



Reassembly of species interaction networks – Resistance, resilience and functional recovery of a rainforest ecosystem (DFG Research Unit FOR 5207)

#3, 2025

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I Project speaker's column

Nico Blüthgen, TU Darmstadt

¡Qué proyecto!

Our previous **Reassembly Newsletters** document our discovery phase, full of new impressions in the forest, followed by reflections and new insights from analysing our results. During year three, field work was much less pronounced and then fading out for several of us. Seedlings became saplings and are now quite large tropical trees that are producing fruits. One highlight during 2024 was the symposium at Universidad de las Américas (UDLA) in Quito, where Reassembly connected to the scientific community in Ecuador - hosted by María-José Endara and Juan Guevara Andino (Fig. 1). We had very inspiring keynote talks from our famous project advisors Robin Chazdon, Rob Colwell and Lou Jost, and great discussions with them and many Ecuadorian scientists. The symposium and a follow-up workshop in a Maquipucuna station in the cloud forest showed a great interest among young researchers in Ecuador to connect and collaborate with Reassembly. And our walks through the Canande forest and discussions in the Chocó lab with Robin and Rob left a long lasting impact and helped to consolidate some of the ideas for our project's future. Ideas on the role of remnant trees were stimulated during these hikes, and Robin taught us how some rare palm species and their life forms indicate the history of these forests.

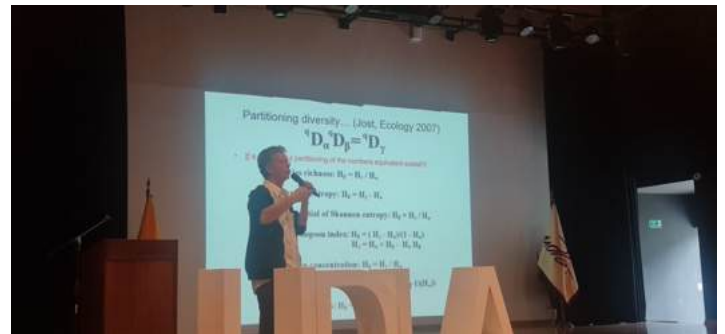


Figure 1: Lou Jost giving his talk during the seminar on "Dynamics of resilience, resistance and functional recovery of tropical ecosystems, at Universidad de las Américas in Quito, March 2024. Photo Courtesy of M.J.Endara

The preparation of our follow-up proposal for a second phase of our Research Unit has started early this year, and speeded up since then. All of us have reflected what we have learned from the ongoing phase so far, and we have compiled our main ideas for the research focus in the next phase. We will continue to work on the plots of the chronosequence, and almost all project leaders will still be involved. Monitoring the same plots after about four years will reveal important information how our models across space (succession age) match the true dynamics in time. Moreover, we will focus on tree-based multilayer networks in secondary forests regenerating from pastures, the role of remnant trees, microclimatic variation and other drivers of spatial variation in forest recovery, particularly during the early stage. Some impressions are included in Edith's report below, who is heavily engaged in the preparation of the new tree plantings that are a core element of the multilayer-networks. There are many, exciting ideas and hypotheses to be tested, but I will not spoiler them all (and all the other secrets) in the Newsletter, of course :)

Another key person has recently left Reassembly to take her next step in her career: our station manager Katrin Krauth. We are grateful for her successful work, personal enthusiasm, effort, patience, and empathetic handling of the people. Julio who already worked at the Chocó lab has taken over the station manager position, and we are glad that he commits his valuable expertise. Although there would be numerous things to add, I would like to hand over the remainder of my Speaker's column to Martin - the other "father" of our Research Unit and CEO of Fundación Jocotoco. Without Martin, Reassembly would not exist. It's his expertise as a biologist and dedicated conservationist - and it's his and Jocotoco's outstanding success in establishing such a huge and relevant network of nature reserves - that made it all happen. What a privilege to work with Jocotoco where scientifically-driven nature conservation is so effectively put into practice, and also so well embedded in local communities. So let us hear what Martin thinks how 'our toddler' is growing.

Fundación Jocotoco

Martin Schaefer

It is good to reflect on Reassembly now, as the intensive fieldwork of the PhD students has come to an end while Edith, Bryan, and others prepare, quite literally, the ground for the next phase of Reassembly. What have we achieved? First and foremost, Reassembly has been a resounding success. This is primarily due to you, the PhD students, hard work during long days and nights on muddy trails. Second, it is also in no small part thanks to our Speaker, Nico, who did a fantastic job in steering and sometimes nudging us towards a common framework, mitigating the small conflicts here and there. There were not many such conflicts, despite us being a diverse group hailing from distinct cultures and perspectives. Again, a success, in no small part due to the long history that many of us share. Third, a dedicated team at Jocotoco did an outstanding job of building the Chocó Lab in record time under the challenging circumstances of a global pandemic in a remote corner of the Chocó—a big thanks to Adela Espinosa, Santiago Arroyo, and the architects involved. Fourth, the plot selection was perfect; it was initially done by Nico, Karsten Mody, and me, based on input from our park guards, and later completed by Nico and Connie. Little did we know about forest recovery at the time. The key ingredient for the compelling and comprehensive design was integrating local knowledge (park guards) with that of tropical ecologists. This is why I am thankful for the work of all of you and Jocotoco's parabiologists and park guards. The products of our joint success are now becoming increasingly visible, as new manuscripts are circulated every month. This is considerably more than most research units accomplish within their first three years.



Figure 2: View of the forest around the "Cabañas" in Canandé

Of course, and despite the constant flow of manuscripts, our understanding of the Chocó rainforest ecosystem remains limited after three years. We started to look at patterns; the underlying processes still need to be uncovered and quantified. Yet, it is remarkable how consistent and complete the recovery of the forest ecosystem has been across taxa and within maximally three decades. That undoubtedly is already one of the key contributions of Reassembly to the global debate in the UN decade on restoration. The message is clear and simple: Nature heals quickly. If we just allow it to recover and if there is enough forest on a landscape level for the recovery to be complete and consistent. Two big "ifs" that are all too often not met, not in the Chocó, not elsewhere in the world. That nature heals quickly is an important message now and will become ever more important in the next few years, as we will see a strong rollback of environmental regulations and protections, not just in the US, but also here in Europe—the delay of enacting the EU regulations on curbing deforestation throughout the supply chains is a good indicator of what is yet to come. To explain why the message that nature can heal quickly is important, let's look at the larger picture. Decades of unfettered environmental destruction now result in humans destroying the very natural foundations on which our cultures, economies, and well-being depend. In an age, where we have more data than ever before, we could learn from the past but choose not to. More and more evidence points to Sumerian, Roman, Mayan and many other empires vanishing owing to the over-exploitation of their natural resources. Collectively, we know this and yet fail to act. Fifty years after the seminal publication of the Club of Rome and more than 30 years after the Earth Summit in Rio, COPs (climate and biodiversity) repeatedly fail to meet global targets. The message is clear: governments won't save us, nor will international treaties. The hailed Paris Agreement intended to limit global heating to 1.5°C above pre-industrial levels. Yet, 2024 has been the first year that we breached the 1.5°C threshold, with a very high probability of it happening again in the next four years. Similarly, none of the ambitious Aichi targets to save the diversity of life was met years ago. And yet, as you have shown nature can heal quickly.

The question to ask here is not how to reconcile global lack of action with nature's ability to heal, as none of us has a global mandate. Rather the question is what can we collectively achieve? I have often been asked, including by some of you, what are Reassembly's benefits to Jocotoco? Even though your data do not influence our management decisions, the benefits are manifold. Quantification of the return of biodiversity is perhaps the most important benefit. Why? Because the conservation sector is inherently weak, relying on storytelling, often an umbrella species as a short-hand for an ecosystem (well-known from WWF campaigns in the 1980-1990s), and normative aims that, at times, are poorly substantiated. We can rarely provide a quantitative answer to what we achieve. Not even to our donors. You all help us doing that.

Another clear benefit is the rapid biodiversity monitoring that Jörg started, and that Jocotoco implemented in other reserves and outside of them. While we are getting used to AI-powered apps that allow us to identify plants and animals in the northern hemisphere, such apps are still non-existent in the tropics. It is not so much the number of species that is challenging, but rather the limited knowledge on their sounds and phenotypes that prevents quick progress. Thanks to the tireless, initial efforts of Jörg's small "army" in October 2021, Jocotoco has invested heavily in biodiversity monitoring and is now at the forefront of a global movement.

The World Bank, the European Central Bank, and other banks are now listening to Jocotoco that AI-based biodiversity monitoring is possible, not expensive, and provides data even in the tropics. Of course, financial markets won't change overnight. However, biodiversity is now a topic that banks are taking seriously. You may add that it is too little



and too late. That is not the point. Neither Reassembly nor Jocotoco can influence banks; it is not what we set out to do. However, if we can contribute an amalgamation of science and conservation that lights the way, it already is a lot. This is the beauty of Reassembly and Jocotoco.



Figure 3: Members of Canandé attending a workshop in Quito. From Left to right: Holger, Miguel Ángel, Bryan, Katrin, Melanie, Leo and Julio. Photo Courtesy: Chocólab

Your work matters. It matters because it contributes towards building a better future, and you help quantifying that path. Since nature can heal quickly, each one of us can have a tremendous impact. That impact is visible. Canandé Reserve tripled in size since the start of Reassembly. The Chocó forests you all roamed will continue to flourish, enabling myriads of interactions in the web of life.

What remains to be done and what could have been done differently?

We should have had the wonderful visit from Robin Chazdon early and not in the middle of the project. Her knowledge is stunning; too bad that few students were able to accompany her on the trails. Comfortingly, Robin confirmed plot selection. She sharpened our view on tree crown formation and its inherent information on past conditions as well as on the age of understory palms. Stunted palms, less than 2m high but a century old, are testimony of a history of forest cover, while artefacts on the ground tell the story of humans living within the forest environment. The very resilience of the Chocó rainforest makes it difficult to piece together this story. In hindsight, I should have prepared better for the first full-blown field season at the beginning of January 2022. With turnover (Adriana moving to Tesoro), Katrin being new,

and high-stress levels and expectations within the sub-projects, it was perhaps to be expected that some conflicts would erupt at that time. At a subsequent meeting in Darmstadt, Nico and I quickly found common ground. Katrin grew quickly in her role and is dearly missed. We have not been terribly successful in enticing others to study the forests and their inhabitants at the Chocó Lab. The workshop in March 2024 provided an opportunity for Ecuadorian researchers to visit the lab that few used. More needs to be done. The (in)famous, yet elusive syntheses of Reassembly will thus be particularly important for placing our findings into a larger context. Ideally, a stronger connection between field results and theory also needs to emerge.



Figure 4: Setting the P-REX experiment in 2022. Photo courtesy of Chocólab

Translating the findings of Reassembly into a larger context remains to be done. For that to be successful, it helps to envision distinct audiences. The larger scientific community that actually reads the syntheses, but also the regional or global audience of practitioners who influence land use changes with their daily decisions. Even well-intentioned actors such as NGOs lack a quantitative understanding of processes and consequences. Analysing underlying processes of forest recovery across multiple trophic levels, while disentangling spatial and temporal effects in phase II is a very useful aim. In conclusion, Reassembly has been a wonderful success, precisely because it measures what we can collectively achieve if we just decide to protect ecosystems, the very nature on which our food, water, and spiritual well-being depends.

SP: Coordination Module

Edith Villa Galaviz, TU Darmstadt

Towards a climax state

In my contribution last year, I described my challenges as the new scientific coordinator. This role is complex; while many responsibilities depend on me, my progress also relies heavily on the input and cooperation of others. This interdependence sometimes slows things down more than people might expect.

The responsibilities of CM, managed through the scientific coordinator, may appear straightforward. However, without administrative experience, it's easy to overlook the extensive effort required. Many complex tasks lie hidden behind simple statements. Take, for example, the phrase: "I went to the beach for the holidays," those few words mask a multitude of logistical efforts, such as saving money, deciding on a destination, setting travel dates, finding affordable accommodations, buying supplies, and often coordinating with others. This planning can take days or even weeks. Similarly, the one-and-a-half-page section on the scientific coordinator's duties in the well-known "Reassembly Book" doesn't capture the countless hours of work and planning they entail. Despite these challenges, I am gradually becoming more skilled at balancing administrative and scientific duties. In the following lines, I'll share some of the small achievements in which I was, in one way or another, involved.



Figure 5: From left to right: Karen, Edith, and Arianna (the mastermind behind forest sounds and cocoa tasting) in the stand of Reassembly for the outreach event "Tag der offenen Tür" of the Technical University of Darmstadt, in Germany, September 2024

CM in administration

Writing letters, arranging invoices, checking the budget, booking hotels and seminar rooms, among other activities I am in charge of, are way too dull to write about. So, for the administrative highlights, I'll focus on this year's most exciting parts. First, I'm pleased to announce that we launched the Gender and Equality Fund for the first time, an initiative suggested by Katrin Heer during our meeting last September. This fund has already supported three small projects led by Ecuatorian women who, without this support, would not have been able to pursue their research. This fund is administrated by the steering committee, whom I would like to thank for their support in this and other activities. Second, I helped organize a couple of outreach activities, and as usual, I helped organize the different meetings we had in Reassembly. Details of these activities are provided below:



Figure 6: The Chocólab team and attendees of the outreach event "Casa Abierta" in Candandé, Ecuador, August 2024.

1. Outreach activities in Ecuador and Germany

This year, CM shared the research we do in Reassembly in two outreach activities: "Tag der offenen Tür" in Germany (Fig. 5) and "Casa Abierta" in Ecuador (Fig. 6). Tag der offenen Tür took place in Darmstadt to celebrate the 150th year of the Botanical Garden of the Technical University of Darmstadt. Reassembly had a stall where all the members of Ecuador. Arianna and I created a stand where visitors could see and listen to some of the animals of the Chocó while enjoying a hot cacao beverage. Meanwhile, Nico amazed experienced minds with a presentation on the Reassembly project, and despite their long life experience, they were curious enough to visit our stand after the talk.

However, our most significant achievement was organizing the "Casa Abierta" event in the Canandé Nature Reserve. The event was the first encounter between the project and the inhabitants of surrounding towns. The particularity of this event is that it did not have the standard approach of researchers explaining their research to locals. In this event, the parabiologists and park guards, who are also locals, presented to their families, neighbors, and acquaintances the work they do for the Reassembly project or the nature reserve. The event consisted of seven presentations at different points in the laboratory of Chocólab. The presentations were five from parabiologists, one by the Chocólab manager, and one by the park guards who had set a stand on the Joco-toco Foundation. Parabiologists explained the activities they do in the projects they support, while the manager of the Chocólab (Katrin) gave the Reassembly project, its structure, importance, and some findings.

The presentation was prepared by CM (scientific coordinator) with information provided by SP2, SP4, SP5, and SP6 and adapted by the Chocólab. The event attracted around 60 visitors of all ages and genders; people expressed having a good time, so we hope to repeat this activity and have some researchers on-site next time.

Lastly, I thank Arianna, Karen, Karla, Eva, Santiago, and Ana R. for providing information, pictures, videos, and ideas for the different events and the Chocólab for organizing the Casa Abierta event. Likewise, as a research unit, we want to acknowledge the Jocotoco Foundation for supporting the event and providing food for attendees through Jocotours.

2. Reassembly meetings

One of the key responsibilities of the scientific coordinator is organizing meetings within the Research Unit, and I'm pleased to share that it's been a productive year in this regard. This year, we launched the Reassembly Monthly Meetings for the first time, aiming to provide a regular update on the progress within our research unit and a platform for those outside CM to stay informed. Although this initiative is still a work in progress, it has significantly fostered a sense of constant connection, improving upon the two annual meetings we previously held.

We, also, held our annual in-person meeting in January in Höchst im Odenwald. This meeting included a workshop on scientific writing, which I conducted, and a statistical workshop in Darmstadt taught by Nico and Michael Staab. In March, as Nico mentioned María José and Juan organized a seminar in Quito, Ecuador.

In addition to these seminars, we hosted two meetings in Darmstadt focused on planning the second phase of our project. To close the year, Karen, Malika, Eva, and I have been organizing a seminar session to showcase presentations from our Research Unit and related projects at the 8th European Conference of Tropical Ecology in Amsterdam. This session won't be the only Reassembly-related event at the conference; on the final day, we will have a workshop on gender and diversity titled "Intersectionality: Mainstreaming Gender Actions in Academia." The workshop will feature Andrea Robles (Particip GmbH), Dr. Ananya Chakraborty (World Resources Institute), and Prof. Dr. Sreerupa Sengupta (Goa Institute of Management) as instructors. Malika, Katrin, Heike, María José, and I have been organizing this event, and we hope it will serve as a meaningful step toward fostering a more inclusive academic environment.

CM in science

Last year, we installed rain gauges and have now collected a year and a half of data from Tesoro and Canandé. Despite last year being an El Niño year, we observed that Tesoro consistently receives more rainfall annually compared to Canandé. We are also pleased to report that we encountered no issues downloading data from the iButtons this year. This information will contribute not only to the field site description paper led by Sebastian but also to a manuscript being prepared by Felicity on the environmental data of the Reassembly project.

In the meantime, I've made progress on the synthesis I lead. While the process has been slow due to ongoing data corrections, I am optimistic that I will submit the paper during the first half of next year. Among the new findings, we observed a general increase in climax and rare species along the chronosequences and a decline in pioneer species. While this trend aligns with expectations, our results do not support the intermediate disturbance hypothesis. Pioneer species showed a sharp decline during early regeneration stages. In contrast, climax species demonstrated a significant increase during later stages of regeneration.

This results in no higher species richness in the secondary forest due to an overlap of pioneer, intermediate, and climax species. Besides, many species do not prefer a successional state (e.g., generalist species) (Fig. 7).

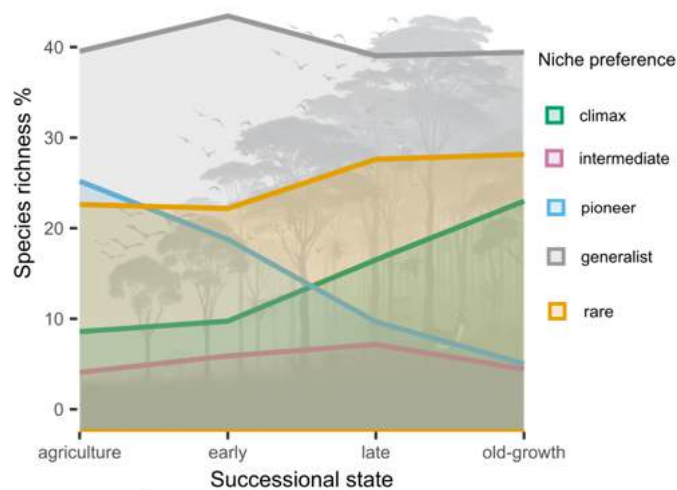


Figure 7: When adding all the data sets analyzed, considering that each one should contribute equally to the total community, we observed the expected increase in climax species and decrease of pioneers as the forests recover

Reassembly's second phase: setting up the new plots

It was just last year when I first learned about the plots in the Reassembly project. It's hard to believe that this year, I returned to establish a new set of 25 plots, subdivided into four blocks, for the project's second phase. This phase will involve planting 16 tree species, each representing different stages of forest regeneration after pasture abandonment, from early recovery to old-growth forest.

Our primary focus is on pastures, especially those in the early years of abandonment. In these areas, grasses grow much faster than forest species, making it difficult for seedlings to survive. One of our biggest challenges in setting up the new plots was removing the grass in a minimally invasive yet practical way, considering Canandé's hilly terrain, staff availability, and other ongoing activities at Chocólab (Fig. 8).

To address this, we covered each 16m x 6m block with plastic sheets and placed 192 tubes to mark the positions of the plants within each block. The work was arduous, particularly under the intense sun, a consequence of the drought Ecuador is currently facing. However, thanks to the dedicated efforts of Julio, Bryan, Leo, Aníbal, Franklin, Jender, and José (the park rangers who stepped in when we were short-handed), we successfully set up the new plots.

In addition to some of the "old" Reassembly plots, the new phase includes several new plots in the southeastern part of Canandé, in an area known as Caserío. This location will host a new field station, set to be completed next year.

A key figure in this second phase is Fredy, a parabiologist who has previously worked with Sebastián. Fredy is an expert in plant identification, capable of recognizing many tree species down to the species level, and he has extensive knowledge of propagation techniques (Fig. 9).

During the initial days of this effort, Sebastián joined us to help create some maps of the trees within the plot for the proposal. He also suggested additional tree species as backups in case we couldn't find the original ones. Furthermore, he assisted with plot setup and came up with the great idea of creating "palo regla" (measuring stick) to measure the distance between plants.



Figure 8: A couple of blocks in one of the new plots for the second phase. We laid plastic sheets to prevent grass from interfering with the survival of the seedlings. Each white marker indicates the position of 10 individuals belonging to the 16 species planned for planting

A special dedication to Chocó lab past and current members

As the main connector between the Chocólab and the rest of the Research Unit, I want to thank all the members of the Chocólab. The team of Tesoro Escondido Reserve has kept their support to the different activities of the Reassembly project, and we are thankful to all its members. Meanwhile, within the team in Canandé, I am happy to have Bryan and Leo, our more extended members, in the Chocólab. Bryan is always giving practical solutions being critical in maintaining the Chocólab running this year. Likewise, Leo has become the herpetology expert among the parabiologists, supporting all the herpetologists in our research unit without stopping to help CM. We are grateful to both of you!

The Chocólab underwent several member changes; Jordi, Jefersson, Jender, Fredy, and Lady left early this year. They highly supported SP4 and SP5, CM, and we wish them all the best! Fortunately, Miguel Angel, who did a great job working on a daily paid basis, joined our team in March. This year, the Chocólab had the help of four fantastic short-term members: Melanie, Holger, Fredy, and briefly Oscar. Melanie and Holger supported a collaborator in Reassembly (Prof. Antonia Abels working with Thomas Schmitt) and Fredy our plant expert. Thank you very much to all of you!

Among all the changes, I think I talk on behalf of the whole Chocólab when I say that the hardest departure was Katrin's, the manager of the Chocólab, who left in October. Katrin did a great job shaping what is now the Chocólab's structure. She also distinguished herself by giving great ideas to CM and other projects. We are very thankful to Katrin and we know she will succeed on her new path! Julio, the previous manager's assistant, took the manager position. We saw Julio's growth as an assistant, and as so it he was the best to do the job. Welcome back!

For those wondering about Tarsilo, Reassembly's mule, he's doing exceptionally well! He's now living with Don Vinicio, who is taking great care of him for a modest fee (money that Tarsilo pays back with all the work that he does for us). Tarsilo has enjoyed excellent health throughout the year, and anyone who hasn't seen him will notice some extra pounds. I hope the coming year brings him even more happiness and good fortune!



Figure 9: Some of the plants for the second phase that are growing in the greenhouse.

SP: Coordination Module

Sebastián Escobar, Universidad de Las Américas

What everyone should know about my work

I am one of the two postdocs in the research unit Reassembly, working with trees, phylogenies, genetic barcodes, among other stuff. I am part of the Coordination Module (CM) and I am in charge of generating forest structure data, assisting logistically to students and researchers, and writing papers! I am employed at Universidad de Las Américas (UDLA) in Quito-Ecuador, where I collaborate directly with Dr. María José Endara and Dr. Juan Guevara, and also coordinate laboratory procedures for genetic and chemistry analyses.

Activities

1. Tree inventory

The tree inventory was finished during 2023, and herbarium work was "finished" during the first semester of the current year. I use "" because herbarium work could last years if we would like to identify each of the collected samples to species level. Nevertheless, for the sake of finishing all assignments on time, I decided to stop herbarium work when > 98% of surveyed individuals were identified to species or morphospecies level. Herbarium work should be resumed later to identify all or most of the surveyed individuals, and to describe potential new species that were found during the tree inventory. So far, we have identified 7408 out of 7542 individuals, representing 539 species and morphospecies. Only 134 individuals are left for further identification, with 73 of them being currently identified through a genetic barcoding approach. This represents the research thesis at UDLA of the undergrad student Mateo Bosquez. He is amplifying the ITS2 region from bark and wood samples collected during the tree inventory. These samples were collected because some trees lacked leaves during the survey or because we were not able to spot their leaves, impeding their morphological identification. Mateo has already generated DNA sequences for these samples, and he is currently comparing his results with the barcode library of Reassembly to provide a species name to those trees. It is expected that these 73 individuals will be identified during the following weeks, increasing the number of identified samples during the tree inventory. In addition, the student Daniela Fierro defended her undergrad research thesis early this year at UDLA. She modified a DNA extraction protocol for wood samples, which was later used by Mateo during his thesis.

2. Site description paper

The much anticipated site description paper was finished during the first trimester of 2024 and submitted to the Journal Ecosphere as an Innovative Viewpoint in March. After two rounds of revisions and other unexpected delays, the paper was accepted for publication in the aforementioned journal. We are currently at the last stages of publication, and we expect that this paper will be available to the public before the end of the current year. Because an early version of the paper was submitted as a preprint to bioRxiv (<https://doi.org/10.1101/2024.03.21.586145>), it has already started accumulating citations from students and researchers from Reassembly. So far, the preprint has been cited three times and many more citations on the actual paper are expected in the following months and years.

This paper describes the experimental design of the Reassembly chronosequence and its scientific background. The chronosequence consists of 62 plots (50 x 50 m), including active agriculture, regenerating

forests, and old-growth forests. The main results of this paper are: 1) The time of regeneration of the plots is not correlated with elevation, showing that old-growth forests are not necessarily located at higher elevations in more remote areas; 2) Forest structure variables and tree species richness increase along the chronosequence of forest regeneration, fully recovering at the same levels of old-growth forests at different time spans. Forest structure variables such as number of stems, vertical vegetation heterogeneity, and light availability are the fastest to recover just after 30 years. Tree species richness was estimated to recover after 76 years while aboveground biomass (AGB) recover after 206 years (Fig. 10), being the forest structure variable to take the longest before reaching old-growth forest levels; 3) Linear models showed that regeneration time is the main factor driving the recovery of forest structure variables and tree species richness. Other explanatory variables such as elevation, precipitation, and soil composition showed almost null effect on the recovery of forest structure and tree richness; 4) Variables such as AGB, basal area, and maximum tree DBH show low resilience and resistance capacity (Fig. 11), being the reason for their estimated long recovery. On the other hand, variables such as number of stems or light availability show either high resistance or resilience capacity, which contributes to a relatively rapid recovery.

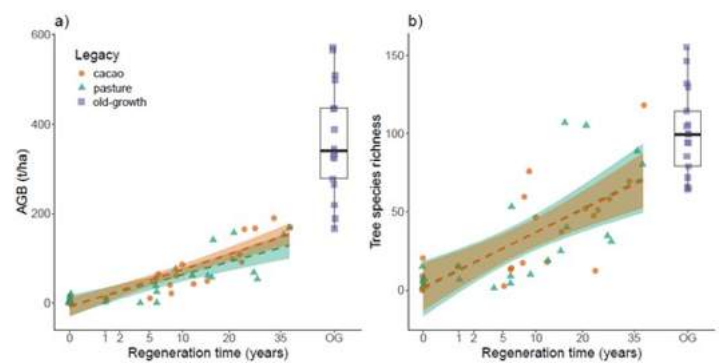


Figure 10: Recovery of aboveground biomass and tree species richness.

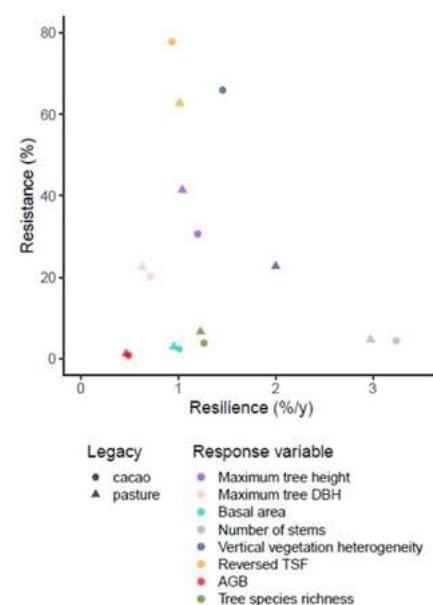


Figure 11: Recovery dynamics of forest structure variables and tree species richness.

3. Phylogenetic synthesis paper

After finishing and submitting the site description paper, I started working on a synthesis paper that uses the community data of trees and animals. A first draft of this paper has been already produced and it will be sent to all Reassembly members in the following days. Although a growing body of evidence has shown that communities can recover after ecosystem disturbance, few of them have explored this issue from an evolutionary perspective. This can be done by implementing phylogenetic trees to community data, which allows exploring the recovery of phylogenetic diversity (PD) and structure along the chronosequence of forest regeneration. Phylogenetic diversity measures the total amount of phylogenetic distance among species within a community based on the length of the phylogenetic tree branches [4]. It theoretically implements multiple dimensions of biodiversity because it is usually correlated with species richness and functional diversity, however this last relationship tends to be statistically significant but weak [6, 3]. Because of this, PD represents a potential useful measure of restoration success [1], and hence the importance of studying its recovery. The recovery of PD was faster compared with the recovery of species richness for angiosperm trees, bats, and dung beetles, while PD recovered after species richness for leaf-litter frogs, frugivore birds, and ants (Fig. 12). The fastest recovery time of PD was determined for ants just after 12 years while the longest recovery time was determined for bats after 91 years.

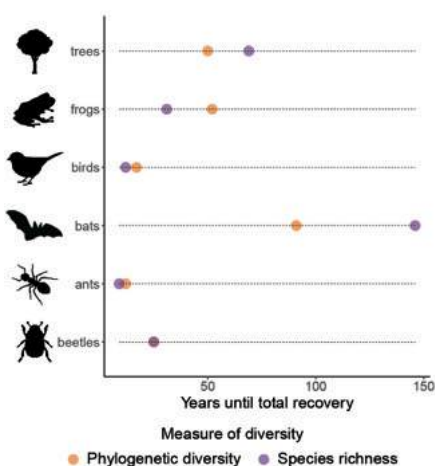


Figure 12: Recovery time of phylogenetic diversity and species richness in trees and animals.

The change of phylogenetic structure was also analyzed. Based on how related species are within a community, communities can be clustered or overdispersed. Phylogenetic clustering usually occurs at early stages of forest regeneration when closely related species coexist within a community [8]. Closely related species tend to share similar niches and display similar phenotypes because of their evolutionary proximity, allowing them to colonize and establish in recently disturbed habitats after counteracting abiotic filters such as high solar radiation, high temperature, or low humidity [7]. On the other hand, phylogenetic overdispersion occurs at late stages of forest regeneration when species within a community are distantly related [2]. These habitats provide a variety of resources and niches that can be used by phylogenetically distant species that tend to display different traits, promoting competition for these resources using different mechanisms [7, 5]. Contrary to previous research and our expectations, we only observed an increase in overdispersion with succession for birds (Fig. 13). For frogs, we observed the opposite pattern. Random patterns of phylogenetic structure were observed for trees, bats, ants, and beetles.

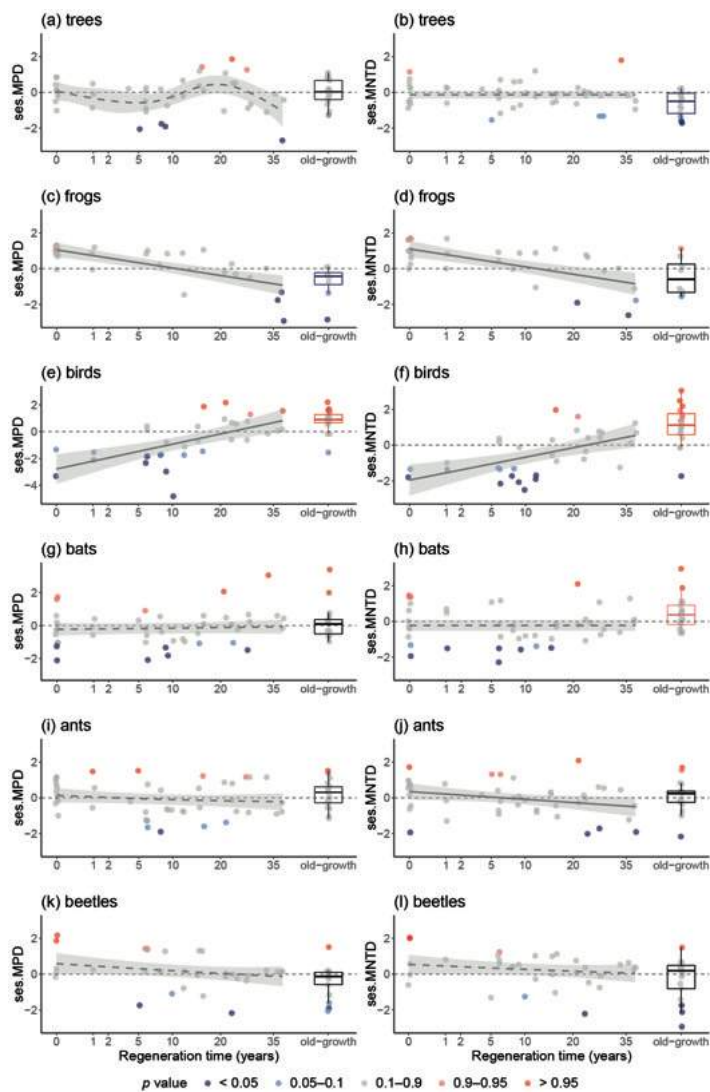



Figure 13: Changes in phylogenetic structure along the chronosequence in trees and animals. Significant values below zero indicate phylogenetic clustering (blue) while those over zero indicate overdispersion (red). Solid trend lines represent statistical significance ($p < 0.05$) in the linear models.

4. Genetic barcoding

During 2024, ITS2 barcodes for most of the species recorded during the tree inventory were generated. So far, ITS2 barcodes have been obtained for around 550 tree species. These barcodes were kindly processed and cleaned by Dr. Alexander Keller and they are already being used by PhD students to identify pollen, seed, and seedling samples. More ITS2 barcodes of different species will be generated and sequenced up to the first trimester of 2025, completing the tree ITS2 barcode library. Additionally, the regions *rbcLa*, *matK*, and *YCF5* have been also amplified for trees and their sequencing is expected to occur during the first trimester of 2025. In this way, the barcode library will increase to four or more regions, potentially becoming an important reference for tree genetic identification in the Chocó. Laboratory procedures were managed and performed by the lab technicians Ing. Doménica López and Ing. Daniela Fierro.



5. Research permits

Although most students and researchers already finished their field work, there were still several permits for processing during this year. In total, 1084 samples were mobilized from Canandé to Quito with eight mobilization permits during this year. Also, eight export permits (one CITES) were processed for sending samples to Germany and the USA.

Plans for 2025

The phylogenetic synthesis paper will be submitted to an appropriate journal during the first weeks of 2025. During the first semester of 2025, I will write a third paper on the changes of the tree community along the chronosequence, including changes on their taxonomic, functional, and phylogenetic diversity. For this paper, I will also explore changes in beta diversity and community composition. I expect to submit this paper during next year's summer. In addition, two papers are expected to be written based on the results obtained in the molecular biology laboratory. These papers will be written by former students and current lab technicians that processed the tree samples. One will be written on the use of wood samples for tree identification, which will include the modified DNA extraction protocol. The second paper will be on the genetic barcode library as a tool for tree identification in the Chocó. Lastly, I plan to perform a pilot study next year with Dr. Katrin Heer on the genetic diversity of seedlings and on seed and pollen dispersal dynamics using genetic tools. Stay tuned!

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SP1: Theory and modelling

Timo Metz, TU Darmstadt

Introduction

This year a lot of my time went into working on a synthesis project of REASSEMBLY which I am leading together with our project's speaker Nico Blüthgen. However, I was also able to spend another 7 weeks in Ecuador, in order to perform some fieldwork at our beautiful study site in Reserva Canandé and take part in a workshop in Quito.

Field impressions

This year I was again going to the field in order to support an experiment of Nico Blüthgen. There, we studied the feeding preferences of orthopterans. I was doing the field work and the experiment with two PhD students of Nico (Margarita Hartlieb and Johanna Berger). During multiple trips to the beautiful forest around our station we collected a large variety of orthopterans and studied their feeding preferences by feeding them young and old leaves of 12 different selected plant species that are common to the area in Reserva Canandé. The experiment involved a lot of work in the lab. We had to cut pieces of a known size from the leaves we collected and quantify the fraction eaten by each individual. While the work in the lab was time-consuming, I also got rewarded with a lot of knowledge about the orthopterans from Canandé. I was able to learn a lot from Margarita and Johanna, who have much more experience with these animals. As a theoretician, a lot of my time is spent on the computer, and I mainly deal with ecological theory, models and data. It was very good to experience a different aspect of ecology, and get to know how an experiment is performed. Currently, we are analyzing the data from the experiment, and a publication will follow at some point.

This year I was also able to visit the beautiful Reserva Tesoro Escondido. Yadira, who is the field director of that reserve, was guiding Margarita, Johanna and me to many REASSEMBLY plots in the reserve. The forest in Tesoro Escondido is truly amazing, and we were also able to see the endangered brown-headed spider monkey (*Ateles fusciceps fusciceps*). The reserve provides an important habitat for that species and contributes significantly to protect it.



Figure 15: A beautiful sunrise at our station in Reserva Canandé.



(a) Preparing food for the orthopterans (b) Really getting used to stick insects

Figure 16: In the lab

Impressions from the workshop at Universidad de Las Américas and Reserva Maquipucuna

During my stay in Ecuador I was also able to go to a workshop at the Universidad de Las Américas (UDLA) in Quito organized by REASSEMBLY. The other PhD students of REASSEMBLY and me could present a poster. I presented the work that I have done for the synthesis project. At the workshop there were presentations by our speaker Nico Blüthgen and Martin Schäfer, who is the CEO of Fundación Jocotoco. Furthermore, there were also talks by the project's scientific advisor Robin Chazdon as well as Rob Colwell and Lou Jost, who are experts on the analysis of ecological data. On the second day of the workshop we went to the beautiful Maquipucuna reserve. We listened to presentations of Ecuadorian researchers and were able to do some hikes in the beautiful reserve. Unfortunately, we could not see the famous Oso Andino (Andean bear), because it was not the right time to see this beautiful animal at this place. However, there were many nice birds and other animals to see that made the stay at Reserva Maquipucuna rewarding. After the workshop, Robin Chazdon and Rob Colwell came to Canandé for a few days. During multiple hikes with Robin and Rob to different plots in the study site, we could learn a lot about secondary forests, the analysis of ecological data and how to improve the study design. I am very grateful that I had the opportunity to meet these amazing and inspiring scientists.



(a) Getting used to stick insects



(b) Nico, Margarita and Johanna

Figure 14: Working with orthopterans and phasmids



Figure 17: Going to the field with our amazing guide Yadira (second on the right) in Reserva Tesoro Escondido.

Synthesis work

Currently, I am working on a synthesis paper that uses community data from various taxa that are studied within the REASSEMBLY research unit. I calculate the recovery trajectories of biodiversity for these taxa along the chronosequence by calculating the recovery time and partitioning the recovery time into two distinct stability components: resistance and resilience. Resistance refers to the biodiversity that is left in the active agriculture plots compared to the old-growth forest plots as a reference. Resilience refers to the speed of recovery back to old-growth forest conditions. I am mostly interested in the recovery of the species composition, but I also study the species diversity and abundance. The results that we obtain are very interesting and promising. However, I will not tell too much about the results here to keep you curious about the publication that will follow from this work.

Outlook

All collaborators of that synthesis project have contributed a lot to make the project result in a very nice paper. I hope to be able to submit the synthesis paper late 2024 or early 2025. As the work is in an advanced stage, I am quite confident that this could be possible.



SPi: Dynamics of weighted bipartite networks with intrinsic node properties

William J. Castillo

Albert-Ludwigs-Universität Freiburg

What we do

One of the main goals of the Reassembly Research Unit is to identify the rules underlying the reassembly of populations and communities in the rainforest through the dynamic assembly of biological interaction networks. In other words, we want to describe the behaviour of the large-scale properties of the forest based on the properties, interactions and dynamics of the elements that make up the rainforest. In this document, we provide a condensed description of our approach toward achieving this objective. We developed a model that connects the dynamics of a real ecological network, incorporating the functional traits and phenology of interacting species, with the description of the community structure [6].

Dataset

The dataset used to develop our model, Burkle et al. [4, 5], investigated the effects of wildfire severity on ecological drivers of interaction in plant-bee communities, considering the role of bees as pollinators. In this context, the two disjoint sets of nodes in the bipartite network represent plant and bee species. Specifically, 116 plant species and 191 bee species are connected with weighted links indicating the number of interactions between each pair of nodes of these trophic levels (Figure ??). Also, the functional traits of plant (plant height, number of flowers per stem, flower head dimensions) and bee species (intertegular distance, size, abundance) were recorded. This implies that nodes possess inherent properties that are critical in shaping the dynamics of competition for interactions.

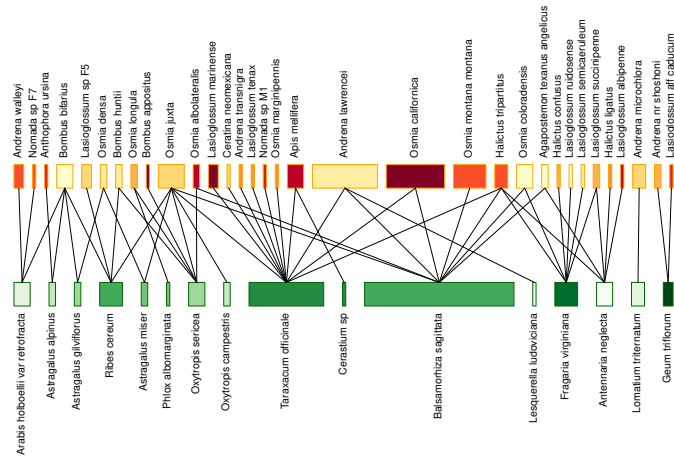


Figure 18: Bipartite network representing the interaction of bee and plant species collected in the Northern Rocky Mountains of Montana, USA. The top/bottom boxes represent bee/plant species. The size of these boxes is a qualitative representation of the number of interactions that each species has.

The data collection process recorded the time that each bee visited a flower, allowing the creation of a time series where each step represents a state in the assembly process of a plant-pollination interaction network (Figure 19). A total of 2589 biotic interactions are distributed over 53 time steps with an average interval of 1.7 days and an average of approximately 49 interactions per day (Figure ??). We observed a notable increase in

the number of interactions over time, peaking towards the end of the season. This trend appears to be driven by the phenology of both plant and bee species and we incorporated it into our model as a second-degree polynomial, $m(t^2)$, with parameters derived from the total number of interactions per time step (see Figure 19). This representation of the phenology, with a coefficient of determination of 0.21, provide a better approximation of the dynamical evolution of the real bipartite network, while still allowing for an analytical solution of the equations.

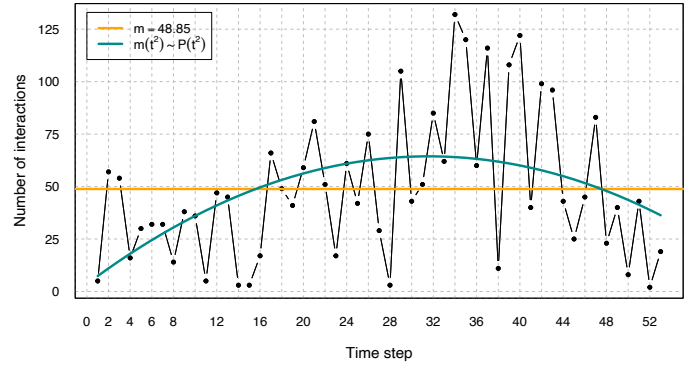


Figure 19: Total number of plant-pollinator interactions recorded at each time step over a period of 53 steps starting on 20 May 2014. The yellow line shows the average number of interactions. Meanwhile, the green line represents the variation in the number of interactions over time, modelled by a second degree polynomial, $m(t^2)$.

Method

Among several robust results that represent the dynamic ensemble of networks [3], we will base our study on the model of scale-free networks [1]. Therefore, the dynamical process that assembles a real weighted bipartite network is described by an extension of the model developed by Bianconi, G. et al. [2]. We associate the competition for interactions with species of a different taxonomic level with the intrinsic attribute of each node i . This attribute η_i , where $\{\eta_i\}_{i \in \mathbb{N}}$ has a desity distribution $\delta(\eta)$, defines the temporal evolution of the strength of the node (i.e., the number of interactions of a node) as:

$$s_i(t, t_0) = m(t^2) \left(\frac{t}{t_0} \right)^{\frac{2\eta_i + \eta_{max}}{C}}, \quad (1)$$

where $m(t^2)$ represents the effect of phenology in the assembly process, t_0 is the first time that the node i connects to the network, and C is a scalar value defined by the dynamical ensemble of the network:

$$1 = \int_0^{\eta_{max}} d\eta \rho(\eta) \frac{\eta}{C - \eta}, \quad (2)$$

with η_{max} is the maximum value of $\{\eta_i\}_{i \in \mathbb{N}}$.

Results and Discussion

Consistent with equation (1), 93.3% of the tested plant species and 96.9% of the tested bee species exhibit interaction dynamics that change over time, following a power law function (Figure 20). Therefore, to assess the model we focus on the dynamic exponents $\beta(\eta_i) = \frac{2\eta_i + \eta_{max}}{C}$. For each plant and bee species, we compare the exponent of the power law fitted from the empirical data (the number of interactions over time) with the exponent of the power law predicted by their respective theoretical model. In a logarithmic plot (Figure 21), we thus compare the slope of the power law curve (represented by black dashed lines) fitted from the empirical data (depicted as black dots) with the slopes of the



power laws produced by the theoretical models (depicted by solid lines). Additionally, we selected three functional traits that capture different mechanisms by which plant and bee species compete for interactions, each characterized by an approximate density distribution $\rho(\eta_i)$ (Table 1).

The dynamics of a species interaction depend on the community of species at the same trophic level and their capacity to engage in interactions. Furthermore, we find that the model's fit improves across all tested traits as we incorporate additional traits when calculating the dynamic exponents. This underscores the importance of the final network size, as these exponents are sensitive to the density distribution of the traits involved. The representation of plant and bee species phenology, $m(t^2)$, also depends on the community of species that comprise the network (Figure 19). This second-degree polynomial improves the fit and provides flexibility and adaptability to the model. The initial conditions for the dynamic evolution of a species of interest can always be adjusted with a proper selection of the parameters of such a polynomial (Figure 21).

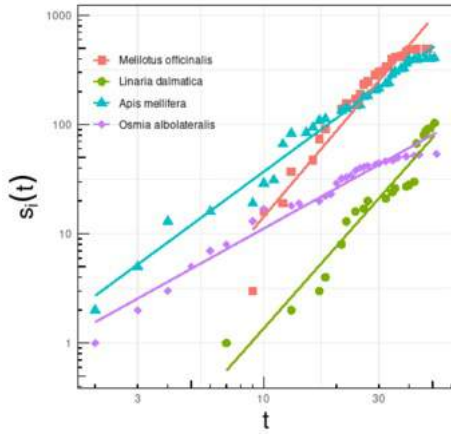


Figure 20: Time evolution of node's strength for plant (■ and ●) and bee species (▲ and ◆). The lines, with coefficients of determination of 0.93, 0.94, 0.98 and 0.97 respectively, represent the linear extrapolation of the dynamic evolution of each species.

Table 1: Traits of flowers and pollinators included in our analysis. The notation $\rho(\eta_i)$ indicates the distribution that best describes the trait distribution for each species. Additionally, error statistics are provided for each trait, including the residual sum of squares (RSS) and the root mean squared error (RMSE).

Level	Trait	$\rho(\eta_i)$	RSS	RMSE
Plant species	Plant height	Log-normal	344.70	2.14
	N. Flower Inf.	Exponential	388.70	2.28
	Capitula width	Log-normal	385.93	2.27
Bee species	ITD	Normal	2113.34	3.99
	Body size	Log-normal	2141.95	4.01
	Abundance	Exponential	2219.18	4.08

In both trophic levels, our model approximately reproduces the dynamics of the species community (Figure 22). For each trait, the set of dynamic exponents produced by our model has a mean value that closely matches the exponents from the empirical analysis. The range of values of the empirical exponents of the whole community is larger than the range of dynamic exponents produced by the two models within each functional trait (Figure 22). This discrepancy arises from differences between the assembly process of the real bipartite network and the mechanism we assume to generate our model, as described in detail in [6]. Particularly, the stochastic number of new species per time step in the network deviates from our assumption of adding just one species to the system per time step. Additionally, the relatively small size of the

network produces deviations in the expected behaviour described in the theory, known as edge effect. Here, in particular, the steep decline in interaction rate at the end of season is not matched well by the quadratic function, leading to what appears to be a saturation.

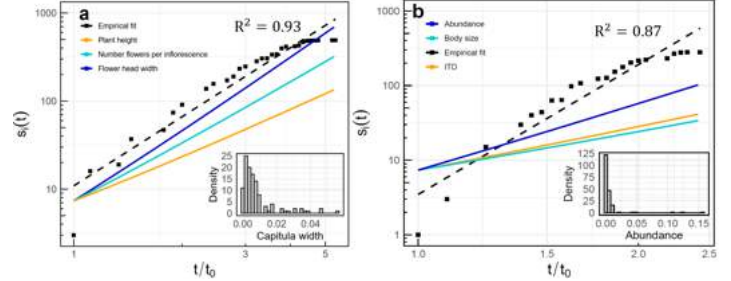


Figure 21: Interaction dynamics of **a.** *Melilotus officinalis*, and **b.** *Heriades cressoni*. The inserted figures represent the density distribution $\rho(\eta)$ of the trait that yields the optimal fit for the data.

From this analysis alone, we cannot establish a trait that performs significantly better for both trophic levels. The trait that best describes the dynamic interactions of the species depends on each individual species (Figure 21). The sum of square residual (RSS) and root-mean-square error (RMSE) of the model for each trait are similar between models of the same level in the food chain (Table 1).

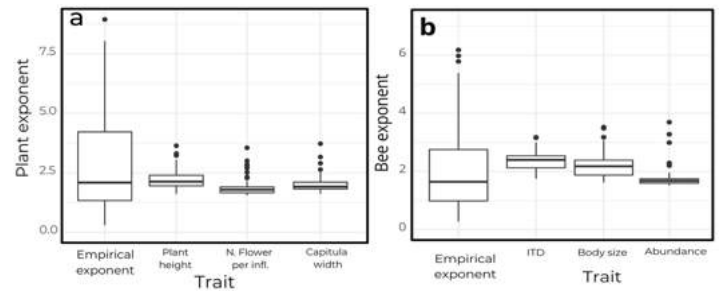


Figure 22: Distribution of dynamic exponents for **a.** plants and **b.** pollinators with three functional traits each. The empirical exponent corresponds to the slope of the best fit of the data in a logarithmic plot.

Conclusions

Despite the relatively small size of the system we are studying, our model demonstrates the applicability of complex network theory to ecological networks. Building upon the Bianconi-Barabási model, our approach reveals that a new species in the network with few interactions can acquire interactions at a high rate if it has a large trait value. This highlights the model's ability to potentially capture the dynamics of species interactions by integrating morphology and phenology. Its simplicity allows for an approximate reproduction of community dynamics across both trophic levels.

Throughout the development of the model, we thoroughly explored various topological features of bipartite networks and alternative assumptions regarding the mechanics of the assembly process. However, none of these models yielded superior results compared to those presented in this work. Moving forward, further development of the model would benefit from datasets representing larger networks with even higher sampling intensities throughout the seasons. Additionally, datasets collected in non-seasonal environments, such as the tropics, would provide valuable insights for enhancing the model's robustness and applicability.

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SP2: Leaf-litter processes on the forest floor - Decomposition and predator-prey networks

Arianna Tartara, TU Darmstadt

Recap

This past year felt considerably different from the previous ones. After two years marked by fieldwork immersed in the vibrant ecosystems of the lowland Chocó, I found myself shifting gears entirely. This last twelve months were dedicated to the lab and to making sense of the wealth of data I had collected during earlier field seasons. More than ever, I came to terms with the complexity of my project. Spanning multiple facets of tropical ecology, it represents for me a thrilling yet a challenging experience. Over the year, I made substantial progress on three key fronts: leaf litter decomposition, arthropod communities, and the chemistry of poison frog alkaloids.

Leaf litter decomposition and related processes

One of the highlights of this year was deepening my understanding of the dynamics of leaf litter decomposition along a chronosequence of forest recovery. Using litterbags (LMB) and teabags (TMB), I uncovered intriguing patterns in decomposition, discerning between decomposer communities by mesh size (small arthropods and microbes, respectively). Firstly, decomposition in LMB followed a U-shaped trend, suggesting a more nuanced response by arthropod decomposer communities in reaction to forest succession. In contrast, microbial communities exhibited a steady increase in activity over time in the above-ground TMB. Both findings align with the idea that older forests foster higher decomposition rates, likely due to their more stable microclimates and the presence of well-developed decomposer communities. This trend could reflect enhanced activity by microbial decomposers, such as fungi and bacteria, supported by the structural complexity of mature forests. Below-ground TMB showed a weak negative correlation with forest succession stages, with consistently higher decomposition rates than above-ground samples. This suggests that below-ground processes may recover differently, influenced more by factors like soil pH and nutrient availability than by above-ground vegetation structure.

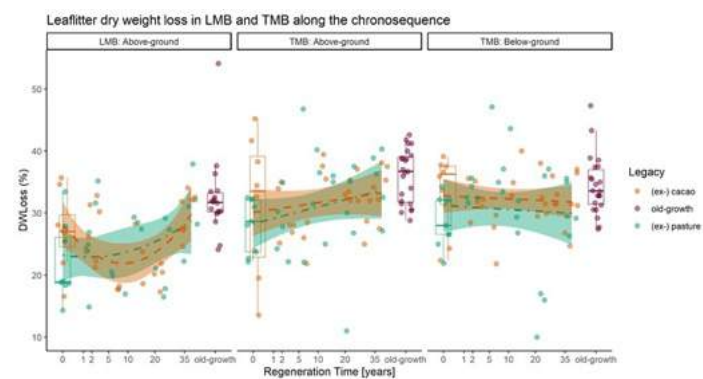


Figure 23: Dry weight loss of leaf litter after 45 days of incubation in the field, comparing LMB (arthropods and microbes) and TMB (only microbes).

Environmental factors such as temperature, canopy closure, and aboveground biomass played significant roles, while topographic variables like elevation had a more modest but still measurable influence. Interestingly, the accumulation of leaf litter on the forest floor peaked

mid-chronosequence, though this didn't directly affect decomposition rates.

Small-scale disturbances added another layer of complexity to these processes. Through the PREX experiment, I observed that pulse perturbation temporarily reduced decomposition rates. However, nature showed its resilience, with decomposition recovering dynamically over time. Meanwhile, fencing enclosures to exclude mammals had no measurable effect, which aligns with expectations given the scale of the decomposer communities studied.

Arthropod community

Parallel to this work, I delved deeper into the intricate world of leaf litter arthropods. With the invaluable help of two collaborators, Florian and Isabel, we processed an immense number of samples and sent many for DNA analysis. The barcodes have recently arrived and I am eager to further explore the taxonomy. Early results revealed that both the abundance and species richness of leaf litter arthropods tend to decline as forests regenerate, though these trends largely vary across functional groups. This decreasing trend in abundance along the chronosequence was also confirmed in the arthropod communities colonising LMBs from the decomposition experiment. Interestingly, as the forest recovered, the richness of arthropod orders in LMBs increased. The next step will involve enriching our analysis with the newly acquired taxonomic data from the DNA barcodes.

Poison frogs' alkaloids

On another front, significant progress was made in analysing the alkaloids of three species of poison frogs from Canandé. Thanks to the incredible patience of Dr. Sebastian Escobar and Dr. Ralph Saporito, the frog skin samples that were carefully collected in the field finally made their way to Saporito's lab in Cleveland. There, I had the opportunity to extract and analyse the alkaloids using advanced GC-MS techniques. Currently, I am focusing on the interpretation of the results, matching the obtained mass spectra to Dr. Saporito's extensive alkaloid library. As a preliminary result, we confirmed that *Oophaga sylvatica*, true to its reputation, exhibited a rich diversity of alkaloids, while *Hyloxalus toachi* and *Epipedobates* aff. *Espinosa* samples contained none. The latter consists of an extremely surprising outcome: past literature reports findings of alkaloids in this species, but we confidently observed none in our samples. Overall, despite the long bureaucratic journey of the samples, the alkaloid component of the project has been an exciting and rewarding challenge so far. I am hopeful that combined with Karla Neira's dedicated efforts to identify dendrobatid stomach contents, this study will allow to offer new insights on the dietary habits and ecological interactions that underpin the frogs' chemical defences.

Getting to the end

As I step into my fourth year, I'm filled with anticipation. With much of the foundational work behind me, the coming months will be focused on synthesizing my findings and piecing together the broader narrative of forest recovery, decomposition, and chemical ecology.

SP2: Food webs and alkaloid defenses - frogs and litter fauna

Karla Neira-Salamea MfN/HU, Berlin – UDLA, Quito

A journey across continents

2024 was nothing like the years before. It started with a big move: relocating from Ecuador to Berlin. Even though I had lived in Germany during my master's, this change hit me hard emotionally, making me reflect a lot on what it means to be a woman from the Global South in science. Sure, there is privilege in even being here, but that does not erase the challenges. Doing a PhD is tough on its own, now imagine doing it as a woman in a male-dominated field. Add to that being a Latina in Europe, navigating cultural differences, implicit biases, and often feeling the need to work twice as hard to prove your worth. These experiences have fueled my commitment to staying mindful of these challenges and working toward more inclusive spaces in science—especially for women from the Global South.

Amid all this reflection, my research kept me grounded. With my fieldwork in the Choco Forest behind me, it was time to fully immerse myself into the data and figure out how forest regeneration works through the lens of understory frogs. I spent months knee-deep in statistics, and when the results finally came in, I had the privilege of presenting them at the 10th World Congress of Herpetology in Borneo, Malaysia. Never in my wildest dreams did I think I would be giving a talk at a global conference in Southeast Asia while pursuing my PhD.

The trip to Malaysia was unforgettable. Before the conference, some friends from Rödels Lab and I visited Mulu National Park in Borneo, a place with one of the biggest caves in the world, a spectacle of millions of bats flying out to hunt in an incredibly organized manner, and, of course, plenty of frogs. Then came the conference in Kuching, where over 1000 participants from all over the world gathered. My presentation went great, people were interested in my work, and as if that were not enough, I met four other Ecuadorian women herpetologists!



Figure 24: Rödels Lab and friends attending the 10th World Congress of Herpetology in Borneo.

First paper submitted!

At the end of the year, I finished the first chapter of my PhD thesis. In this chapter, I explored how understory frog communities change along the chronosequence. Understory frogs rely on specific microclimates to survive, but with such diverse life histories, their responses to disturbance and regeneration can also vary. I wanted to explore whether forest age, distance from forests, and land-use legacy (cacao or pastures) influenced the richness, diversity, and composition of frog species across the chronosequence. It turns out that all three metrics increased over time, but neither the distance forests nor the land-use legacy significantly impacted this recovery. Forest age-related factors, such as structural complexity and light availability, create new microclimates. These conditions may also limit the presence of certain species, depending on their tolerance to temperature changes. We also believe our findings are connected to the landscape configuration—a highly forested mosaic with patches of old-growth forests, secondary forests, and plantations all interconnected, allowing frogs to move across these habitats.

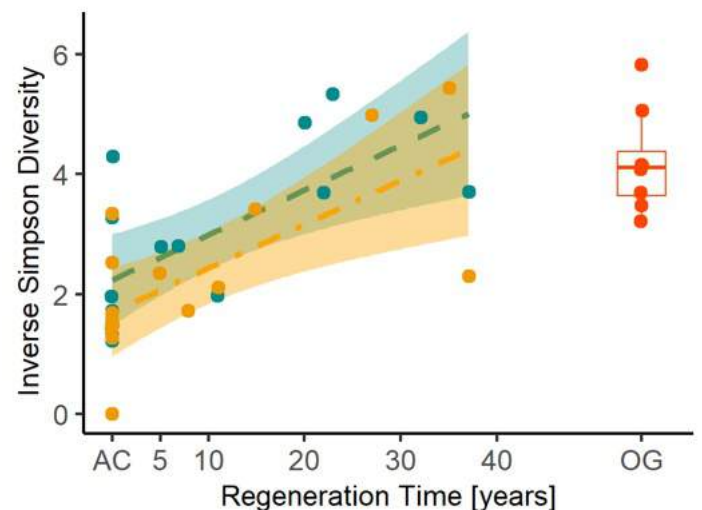


Figure 25: Trajectory of diversity (inverse Simpson Diversity) along the chronosequence, showing an increase over time.

New discoveries, new challenges, new collaborations

A highlight at the end of this year was the publication of a paper where, after 50 years in Ecuador, we described a new species of *Caecilia*. When Sarah Bock, a master's student in our subproject, together with Holger, the parabiologist, discovered a strange, long, purple-and-yellow *Caecilia*, she could not believe her eyes. We immediately assumed it was a new species to science, and we were faced with a challenge. Tesoro's team was not convinced that collecting the animal was the best option—collecting, sadly, means sacrificing the animal—and it is always a tough decision. Why harm something we care about? Why take an animal from a reserve? Herpetologists face these tough questions regularly, but on the other hand, how can we protect something we do not even know? In the end, the animal was sent to the collection at PUCE, curated by Santiago Ron, who opened the doors of his lab to us. After much hard work, led by Sarah, *Caecilia tesoro* was formally described, adding another remarkable species to Ecuador's biodiversity. This also marked the beginning of a new collaboration between MO and Santiago. This is a very positive step, as I think it is great that science continues to build bridges for horizontal collaborations, from North to South.



Figure 26: *Caecilia tesoro* right after being found. Photo: Sarah Bock.

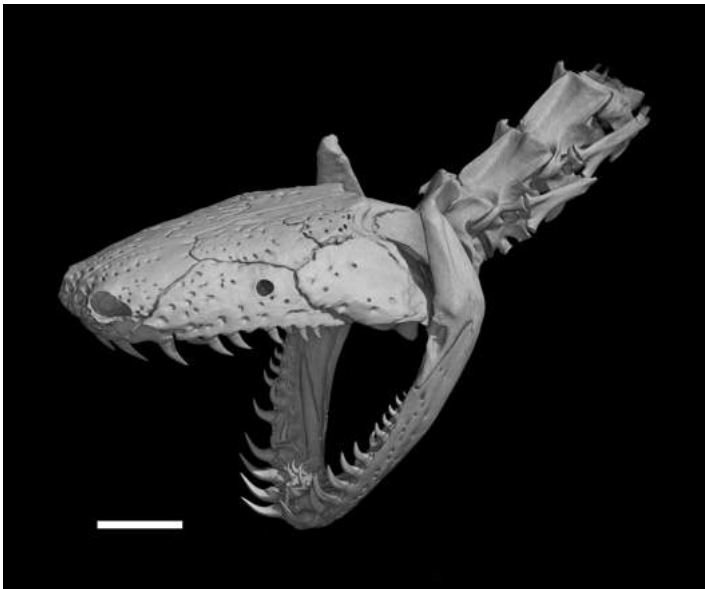


Figure 27: Skull of *Caecilia tesoro* captured using CT scan. Scalebar = 5 mm. Photo: Sarah Bock

Coming back to my main topic, I found that the poison frogs we expected to dominate the trajectories did not quite take the spotlight. Instead, *Pristimantis* frogs stole the show. They are the true queens of the forest, making up half of the species we recorded. Now, I can not wait to learn more about these rain frogs. How does the functional diversity of these communities change as the forest regenerates? What are the frogs eating? It was an extremely challenging task, but Alex Keller and his lab have completed the metabarcoding analysis of frog diets! Now, let's see what we find. Also, what about the trophic network? So many questions still to explore in my last year of PhD.



SP₃: Plant-pollinator interactions

Ugo Mendes Diniz, Technische Universität München

Three years and 25000 insects later...

After three very productive years of fieldwork and data collection, SP₃ managed to assemble an impressive dataset of tens of thousands of insects across many taxonomical groups, including diurnal stingless bees, orchid bees, nocturnal and crepuscular bees, sweat bees, hawkmoths and tiger moths. These data will help us understand how pollinators recover after forest loss, the extent of their resistance and resilience to disturbance, and which factors affect their recovery trajectory along the chronosequence. It is not to be left unmentioned the amount of work that was necessary to produce these results. In the past years, and with the help of our incredible parabiologist Jender Vélez Looor and many great students determined to go through the mud and exhaustion of Canandé, we visited each of the 62 chronosequence plots twice and set about 700 traps of all kinds, not only at the understory but also up to 40 m height in the canopy with the help of our (painful yet rewarding) archery method. I extend my deep gratefulness and appreciation to everyone involved in the progress of SP₃, and I'm excited to see what comes next (hopefully papers).



Figure 28: Setting canopy traps with the bow and the immense assistance of Jender



Figure 29: Last sampling day, with a collection of very happy researchers, from left to right: Kevin Deesy, me, Julia Windl, Jender Vélez and Kathi Veltman

The importance of forest canopies

Among our most exciting results is the seemingly key role of canopies (> 20 m) in both primary and successional forests. We are starting to see how most pollinator groups are more abundant and diverse in the canopies, regardless of disturbance legacy and forest age. These patterns suggest that, even though large canopy trees take a long while (even centuries) to show up in the landscape, vertical stratification starts to appear quite soon. We still need to figure out what drives pollinators up, though. Resource availability probably plays a big role, but we have many different variables to disentangle. However, our results already started to show the beneficial effects of forest restoration early on.



Figure 30: An example of the structure of a tall (> 35 m) canopy in canandé, with some of our traps dangling from a branch

Shedding light on pollinator recovery and distribution

A big part of REASSEMBLY is understanding the resistance and resilience of biodiversity. While many groups seem to take ages to recover to their primary forest state, pollinators seem to be having an easier time. Results so far show a high rate of recovery of abundance, diversity, and functional profile of pollinators, particularly moths and stingless bees



(Fig. 31). This probably has a lot to do with their high dispersal capability, but we still need to figure out the actual drivers. Some groups seem to be more sensitive than others, such as orchid bees (Euglossini), which showed a more delayed recovery and may suggest that some groups serve as indicators of disturbance.

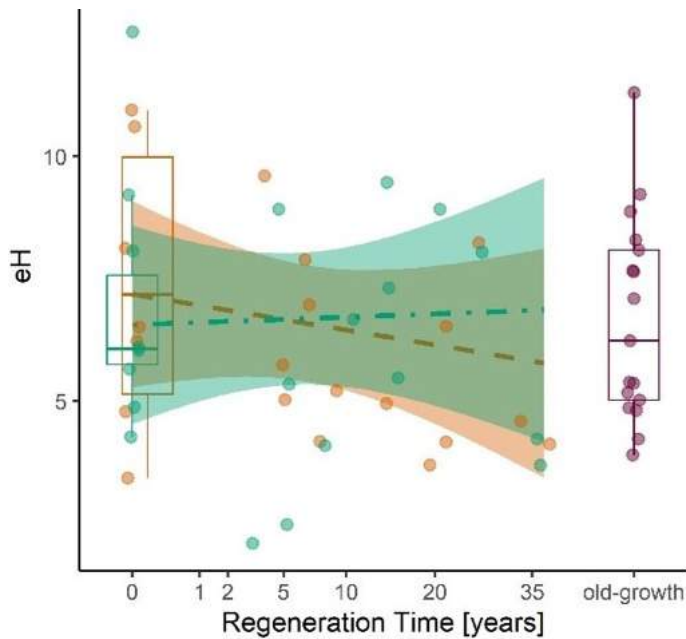


Figure 31: Example of the resistance to disturbance of a group of bees (Meliponini): diversity does not go below old-growth levels even in active disturbances



Figure 32: An orchid bee carrying a pollinia from an orchid on its back. The pollinia, like all pollen samples, underwent metabarcoding so we can assess the structure and recovery of pollination networks.

What lies ahead: networks, plants, and disentangling causes and effects

Even though fieldwork is over, there is still much work ahead. While we will soon be able to show our results on insect recovery, the crown jewel of SP₃ (and REASSEMBLY in general) is yet to come: networks. After extracting DNA and metabarcoding more than 1500 pollen samples, we will finally have a grasp of the structure of plant-pollinator interactions and how they recover along the chronosequence. With it, we also aim to show the role of floral diversity, availability, and functional variability per plot, a dataset containing more than 1000 plant occurrences on the recovery of the multiple levels of pollinator diversity and interactions. In a nutshell, we still need to connect the dots between plot, plant, and insect, and 2025 will surely bring the most insights to SP₃ since the start of the project. Stay tuned!

SP4: Seed dispersal and its important role in forest recovery

Anna Rebello Landim, Senckenberg Biodiversity and Research Centre

What Everyone Should Know About My Work

After successfully collecting data in all 62 plots between 2022 and 2023, this year my work shifted from the field to the office, where I have been analysing the data collected during the first two years of the project. Using a combination of data and simulation models, I study how seed-dispersing animals help forests to recover.



Figure 33: Anna and Jordy after their last they of fieldwork in December 2023.

Seed dispersal allows the recolonization of degraded habitats by plant species from old-growth forests [1]. In tropical forests, most plants depend on frugivorous animals for seed dispersal [2]. Various animal species, particularly birds and mammals, disperse seeds and can play distinct roles in seed dispersal [3]. While large animals such as toucans and spider monkeys are able to disperse seeds over long distances, non-flying mammals such as agoutis disperse seeds of large fruits that lay on the forest floor. These seed-dispersal interactions influence the plant species that can reach degraded habitats, driving forest recovery over time.

Despite the importance of animal-mediated seed dispersal for the natural recovery of tropical forests, many questions regarding the mechanisms behind the recovery of seed-dispersal interactions after deforestation remain unanswered.

Seed dispersal from old growth to regenerating forest patches

In a first study, I explored how the movement of animal seed dispersers affects plant dispersal from old-growth forests (the source) to degraded habitat patches (the target). For that, I simulated seed-dispersal events between source and target forest patches. In our simulations, we focused on how the distance between habitat patches and the diversity

of fruits in the target patch influence the number and diversity of seeds reaching the degraded habitat patch (Fig. 34).

My simulations showed that the number and diversity of seeds decreased with distance, and most seeds were dispersed within 250 meters from the source patch. These values varied depending on the diversity of fruit resources in the target patch: the more fruit resources in a patch, the greater the number and diversity of seeds reaching that target patch. The diversity of seeds reaching the target patch also depended on the level of specialization of the seed-dispersal network in the source patch. In more specialized networks - when plants depend on specific seed dispersers - the diversity of seeds reaching the patch was lower than in generalized networks. Hence, sharing seed dispersers among plant species increased the potential for seed dispersal and forest recovery.

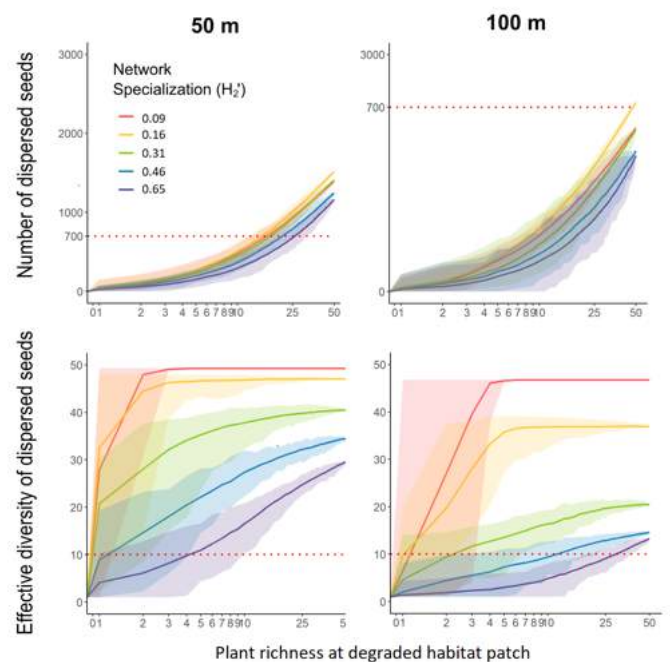


Figure 34: The number and effective diversity of seeds reaching a target patch at 50 and 100 meters from a source patch in the old-growth forest. The x-axis represents the richness of fruiting plant species in the target patch. Different colors represent different levels of network specialization, from very generalized (red) to very specialized (purple).

Recovery time of seed-dispersal interactions

In a second study, I analysed the recovery of seed-dispersal interactions after deforestation, based on the field data that Jordy and I have collected in the past two years. We recorded seed-dispersal interactions using two different methods at each of the 62 plots. For the canopy and midstory of the forest, we conducted direct observations using binoculars and for the forest floor, we used camera-traps and deployed fruits in front of them. I also compiled and measured important functional traits for all plant and animal species involved in these interactions to measure the functional diversity of seed-dispersal interactions.

My preliminary results show that the functional diversity of interactions increases with the recovery age of the plots. I observed functionally more diverse interactions on the older plots and in old-growth forests. In early recovery forests, I mainly observed interactions between small birds and pioneer plants (Fig. 35). According to my model, it seems that the functional diversity of seed-dispersal interactions needs a couple of decades to recover to values comparable to those in the old-growth forest.



Figure 35: Red-capped manakin (*Ceratopipra mentalis*) and flame-rumped tanager (*Ramphocelus flammigerus*). Two common species observed interacting in early-recovery forests. Interactions between large animals and late-successional plants were restricted to later recovery stages.

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SP4: Bats and seed dispersion

Santiago Erazo, University of Ulm, Germany - Pontificia Universidad Católica del Ecuador

Introduction

SP4 is the combination of two diverse and multi-disciplinary groups. We focus on bats, non-flying mammals, and birds (mainly frugivorous), their seed-dispersal interactions, and their importance and role in a forest recovery gradient in the Ecuadorian Chocó. Our group, Marco Tschapka (PI), Santiago Burneo (main collaborator), and I (PhD student) develops around seed dispersion by bats. Matthias Schleuning (PI), Eike Lena Neuschulz (PI), Boris Tinoco (main collaborator), and Anna Rebello Landim (PhD student) focusing on seed-dispersal by frugivorous birds and non-flying mammals. Additionally, SP4 studies seed rain. During the fieldwork, we had the valuable collaboration of trained Parabiologists, mainly Jefferson Tacuri and Jordy Ninabanda. We also had the help of Paola Ayala in different laboratory activities carried out at the Zoology Museum of Pontifical Catholic University of Ecuador (QCAZ).

The study area is located in Esmeraldas, in the Chocó biogeographic region of Ecuador. This region is part of the Tumbes-Chocó-Magdalena hotspot, important for its diversity and endemism [3] and faces constant and increasing threats generated mainly by deforestation for agriculture and timber extraction [1]. The landscape of the study area consists mainly of grassland, cocoa fields, and different levels of forest regeneration. To understand how diversity, functionality, and ecological interactions are affected by regeneration time and landscape composition, we used phyllostomid bats as a study group. This group is considered ideal for this type of study. It has been shown to respond to ecosystem variation, has a wide distribution, high diversity, etc. In addition, they are important contributors to various ecosystem services, such as seed dispersers and pollinators [2].

Bats diversity

To ensure proper fieldwork, constant training has been necessary. The study area was previously visited to understand its geographical and environmental characteristics. This allowed us to be prepared for the different adversities and possible complications that could arise during fieldwork. In addition, before starting fieldwork, a list of possible bat species distributed in the region was compiled from literature, and specimens from the Mammal Collection of QCAZ-M were reviewed to determine the morphological characters that would facilitate their identification in the field.

At the end of 2023, after four field campaigns during the dry and rainy seasons, we completed sampling at the 62 sites, a total of 186 nights and 6138 hours/nets of sampling. A total of 2571 individuals were captured. During fieldwork, it was necessary to collect several specimens, mainly those with very subtle morphological diagnostic characters that generated taxonomic confusion and required a more detailed review for identification. A total of 67 specimens are deposited as a reference collection in the QCAZ-M museum, registered under the Contrato Marco MAAE-DBI-CM-2021-0165, issued by the Ministry of Environment of Ecuador.

In the first months of 2024, the morphological review of the collected specimens was completed. In addition, DNA extraction and the whole process necessary to obtain the genetic sequences of approximately 35 of the specimens collected was carried out. This information was used to update the database and the list of species. A total of 46 species were

recorded, distributed in four families (Emballonuridae, Phyllostomidae, Thyropteridae, and Vespertilionidae). However, only 42 species of phyllostomids were considered as a study group, with 2558 individuals.



Figure 36: Bat diversity: *Vampyroides major*

Landscape composition and Phyllostomid Bats

With the species list and database updated, we were able to continue with the respective analyses to answer our research questions. To analyze how the phyllostomid bat assemblage responds to the composition of the regenerating landscape, we calculated Hill numbers ($q=0$, $q=1$, and $q=2$) as measures of diversity. Among the results, a positive correlation was observed between years of forest regeneration and diversity measures. On the other hand, when considering landscape composition, Generalized Linear Models (GLM) from diversity measures, showed a negative trend with decreasing forest cover, mainly influenced by increasing grassland cover and initial regeneration. The results show the important diversity of bats in the biogeographic Chocó region. The responses of the assemblage to the composition of a landscape with forest regeneration are evidence of the past and present effects of deforestation and modification in the Chocó Region.

The preliminary results of this section of our study of the research were presented at the IV Latin American and the Caribbean Bat Meeting (Congreso Latinoamericano y del Caribe de Murciélagos, IV COLAM), at Cusco, Peru, in August 2024. Also, at the VI Ecuadorian Mammalogy Meeting (Congreso Ecuatoriano de Mastozoología, VI CEM), Tena, Ecuador, in October 2024. At the two congresses, we had the opportunity to meet with important researchers and appreciate the significant studies being carried out in different parts of the world. During both presentations, I received very positive and constructive feedback regarding our research. In addition, I was honored to win the 'Best Postgraduate Student Presentation Award at the VI CEM'.



Figure 37: Congress: VI CEM

Frugivorous Bats and seed dispersion

As part of our objectives, we sought to understand the role of bats as seed dispersers in a regenerated forest landscape. Identify seed diversity and bat-plant interactions to determine possible dispersal patterns and their influence on regeneration. During the fieldwork, it was possible to collect more than 1000 fecal samples among the 2500 bats captured. Samples are deposited at QCAZ-M. In the first quarter of 2024, after the exhaustive work carried out by Paola Ayala, it was possible to process all the samples. The process involved identifying and separating seeds by morphotype, determining their approximate abundance, and preserving the samples appropriately. A lot of time and practice was needed to identify the seeds, where size, shape, color, and texture, among other characteristics, were considered. Approximately 100 seed morphotypes were identified, and distributed among 22 bat species. To confirm the taxonomic identification of the seeds, a sample of each morphotype was prepared and sent to the laboratory of the University of Munich, Germany. In this laboratory, Professor Alexander Keller and his team carried out the corresponding analyses to obtain the barcoding of the different morphotypes. After the analyses, approximately 45 species of seeds dispersed by bats have been identified.

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SP5: Tree seedling recruitment and herbivore interactions during forest recovery

Eva Tamargo López, Philipps-Universität Marburg

Work progress

2024 was the year of fieldwork closure for SP5. Within another 4 months in the amazing forest of Canandé and Tesoro escondido, the last year of monitoring passed by with a lot of fun and new memories. With the help of the three new master students (Stella Drechsler, Niko Ioannidis and Marco Hügel) and our new parabiologist Miguel Ángel Tacuri we accomplished to monitor our 39 plots, with an extra arthropod sampling carried out by Niko and Miguel. In order to increase the comprehension on anti-herbivore defenses in some of the most common species in the study area, we also collect volatiles (or volatile organic compounds) of four common tree species: *Brosimum utile*, *Banara guianensis*, *Protium equadorensense* and *Wettinia quinaria*. The start of the field work was supported by the presence of Nina Farwig and Sybille Unsicker in Canandé, two of the SP5 PIs. Their presence was a great help to improve our methodology and allowed us to enjoy their nice company and great snacks in these tropical forests (fig.38).



Figure 38: SP5 Field team 2024

With the invaluable help of Miguel, I also managed to monitor the other 24 non-PREX plots for the first time. It was an exciting adventure, that allowed me to visit the complete study area of Reassembly. 2024 was an emotional year, full of farewells, which shows other perspectives of the advantages of working in this amazing area, as being able to know beautiful people that will always remain in my heart.

Besides the field work in our tropical paradise, we also made some achievement. I was able to present our work “Recovery of tree seedling-herbivore interactions along a tropical chronosequence” at the annual meeting of the European Society for Tropical Ecology in Lisbon in February 2024 (fig.39). This was a great opportunity to present our advances to the scientific community, and to connect with researchers working in the same research area as me.



Figure 39: Presentation in the European Society for Tropical Ecology in Lisbon (Feb.24)

We are advancing fast with the species barcoding identification as well, adding further detail to our data. This is only possible thanks to the expert help of Sebastian Escobar (CM) and Alexander Keller and his team (SP3).

Third field season-PREX focuss and arthropod sampling

Three years after the disturbance experiment, we now started to focuss on the PREX data. We already recorded recovery of tree seedlings in 25 of the 39 disturbed plots. I am looking forward to explore how the forest, the adult trees in the surrounding and the forest recovery time are influencing the recovering seedling communities after the disturbance. This will be the main focuss of Stella as well, who will concentrate on the Perturbation - Recovery Experiment in her master thesis (fig.40).



Figure 40: Stella Drechsler measuring a *Wettinia quinaria* on a fenced undisturbed treatment

It is also exciting to add information on the arthropod recovery. This will be Niko’s master thesis focuss in the next year, and it will help increase our understanding of the tree-seedling interactions, since we will depict, not only the seedling community recovery, but also its counterpart, the insect community. Its interesting to note that, even though we didn’t participate in the BugNet project for timing reasons, we followed their sampling protocol [1] to carry out our sampling. This can lead to interesting conclusions about the arthropod recovery, since this international project has only a few points in South America (fig.41).



Figure 41: Miguel Tacuri and Niko Ioannidis carrying out understory insect sampling in a young pasture plot

First paper draft and future expectations

After extensive data cleaning and analysis, we're finally starting to see the light at the end of the tunnel! SP5 is about to submit its first manuscript on the taxonomic and functional recovery of tree-seedlings along our tropical chronosequence. Working on this first chapter of my PhD has been exciting for me. I can finally see how my hard work in the field shape up in a beautiful manuscript; and this has allowed me to understand some of the dynamics in forest recovery. In this manuscript we explain that the fast taxonomic recovery (fig.42) might be related to the forest coverage in the surrounding landscape. We also see a positive trend in the recovery of functional diversity with increasing values of diversity towards old-growth forest. With the additional information collected and processed this year, we identified a possible functional arrestment in pasture legacies for some traits such as leaf toughness. Further details will be given in the manuscript - so stay tuned!

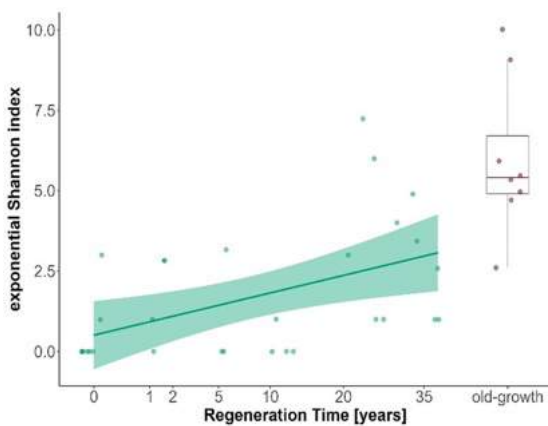


Figure 42: Recovery of species diversity with forest age, showing a fast increase in exponential Shannon index with time, without reaching yet old-growth forest levels, as shown by the old-growth forest boxplot.

Future expectations

Our incoming plans are:

1.- Publication on Herbivory-network recovery. This publication will be a joint work with Marco Hügel and Lukas Werner to unravel the processes behind the herbivory recovery patterns.

2.- Publication on tree-seedling recovery after an anthropogenic perturbation (PREX). Together with Stella Drechsler we will identify the main factors influencing tree-seedling recovery after a strong clearance perturbation in a neotropical rainforest.

3.- Canandé and Tesoro Tree-seedling field guide. Lastly, once the barcoding of our samples is complete, we will compile a Tree-seedling field guide to help the next researchers visiting the amazing Chocó forest in Canandé and Tesoro escondido.

Conclusion and outlook

Our work is providing important insights into the dynamics of tree-seedling recovery along our successional gradient. Seedling diversity increases consistently once lands are abandoned and succession starts, but this process can be slowed down by the legacy of human impact.

In conclusion, even though natural regeneration can push forward ecosystem recovery, its important to shed light on (a)biotic factors promoting or hindering this process. This can help implement actions to improve the forest recovery from all perspectives.

To conclude, our project is advancing steadily. 2025 will be the year were all our work closes up in three beautiful publications with all the knowledge we acquired in tree-seedling and herbivore interactions recovery in Tropical Lowland Evergreen Forest.



Figure 43: The beauty of Canande, Jocotoco's Reserve. Photo from Niko Ioannidis

References

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SP6: Dung beetles and forest recovery

Karen Marie Pedersen, TU Darmstadt with contributions from Jan Johan, and Anne-Sophia Jatsch

Who makes up SP6

This year, our team grew again and now consists of three supervisors, Nico Blüthgen, Thomas Schmitt, and Diego Marín-Armijos, collaborator Santiago Villamarin-Cortez, Ph.D. student Karen Marie Pedersen, master's student Jan Johan, field assistant Anne-Sophia Jatsch¹, and our research assistant and expert dung beetle dissector Simon Heck. Collectively, we study dung beetles in the context of REASSEMBLY.

What did we accomplish this year

I think my personal attraction to dung beetles stems from their dual contributions to decomposition and seed dispersal [2], in addition to their excellent personalities. In previous years, I have written a lot about my fieldwork and a bit less about the other aspects of research. This year was the first year that I did not collect data in the field. This allowed me to focus more on writing, data analysis, and improving my mathematical and data analytic skills (still a work in progress). We had a paper come out in March and we were able to submit the multi-resource dung beetle networks in the context of forest recovery paper in June, and we hope to resubmit the revised version in the next month (December). While papers are the most prestigious product of our work, there are many time consuming steps before the paper. Each step produces its own product. This year we generated other such products. These included organized the information around species keys for the dung beetles in Canandé, which will allow others to work with this group more easily, barcodes for most dung beetle species, photos of the species of dung beetles, clean seed dispersal data. We also started the analysis for the seed dispersal paper in earnest, made progress on the analysis of the dung removal data (collected by the modular cameras), began collecting dung beetles with volatile traps, and began the lab work for the metabarcoding of the dung beetle gut contents.



(a) Anne with dung beetle bait in the field.



(b) Anne working with the volatile baits.

Figure 44: I asked Anne to send me photos of herself in the field. These are those photos, and I think they perfectly capture her enthusiasm. I cannot wait to see the orchid bees.

Field Work

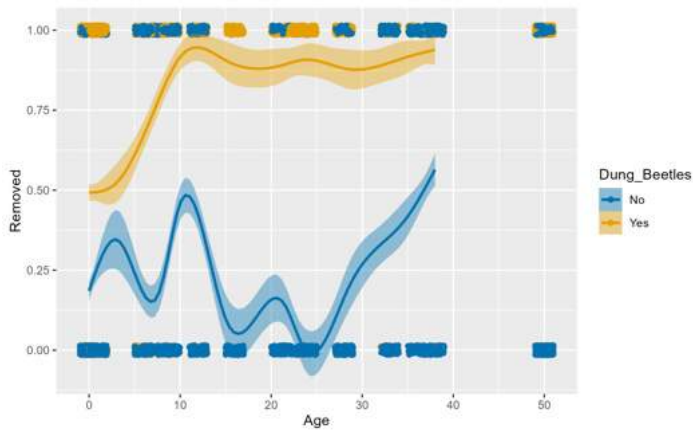
I was not personally in the field this year. However, the final field collections using volatile traps were installed by Anne in the field this year. These traps use volatiles that are known dung volatiles in different combinations. However, due to the extremely dry year there have been very few dung beetles collected even with the dung baits which typically work better than the volatile traps. This means that the data from these traps will probably not be used to study dung beetles. However, this is not to say the traps are not producing data. Orchid bees seem to be attracted to the traps. This means there will likely be a shift to study the orchid bees and their volatile preferences analyzed. Anne has a great attitude, which is perfect for this type of fieldwork (fig 44).

Secondary seed dispersal

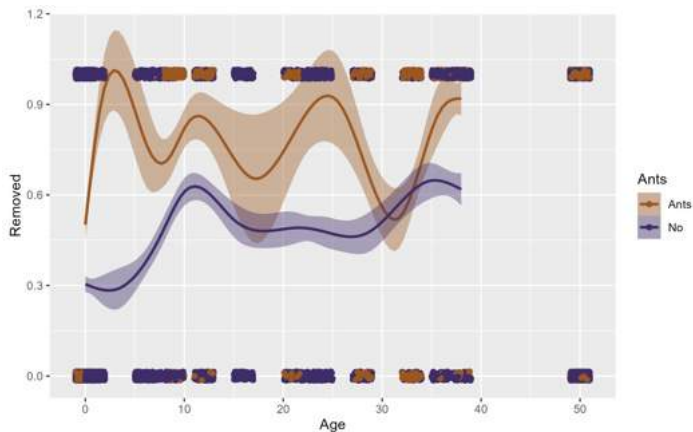
Within the PREX, we set out 200 g of pig dung with standardized seed mixtures with seeds ranging from a length of 1 mm to 30 mm, representing a realistic range of seed sizes. Seeds were collected from local trees. Two seed dung mixes were placed in each PREX treatment, one with a dung beetle enclosure over the top and one open to the beetles. We then came back after four days to count the number of remaining seeds, measure the distance from the central point, count the number of dung beetle tunnels, and measure the tunnel mouths. This year, I got access to the complete data set thanks to Edith bringing me back the field notebooks. I was then able to enter the remaining data into a spreadsheet. This is a large data set with 6840 rows and 14 columns which is 95,760 cells, for the seed-specific data. There are also treatment-specific data in other data sheets. This is too much to check by hand accurately so I checked the data entry using R code that identified missing treatments, outliers, and spelling mistakes. This took some time but it was worth it in the end.

I present some preliminary analysis here as clean data was only produced on the 11th of November 2024. The results with these complete but clean data are not so different from last year's partial and dirty data. So if it feels a bit like *deja vu* you are not wrong. Using the completed data set, we wanted to see which variables of the collected variables are important for seed removal. For this, we ran a GLMM with a binomial distribution. Within the model, our fixed effects were dung beetles present or absent, the presence or absence of ants, forest age as a rank variable, then scaled, seed length, if the subplot was fenced or unfenced, and if the plot was disturbed or undisturbed. We included treatment ID (which corresponds to location) was included as a random factor in the model. The PREX variables (fencing and disturbance) are not significant. Other variables are significant: dung beetle presence increases seed removal (p -value < 0.0001), the presence of ants also increases seed removal (p -value < 0.0001), the rank forest age also increases seed removal (p -value $= 0.0003$), and longer seeds are less likely to be removed (p -value < 0.0001) (fig 45). The seed removal by ants is likely to be destructive as we observed seed consumption by ants in the field thus a net negative for seed survival. Seed removal by dung beetles is not immediately destructive as the dung beetles do not consume the seeds and instead make it harder for seed predators like rodents and ants to find them thus more likely to be a net positive for seed survival.

¹Due to the drought this year there are very few dung beetles, so Anne may end up studying orchid bees and other insects attracted to volatile traps.



(a) Plot of the seeds that are either removed 1, or not removed 0 on the y-axis, and forest age on the x-axis. Each seed in the data set is represented by a circle, and treatments with dung beetles are colored in yellow, those where beetles were excluded are in blue.



(b) Plot of the seeds that are either removed 1, or not removed 0 on the y-axis, and forest age on the x-axis. Each seed in the data set is represented by a circle, and treatments with ants are colored in brown, those where ants were not observed are purple.

Figure 45: Seed removal across the chronosequence. The scatter plot looks like the presences of ants create a lot of noise in the seed removal data.

Dung beetle dissections for mammal dung beetle networks

I had asked Alex Keller if he could try his pipeline for metabarcoding with COI with the dung beetles. From the beginning, I was skeptical that primers that do not filter for some organisms would work well because you would expect a lot of dung beetle DNA relative to target mammal DNA in the dung beetle digestive tracks. However, you never know until you try, and he graciously tested the protocol. Unfortunately, the results were mostly dung beetle DNA. After that I knew we would have to use the mammal primers like we did previously [3]. This time we have modified them to work with an Illumina sequencer, and I am hopeful that we might get data from a larger number of beetles this time than last time. However, molecular work is always a bit finicky, and small changes can sometimes present unanticipated problems. Now that we have materials we have started the dissections of the dung beetles collected in the multi-resource study for gut content analysis. David Donoso very kindly transported the dung beetles from the second round of collections from Ecuador to Germany so we have even more samples than we did at the start of the year. Beginning this process was much

slower than anticipated because purchasing materials is somehow never a straightforward process. It seems like you it should follow a logical order. First should make your list, find the lowest price and then buy the materials. In practice, this never seems to work. We spent four months going back and forth with one of the suppliers before we could purchase some of the needed reagents and comply with the university requirements. Another supplier shipped the materials three months after they were ordered. This, among other aspects, caused a lot of frustration and delay. Some of this is, of course, due to my inexperience and lack of tolerance for incredibly tedious tasks with many seemingly silly obstacles. I anticipate that we will get some great data from this in the next year, and I am excited to write that paper.

Dung beetle guide

This year, I spent a lot of time organizing and generating information and materials to facilitate the identification of dung beetles in Canandé by students. To do this, I created a species list and organized all the genus and species characters and citations when possible. Then took stacked photos of the beetles I had pinned. The photos were too big to be included in a single document, so I wrote Python code to automatically resize them. Then I took the Excel file and the photos and, in an rmarkdown file, wrote a couple functions that automatically extracted all the smaller photos from the directory with the species photos and the cells with the Excel species characters descriptions. This generated a rather ugly but serviceable document that will provide the foundation for a more professional dung beetle guide (fig 46).



Characters for the species *Eurysternus foedus*: Species within the foedus species group have a body size between 12.0 and 25.0 mm. The body surface covered by short setae of size uniform, but with some longer tufts at the elytral apex and on margins of head and pronotum. Eyes poorly visible in dorsal view. The pronotal surface is irregular with concavities or depressions. The elytra have variable often alveolate microsculpture on the surface. The elytral interstriae are narrow. The posterior coxae are unicolor. The metatibial spine sessile in males. *E. foedus* can be differentiated from *E. strobilus* with the following characters. Body size is

Figure 46: An example of one of the sets of photos and species character descriptions from the draft dung beetle guide.

Dung beetle activity

Jan started as a bachelor student in SP6, and we are very pleased he has continued to work with us as a master student. He has some valuable technical skills which made him a good fit for our work with the dung beetle cameras. The goal for the cameras was to understand better dung beetle activity windows and rates of dung removal as the forest recovers. I asked him to provide a brief overview of the progress he made over the last year, and that text is included below.

This project has always been a challenge. From trying to design a waterproof low-cost camera system to dealing with the messy data it produced. Before it started, I had never heard the term “microcontroller”



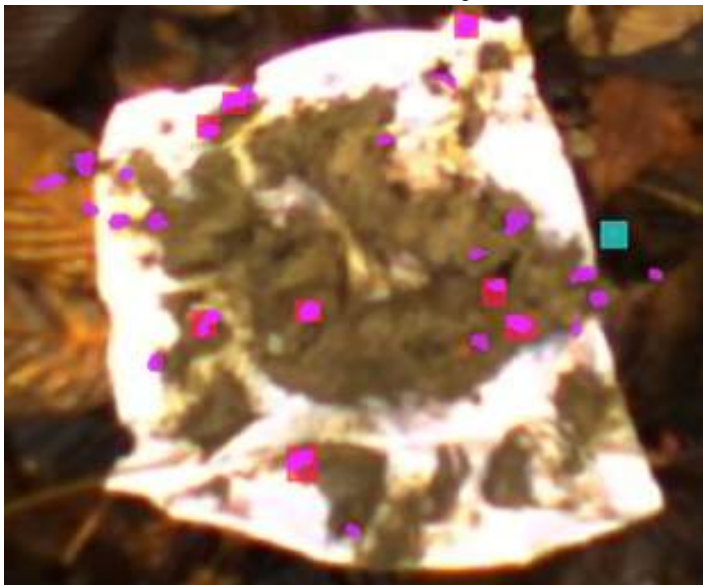
and thought machine learning was sorcery. At the end of the field season, we found ourselves with some pretty decent and user-friendly monitoring devices. And as to the sorcery: I'm getting there! So far we have 1327 dung beetle annotations on 699 images. The annotation process is not finished yet but has become much faster with the help of a computer vision algorithm I figured out based on a previous paper [1]. It allows me to highlight motion in the timelapse photos (fig 47).

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(a) The boxes are annotated dung beetles.



(b) Highlighted in purple boxes are objects in motion.

Figure 47: This method revealed some dung beetles that I had missed before and greatly increased my annotation speed. It has also allowed me to increase the coverage of annotated images across the whole time-lapse. Again based on the paper mentioned above, it looks like some tweaking of the model has increased the mean average precision by 0.5 recall by at least 1.5. This is still to be further investigated.



SP7: Interactions between saproxylic insects and consequences for wood decomposition

Nina Grella, Universität Bayreuth

Work progress

2024 was the year in which SP7 finally finished the last field season and where we retrieved all data from our experiments. In 2023 we installed a big dead wood decomposition experiment on the PREX plots with more than 1000 pieces of wood. We left the dead wood on the plots for investigating the decomposition rates depending on forest age, disturbance, and fence treatments. After removing and measuring the first half of the woods in autumn 2023, we retrieved the second half this spring after giving it one year time to be decomposed by arthropods and fungi. The biggest part of the field work was mainly conducted by our amazing parabiologist Holger, with whom we collected wood data in the seasons before. I and the rest of the team from SP7 were very happy to have Holger in our team and to be able to count on his reliability and creativity in solving problems.

During this time, I was working in Bayreuth on the ant and termite samples from the previous seasons. I grouped them into morphospecies and prepared them for being barcoded (Fig 50, 49). Now, by the end of the year, I have obtained 2700 DNA sequences from the thousands of insects that I have collected and already identified most of their species with the help of David Donoso using phylogenetic trees and morphological traits. This year I was very thrilled that my very first first-author paper about vertebrate communities along the forest recovery gradient got accepted for publication recently [1]. This paper was based on data derived from camera traps that Jörg Müllers team had installed on the plots at the beginning of the Reassembly project. With this study we showed that regenerating forests have a high potential for the recovery of vertebrate diversity and laid the foundation for other studies on rapid vertebrate assessments using camera traps in our study area.



Figure 48: Nina working on insect identification at the microscope in Bayreuth

Conferences

In September 2024 I had the chance to present the results of my analysis of flying ant and termite alates in our study area at the 53rd annual conference of the German ecological society in Freising. The data was collected by Jörg Müllers team, who sampled a variety of insects

with light traps, and I was given the opportunity to analyze the ant and termite communities. This was especially interesting to me, because the distribution of flying reproductives can contribute to disentangling the effects of habitat filtering and dispersal limitation of social insects.

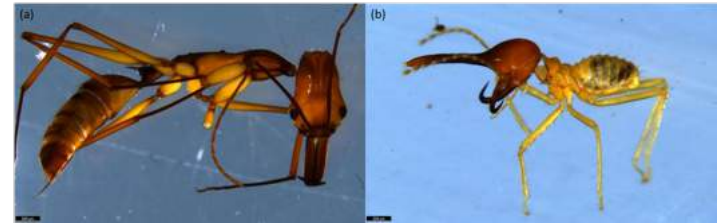


Figure 49: Two pretty insect specimen collected in Canandé. (a) the trap-jaw ant *Odontomachus hastatus* and (b) a termite belonging to the genus *Rhynchotermes*

Previous work by former PhD student Philipp Hönle has shown that species richness of ant workers originating from sessile nests does not differ along our regeneration gradient, but that community composition does depending on forest age [2, 3]. With the data of reproductive alates, that swarm form their nests for mating and the subsequent foundation of new colonies, I showed that community composition does not differ along the regeneration gradient, but is driven by the plots location for ants and termites (Fig. 50). This indicates that dispersal limitation is not an important factor explaining different community composition of workers depending on plot regeneration ages and delivers evidence that habitat filtering could be an important mechanism shaping ant and termite communities in our study area. For termites I will soon have the results about the distribution of workers along the regeneration gradient from my own field work. I am looking forward to combining all of this information and putting it in into a bigger picture for explaining mechanisms of social insect distributions and I am excited to present these results in February 2025 at the 8th European Conference of Tropical Ecology in Amsterdam.

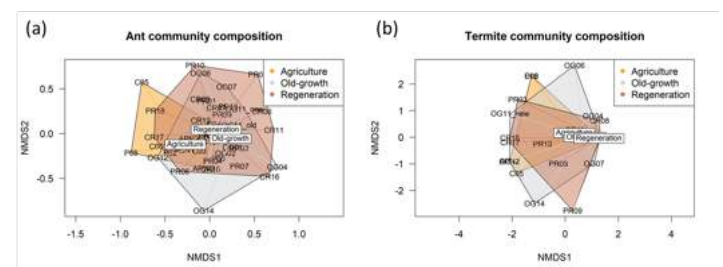


Figure 50: NMDS of ant (a) and termite (b) alates caught in light traps in agricultural land, regenerating forests, and old-growth forests.

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SP7b: Deadwood and saproxylic insects

Ana Falconí López, Universität Würzburg



Figure 51: Ana in Tesoro Escondido Reserve

What everyone should know about my work

In SP7 we investigate deadwood decomposition and the interactions between saproxylic insects, fungi, and deadwood along the forest recovery gradient.

Deadwood is a critical resource for global forest biodiversity, providing habitat for a wide range of interacting invertebrates and fungi. While many species benefit opportunistically from deadwood, approximately one-third of all forest insect species are saproxylic, relying exclusively on it during some part of their life cycle. Unfortunately, many of these species are now at risk in intensively managed landscapes. Over the past decades, numerous studies have focused on conserving this fauna, particularly examining the impacts of forest management practices and natural disturbances. However, significant knowledge gaps persist, especially concerning subtropical and tropical forests, where further research is urgently needed.

To address these gaps, and after three years of field work (2022-2024), we successfully completed all the experiments planned for our project (Figure 50). These have been years of learning and self-knowledge, in which we have valued teamwork and highlighted the great work of our parabiologists.

A brief summary of the year

I started 2024 by travelling to Germany for our January workshop, where we were able to see the progress and preliminary results of all our colleagues in the different Reassembly projects. On this occasion I was able to present the preliminary results of my second article on the diversity and host-networks of saproxylic beetles. Then I travelled to the Bavarian Forest for a month and a half to finish my first chapter article (Patterns of deadwood amount and deadwood diversity) and worked with my tutor Jörg to solve all the reviewers' comments and submit it for final review.



Figure 52: WP5 Insect exclusion experiment: we removed the last exposed deadwood from different cages and no cages on each plot after one year

I returned to Ecuador in mid-February and was able to organize all the logistics for my last field trip to the Canandé and Tesoro Escondido Reserves from February to March 2024. For this field trip, we had planned to collect the timbers from our last insect exclusion experiment on the 32 PREX plots, we still had to collect the timbers after one year of having placed them in the different cages and plots (Figure 51). We then cut the ends of each log to take samples for fungi and to measure wood decomposition as mass loss (weight and volume); the volume of the 5 cm sections were measured by water displacement; the cut sections were dried at 80 °C until the mass remains constant (Figure 52).



Figure 53: WP5 experiment: cut sections of wood dried at 80 °C until the mass remains constant

After the field work, I was able to send all my microplates with beetles collected from my last field seasons (Figure 53). Finally, I obtained the barcoding results, in order to organize the species with the guidance of my tutors David and Jörg; we were able to identify about 90 beetle species.

This data will help us to i) characterize the responses of saproxylic communities to forest degradation, ii) analyze the re-assembly of complex networks of saproxylic communities following anthropogenic disturbance, and iii) quantify the effect of saproxylic communities and their biotic interactions on decomposition rates along the forest recovery gradient in a tropical rainforest.

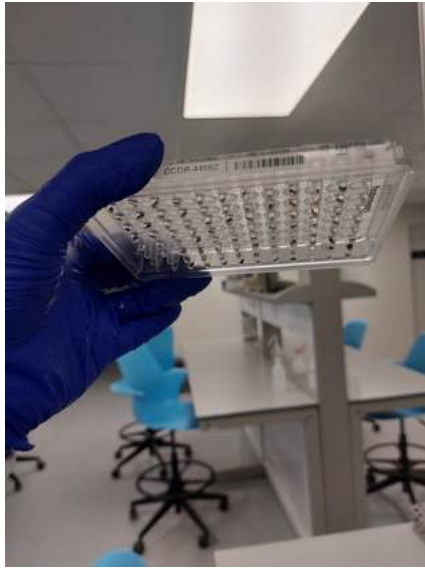


Figure 54: Beetles microplates

In March, I had the opportunity to participate in the workshop organized by REASSEMBLY at Universidad de las Américas (UDLA) in Quito (Figures 54 and 55). Along with the other PhD students, I presented a poster. My contribution focused on the research I have conducted for my two articles, which explore dead wood patterns and beetle-host networks.



Figure 55: UDLA workshop (website UDLA, 2024)



Figure 56: Reassembly (website UDLA, 2024)

The amazing and not so well-known world of saproxylic insects and dead wood in the Tropics

Finally, my first article 'Patterns of deadwood amount and deadwood diversity along a natural forest recovery gradient from agriculture to old

growth lowland tropical forests' was accepted in May and I was very happy to be able to contribute to this area that is still not so thoroughly explored in the tropics. Our findings showed no significant increase in deadwood volume over time during forest recovery. However, diversity in the size, decay stages, and types of coarse woody debris (CWD) did increase along the recovery gradient, regardless of the previous land use. Fine woody debris (FWD) mass increased overall across the gradient, driven primarily by a steep increase in former pastures, while no notable changes were observed in areas previously used for cacao plantations. We suggest that the variety of sizes and decomposition stages of deadwood present in these two major tropical agricultural systems may offer valuable resources for saproxylic organisms and represent an underappreciated carbon storage potential outside of old-growth forests (Figure 56).

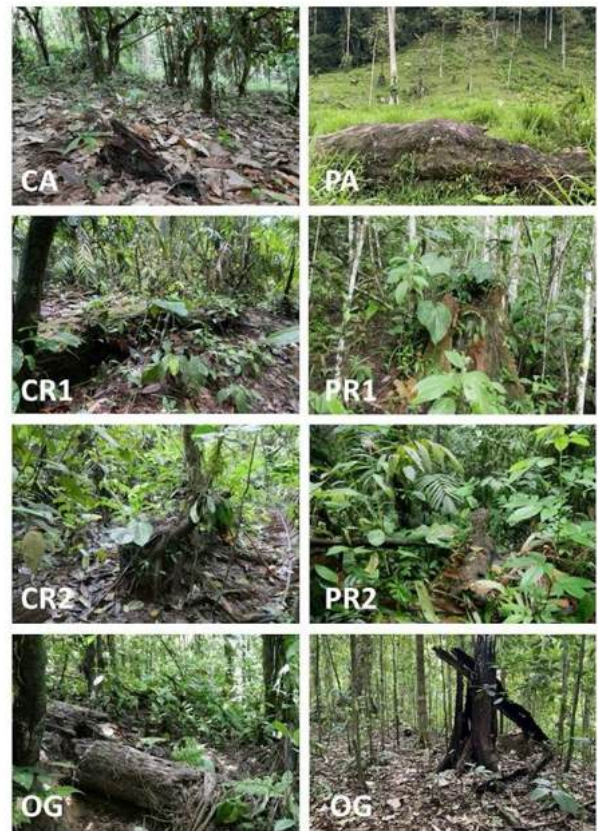


Figure 57: Some types of deadwood found in my research, first article (Falconí-López et al. 2024)

Currently, I am working on my second article in which I am analysing the diversity and host networks of saproxylic beetles along a recovery gradient. The data came from our WP3 sub-project experiment where we exposed logs of five different tree species, covering a range of major decomposition rates, along a chronosequence from active grasslands (AP) and cocoa plantations (CA), secondary forests originating from previously used grasslands and cocoa plantations at an early stage of recovery (<20y), secondary forests at a late stage of recovery (20-40y), to old-growth forests (OG). We identified beetle species with support of DNA barcoding and used generalized linear models, rarefaction-extrapolation curves and recently developed network diversity measures.



Outlook

The field research phase is over. It was a mixture of great physical and mental effort, between the mud, long working days in the 62 plots and many nights in the incredible laboratory of the Canandé scientific station; as a result we have been able to obtain this valuable information and findings (Figure 57). This was possible due to the teamwork and logistical coordination with the station managers and our amazing parabiologists Holger and Silvia.

Next year I will live and work in the Bavarian Forest. With the great support and guidance of my incredible supervisor Jörg Müller, I will try to finish two more articles on wood decomposition and the diversity and host-networks of wood-inhabiting fungi along a recovery gradient. Living in Germany is going to be an amazing experience.

Also, next year I will present the results of my second article at The 8th European Conference of Tropical Ecology will be held in Amsterdam (the Netherlands) from 24 to 28 February 2025. This will be a great opportunity to present my findings to the scientific community and to connect with other researchers working in the same area.

The last year of my PhD will be an opportunity to grow in my writing, statistics and research skills. I look forward to it!



Figure 58: Ana at Mirador in Canandé Reserve

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SPX: Spider Monkeys and Seed Dispersal

Malika Gottstein, Uni Freiburg

Who we are

This year, our team working on the spider monkey project grew significantly. Alongside my supervisors, Katrin Heer, Eckhard W. Heymann, Citlalli Morelos-Juárez, and parabiologist Ariel Villigua, we received invaluable support from the Forest Genetics Lab team in Freiburg. Special thanks to lab technicians Sandra Link and Luisa Grove, student assistant Maike Menger, and postdoc Carina Carneiro de Melo Moura for their dedicated contributions. I am deeply grateful for everyone's hard work and collaboration in advancing this project!

Work progress

This year, we made significant progress toward achieving the goals of our project, which include assessing the diversity, quantity, and quality of seeds dispersed by spider monkeys, observing seed dispersal distances, and investigating gene flow through seed dispersal.

In 2023, we collected ecological data on spider monkey movement, feeding habits, and behavior in Tesoro Escondido. As the largest arboreal frugivores in the Chocó region, spider monkeys play a critical role in seed dispersal [1, 2].

This year, we analyzed data from 150 hours of spider monkey observations and 270 fecal samples to study their diet and seed dispersal. During these observations, we recorded nearly 600 feeding events (defined as an individual feeding on a specific food item). Spider monkeys predominantly fed on fruit (91% of recorded feeding events), with occasional consumption of leaves, flowers, bark, aerial plant roots, insects, and lichens. Ripe fruit accounted for 83% of their feeding events. Importantly, 63% of the feeding events involved the ingestion of seeds from ripe fruits, suggesting potential seed dispersal. Also, 95% of the collected fecal samples contained seeds.



Figure 59: Preparation of leaves of *P. guianensis* for DNA extraction

We identified 86 plant species from 39 families to be part of the spider monkeys' diet in Tesoro Escondido. Alex Keller and his lab were a huge help to identify those seeds that could not be identified in the field through barcoding, thanks a lot!

Spider monkeys primarily consumed fruits from Moraceae (mainly *Brosimum utile*) and Urticaceae (mainly *Pourouma guianensis*). In 2023,

we collected leaf and cambium samples from these two species in Tesoro Escondido. Over an area of 12 ha, we sampled all adult *B. utile* and *P. guianensis* individuals, as well as seedlings along transects (4 x 200 m).

At the beginning of this year, we extracted DNA from a total of 479 samples 59. We are currently working on genotyping these samples using a ddRADseq approach. The initial results are promising, and we hope to conduct parentage analysis and examine spatial genetic structure for both species as indirect measures of seed dispersal distances.



Figure 60: Camera trap capture of *Proechimys* sp. dispersing seeds of *P. guianensis*.

While other animals also disperse *B. utile* and *P. guianensis* 60, we believe that our genetic data will provide valuable insights into gene flow via seed dispersal, particularly by spider monkeys.

Public outreach

We are excited to have shared our project and some preliminary findings at three conferences this year. I presented at the European Conference of Tropical Ecology in Lisbon (February 2024) and the Gesellschaft für Primatologie conference in Konstanz (March 2024). Ariel presented our project at the Congreso Nacional de Mastozoología in Tena (October 2024).

Conclusions

We are pleased with the progress we have made this year. Highlights for me include learning new techniques in the lab and attending the conferences to share our research. The continuous support from all those involved in this project has truly been one of the year's standout experiences!

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Imprint

This is a product of the DFG Research Unit 5207, Reassembly of Species Interaction Networks.

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