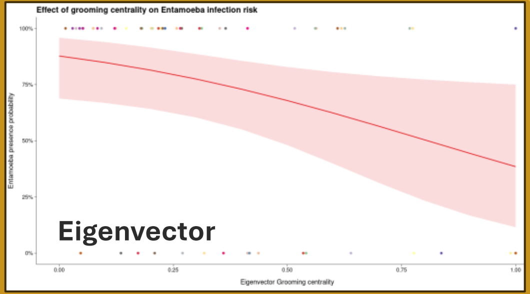



***Balantiodes sp* presence ↗ :**

- ↗ **subordinate** (p = 0.027)
- ↗ **grooming out** (p = 0.049)




***Iodamoeba sp* presence ↗ :**

- ↗ **HM interactions** (p = 0.022)

***Entamoeba sp* presence ↘ :**

- ↗ **eigenvector** (p = 0.032)

**No significant effects** of the explanatory variables on the presence of **helminthic GI parasites**

# Discussion & Conclusion

## Parasitology:

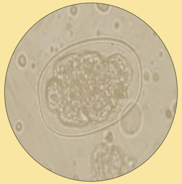
### Protozoa

*Entamoeba sp*

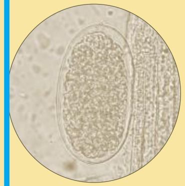
*Iodamoeba sp*

*Balantiodes sp*

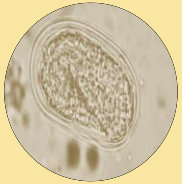
### Helminths



Hookworm



*Oesophagostomum sp*



Strongyloides sp

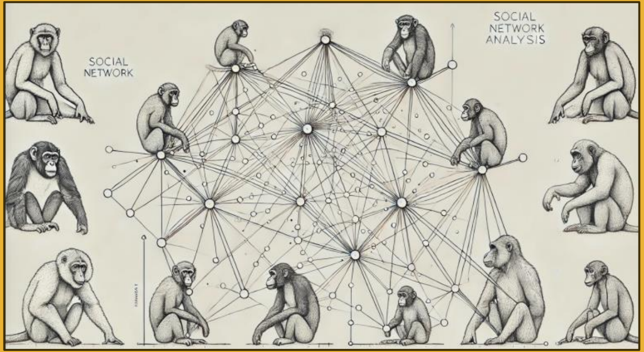
*Trichuris sp*

- ***Entamoeba sp*** → **most found**
  → could be **pathogenic** (cf. *E hystolitica*)

- **Hookworm** → **most found**
  → ***Ancylostoma sp*** or ***Necator sp***

- **Common GI parasites** usually found in primates
- **All GI parasites** found → **direct life cycle**
- **All genera** of **helminths** found → include species that can **cause intestinal diseases**

## Risk factors influencing GI parasite species presence and richness:




Social network pathways → **alone** not explain GI parasite infection, **infection sources = multiple**

- **Social centrality** in **grooming network** → ↘ parasite diversity

**Social buffering effect:** Central individuals have **better health status** and **are less likely to be infected**

**Synanthropic behavior increases** exposure to parasites

GI parasites: **not uncommon, direct life cycle**
**environment** → possible **source of infection**

# Thank you for your attention

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