SPAAM^5

The Fifth Annual Meeting of
Standards, Precautions & Advances
in Ancient Metagenomics
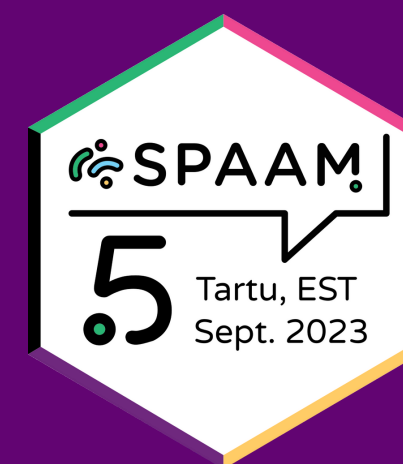
SPAAM

5 Tartu, EST
Sept. 2023

Part One: The In-Person Meeting
September 12th – Tartu, Estonia

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Welcome to SPAAM5

Hello and welcome to SPAAM5,

The SPAAM5 organizers are very happy to welcome you to the first open in-person SPAAM meeting on the eve of ISBA10 in Tartu, Estonia.

We hope this will be a great opportunity for all of us to get to know each other and discuss specific topics in our common fields of study. We are looking forward to meeting you and sharing our enthusiasm for ancient microbes.

Let's have a SPAAMtastic day!

The SPAAM5 organizers

Venue: Tartu Nature House, Lille 10 Tartu 51010, Estonia

SPAAM 5
Tartu, EST
Sept. 2023

Sierra Blunt
University of Bordeaux, PACEA
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I'm a PhD candidate working on the evolution of ancient oral microbiomes throughout periods of cultural and demographic transition in France.

Meriam Guellil
University of Vienna, Department of Evolutionary Anthropology
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I am a senior postdoctoral researcher and project leader at the University of Vienna. I specialises in ancient microbial phylogenomics and metagenomics, with a focus on human pathogens.

Alina Hiss
Max Planck Insititute for Evolutionary Anthropology
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I'm a PhD student working on ancient pathogens, specifically genomes of the Hepatitis B virus that were recovered from individuals living in the Carpatian basin during the early Medieval time.

Megan Michel
Harvard University Department of Human Evolutionary Biology and Max Planck Institute for Evolutionary Anthropology
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I'm a PhD student interested in exploring human/pathogen coevolution using genomic analyses of ancient pathogen DNA.

Zoé Pochon
Stockholm University, Centre for Palaeogenetics,
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PhD student trained in biology and history and interested in using archaeogenetics to bring new clues to scientific debates. Currently helping to develop aMeta and screening for pathogens in Scandinavia.

Morning Program

9.30 to 10.00 – Welcome

10.00 to 10.15 – Opening remarks

10.15 to 10.35 – Featured Talk

- **Metadata and smiley plots: the latest community projects from the SPAAM** – James Fellows Yates

10.35 to 11.00 – Session 1: Eukaryotic Metagenomics

Flash Talks

- **Impact and quantification of faunal aDNA that maps to the human genome** – Niall Cooke
- **Metagenomic analysis of ancient cat remains: challenges and perspectives** – Marica Baldoni
- **Metagenomic perspectives on traditional beer brewing: New insights from Scandinavian yeast rings** – Oya Inanli

11.00 to 12.00 – Coffee and Discussion groups

12.00 to 12.30 – Session 2: Microbiomes

Flash Talks

- **Considerations for de novo ancient metagenome assembly** – Irina Velsko
- **Biomolecular perspectives on the uses of birch bark tar in prehistoric Europe** – Anna White
- **Oral Odysseys: Unravelling distinct evolutionary journeys of oral microbes** - Sarah Johnson
- **How to re-think a study: the case of Edix Hill** - Biancamaria Bonucci

12.30 to 12.35 – SPAAMtisch presentation – Biancamaria Bonucci and Maria Lopopolo

12.35 to 14.00 – Lunch break

Afternoon Program

14.00 to 14.20 – Featured Talk

- **Community development of a data curation and exploration tool for ancient metagenomics** – Maxime Borry

14.20 to 14.50 – Session 3: New Tools and Methods

Flash Talks
- **Navigating the Landscape of Authentication Tools in Ancient Metagenomics: Towards Establishing Common Practices** – Sterling Wright
- **The skeleton is a complex dataset. Let's use it to inform pathogen screening** – Kelly Blevins
- **Assessing antimicrobial peptides, resistance genes, and functional gene clusters in ancient microbial DNA** – Jasmin Frangenberg

14.50 to 15.10 – Session 4: Sedimentary aDNA

Flash Talks
- **The complex colonisation and survival history of microbes in the 14-thousand-year sediment of Lake Constance** – Yi Wang
- **Computational Challenges In Environmental Ancient Dna Analysis** – Nikolay Oskolkov

15.10 to 16.10 – Coffee and Discussion groups

16.10 to 16.30 – Session 5: The Future of SPAAM

Flash Talks
- **SPAAM Steering Committee**
- **SPAAM Blog**

16.30 to 17.15 – Discussion

17.15 to 17.30 – Closing remarks and announcements

Metadata and smiley plots: the latest community projects from the SPAAM

James Fellows Yates

Following the success of the AncientMetagenomeDir and AMDirT projects from SPAAM, in this talk I will introduce two new community projects. I will introduce the next stage of improving research experience in reporting and accessing ancient DNA metadata of samples and libraries with the MInAS project – a project aiming to cover the entire palaeogenomics community. I will also introduce a new lighthearted creative project in collaboration with the newly established HAAM community to help you with interpreting those weird and funky damage plots we so often encounter. I will describe the purposes of both projects and explain members of the community can get stuck-in and involved!

Community development of a data curation and exploration tool for ancient metagenomics

Maxime Borry and the SPAAM Community

Since the publication of the first ancient metagenomics project, the number of published ancient metagenomics samples has been increasing every year. However, thanks to the contributions of the SPAAM community members, almost all of these studies have been curated in a single database, the "AncientMetagenomeDir". To facilitate the curation of theses studies, and exploration of this database, the SPAAM community has been developing the companion tool AMDirT. With the latest release of this tool, we now present multiple new features for advanced and facilitated data exploration, automated and enhanced data curation, and a general improvement to the documentation and testing of the AMDirT software.
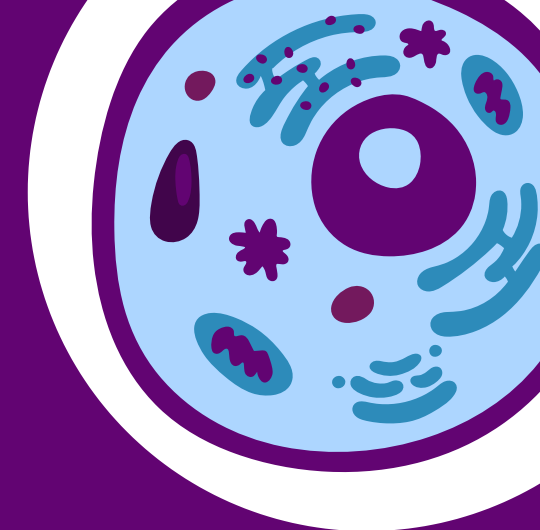
Impact and quantification of faunal aDNA that maps to the human genome
Niall Cooke

Recent advances have enabled the retrieval and analysis of genome-wide human nuclear DNA directly from sediment samples. However, the metagenomic nature of a sediment sample - in which DNA from multiple species are present - complicates potential analyses, as genetic material from non-human sources may be challenging to distinguish from human DNA. In this talk, I will discuss the impact that faunal DNA that has mismapped to the human genome has on downstream analyses, and present a method for quantifying it.

Metagenomic analysis of ancient cat remains: challenges and perspectives
Marica Baldoni

Cats are intriguing "domestic" animals that most likely started their interaction with humans more than 11 thousand years ago in the Fertile Crescent. Due to their long-standing relationship with humans as pest-control agents and companions, cats are renowned hosts of several zoonotic diseases. The challenging objective of our research is the identification of ancient pathogens in cats distributed across Europe, North Africa, and Southwest Asia dating from prehistory to historic times. After a preliminary screening the metagenomic research is now moving forward with the analysis of bitumen from ancient Egyptian mummies and dental calculus remains. Here we present the methodological strategies, the challenges, and the open questions related to ancient cat metagenomics along with the preliminary results obtained from the metagenomic screening.

Metagenomic perspectives on traditional beer brewing: New insights from Scandinavian yeast rings
Oya Inanli

Traditional "kveik" yeasts are still used in farmhouse beer brewing in Western Norway. However, the origins of kveik yeast are debated, and it is unclear to what extent the strains being used today reflect past diversity. This project explores the potential of recovering ancient yeast strains from historical yeast rings and fermentation barrels to expand our understanding of traditional brewing practices and the evolution of fermentation microbiome.
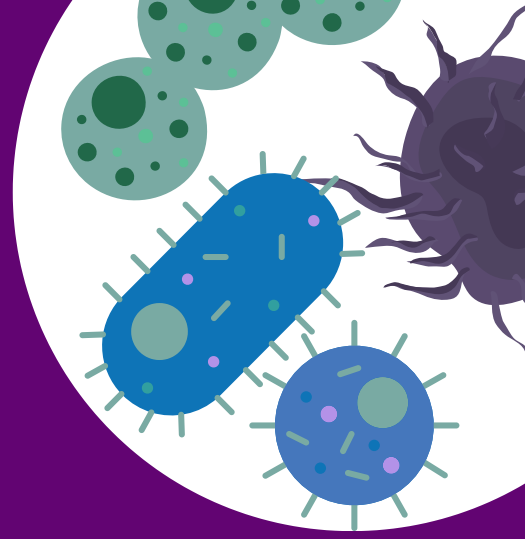
Considerations for de novo ancient metagenome assembly
Irina Velsko

De novo assembly of ancient metagenomics samples to assess taxonomic diversity is increasingly feasible and gaining popularity. This approach enables reconstruction of nearly complete microbial genomes without relying on the currently available references in genome databases such as NCBI, thereby potentially revealing uncatalogued genetic and genomic diversity. However, the tools currently available for metagenome assembly were created to process modern metagenomic samples, and characteristic ancient DNA damage disadvantages the assembly process and outcomes. I will briefly discuss the characteristics of ancient metagenomics samples that affect de novo assembly, and some ways to overcome these disadvantages.

### Biomolecular perspectives on the uses of birch bark tar in prehistoric Europe
Anna White

Ancient DNA analyses provide a new way of analysing ancient birch tar that can provide new insights into its uses in the past. We can determine whether or not the pieces were chewed and identify potential additives. Here I'll discuss the importance and challenges of authenticating ancient DNA from metagenomic sample sets.

Oral Odysseys: Unravelling distinct evolutionary journeys of oral microbes
Sarah Johnson

The biological impact of European Contact in the Americas has been well-documented among human populations. In our research examining ancestral Native American oral microbiomes, we find that there is variability in the evolutionary trajectories of microbes within the same oral ecology, with some species showing strain persistence and others showing replacement over time.
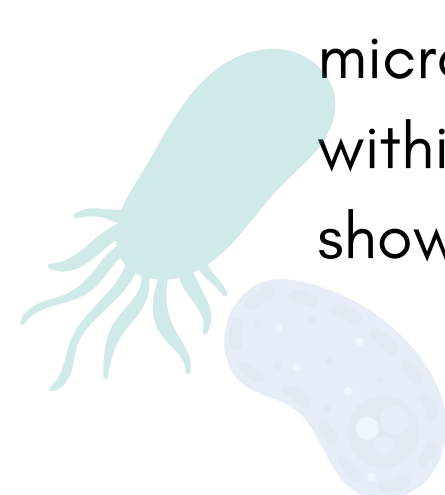
How to re-think a study: the case of Edix Hill
Biancamaria Bonucci

In this study, we generated shotgun metagenomic libraries from dental calculus coming from 74 individuals buried in the Anglo-Saxon cemetery of Edix Hill. The preliminary results showed a prevalence of species associated with a poor oral health. New libraries and deeper sequencing will allow us to better investigate the relationship between oral health and kinship of this Early medieval population.

Navigating the Landscape of Authentication Tools in Ancient Metagenomics: Towards Establishing Common Practices
Sterling Wright

Numerous authentication tools designed to verify the reliability of ancient metagenomic data have recently been developed. However, the accelerated progress of such tools poses a challenge for researchers in determining the most appropriate authentication practices. This talk seeks to discuss the various authentication methods that have been put forward recently, hoping to spur discussions among researchers in addressing whether common practices should be agreed upon to ensure reproducibility and the integrity of ancient metagenomic analyses.

**The skeleton is a complex dataset. Let's use it to inform pathogen screening**
Kelly Blevins

Metagenomic screening for ancient pathogens is largely opportunistic from libraries generated for host DNA recovery or targeted for causative agents of three highly "archaeologically visible" diseases: leprosy, tuberculosis, and treponemal disease. Many infectious agents, however, can infect bone and theoretically be recovered through strategic sampling of skeletal material. This talk will explore some common skeletal pathologies and how we can use their hypothesised aetiologies to inform sampling strategies for metagenomic pathogen screening.

Assessing antimicrobial peptides, resistance genes, and functional gene clusters in ancient microbial DNA
Jasmin Frangenberg
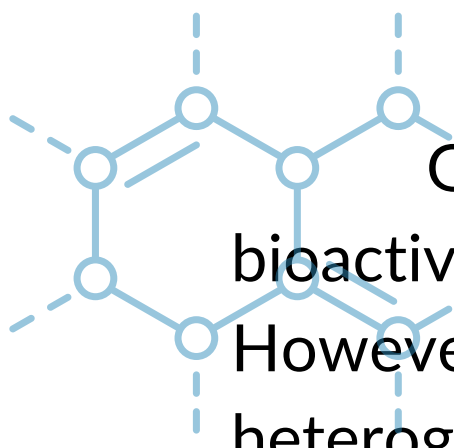
Genome-mining of ancient DNA (aDNA) is a powerful strategy to discover new bioactive natural products and to study their evolution and structural diversity. However, the diversity in computational platforms, accessibility, scalability, and heterogeneous reporting of results hampers the effectiveness and usability of such analysis tools. Here, we present nf-core/funcscan, a Nextflow pipeline for the screening of functional and biosynthetic genes from assembled contigs and we demonstrate this functionality on a dataset of aDNA from paleofeces. nf-core/funcscan allows researchers of different scientific fields and backgrounds to efficiently mine genomic data for antimicrobial peptides, antibiotic resistance genes, and biosynthetic gene clusters.
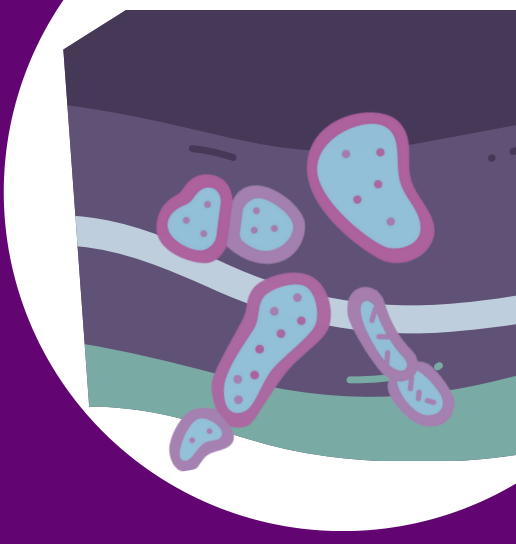
The complex colonisation and survival history of microbes in the 14-thousand-year sediment of Lake Constance

Yi Wang

We extracted a 34-sample metagenomic series from the sediment of Lake Constance and identified more than 6700 bacterial and 280 archaeal species using taxonomic profiling. Co-abundance based network analysis shows that closely connected communities mostly consist of low abundance species. Predominant species, some still living in the sediment, also have distinctive distribution patterns linked to ecological changes through time.
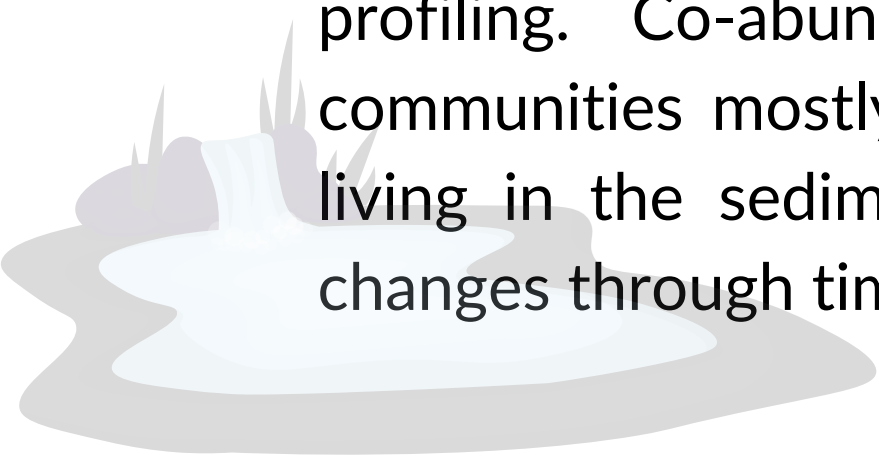
Computational Challenges In Environmental Ancient Dna Analysis

Nikolay Oskolkov

Environmental and sedimentary ancient DNA (sedaDNA) can deliver important temporally resolved information about hominin and animal evolution where historical bones and teeth are not available. However, the natural lack of prior knowledge about the content of environmental samples leads to particularly high demands on the reference databases which should be large enough for an unbiased profiling of the organisms present in the samples. In this presentation, I will discuss a few possible ways to construct large and representative across tree-of-life databases, and overcome technical limitations due to the limited computer memory.
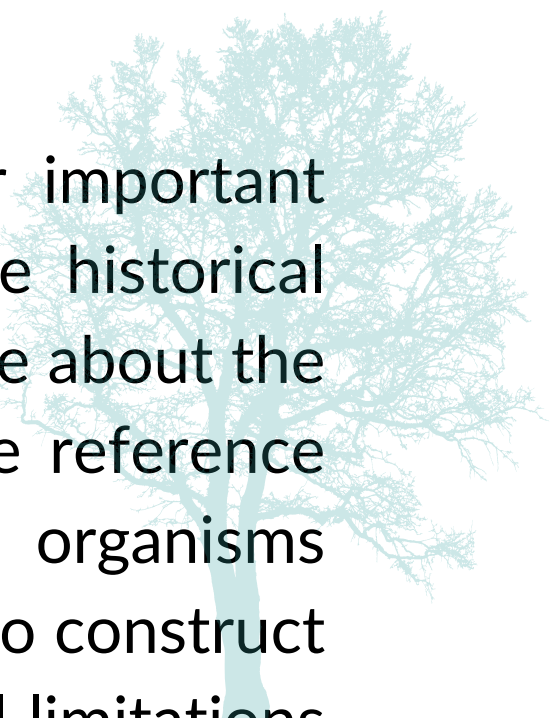
SPAAMtisch and Session 5 – The Future of SPAAM

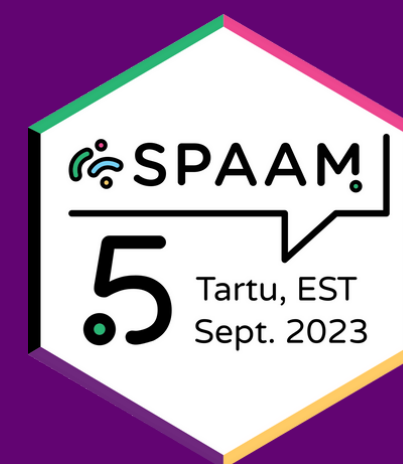SPAAMtisch - Biancamaria Bonucci and Maria Lopopolo

SPAAM Steering Committee - Shreya Ramachandran

SPAAM Blog - Eleanor Green

Code of Conduct

TL;DR

All attendees and members of SPAAM are expected to be respectful towards all members regardless of background, and actively participate in creating a welcoming and friendly community.

Unacceptable or illegal behaviour will not be tolerated and the organisers reserve the right to remove anyone violating the Code of Conduct from both in-person or online channels.
If at any point you feel unsafe or the code of conduct is violated, please contact any of the following SPAAM members who will deal with any issues respectfully and anonymously, as required. This is only for guidance, and the main body of this page is the enforceable document.

1. Purpose

A primary goal of SPAAM is to be inclusive to the largest number of contributors, with the most varied and diverse backgrounds possible. As such, we are committed to providing a friendly, safe and welcoming environment for all, regardless of gender, sexual orientation, ability, ethnicity, socio-economic status, and religion (or lack thereof).

This code of conduct outlines our expectations for all those who participate in our community, as well as the consequences for unacceptable behaviour.

All attendees at our conference are required to agree to and comply with with the following code of conduct. Organisers will enforce this code throughout the event. We expect cooperation from all participants to help ensure a safe and positive environment for everybody.

2. Citizenship

A supplemental goal of this Code of Conduct is to increase 'citizenship' by encouraging participants to recognize and strengthen the relationships between our actions and their effects on our community.

Communities mirror the societies in which they exist and positive action is essential to counteract the many forms of inequality and abuses of power that exist in society.

If you see someone who is making an extra effort to ensure our community is welcoming, friendly, and encourages all participants to contribute to the fullest extent, we want to know (either in person, Slack, or email – see section 8).

3. Expected Behaviour

The following behaviours are expected and requested of all community members:

- Participate in an authentic and active way. In doing so, you contribute to the health and longevity of this community.
- Exercise consideration and respect in your speech and actions.
- Attempt to respectfully resolve issues before conflicts arise.
- Refrain from demeaning, discriminatory, or harassing behaviour and speech.
- Be mindful of your surroundings and of your fellow participants. Alert organisers if you notice a dangerous situation, someone in distress, or violations of this Code of Conduct, even if they seem inconsequential.
- Remember that events may be shared with members of the public; please be respectful to all patrons of these locations.

4. Unacceptable Behaviour

The following behaviours are considered harassment and are unacceptable within our community, both in person and online:

- Violence, threats of violence or violent language directed against another person.
- Sexist, racist, homophobic, transphobic, ableist or otherwise discriminatory jokes and language.
- Posting or displaying sexually explicit or violent material.
- Posting or threatening to post other people's personally identifying information ("doxxing").
- Personal insults, particularly those related to gender, sexual orientation, race, religion, or disability.
- Inappropriate photography or recording.
- Inappropriate physical contact. You should have someone's consent before touching them.
- Unwelcome sexual attention. This includes, sexualized comments or jokes; inappropriate touching, groping, and unwelcomed sexual advances.
- Deliberate intimidation, stalking or following (online or in person).
- Advocating for, or encouraging, any of the above behaviour.
- Sustained disruption of community events, including talks and presentations.
- Furthermore, we will follow all legal guidance from the European Commission on non-discrimination

5. Consequences of Unacceptable Behavior

Unacceptable behaviour from any attendee, including those with decision-making authority, will not be tolerated.

Anyone asked to stop unacceptable behaviour is expected to comply immediately.

If an attendee engages in unacceptable behaviour, the community organizers may take any action they deem appropriate, up to and including a temporary ban or permanent expulsion from the event without warning (and without refund in the case of any payments).

6. Reporting Guidelines

If you are subject to or witness unacceptable behaviour, or have any other concerns, please notify any of the event organisers (see section 8) as soon as possible. Organisers will ensure that the report can be given in a safe space, and will be recorded as respectfully as possible.

Additionally, organizers are available to help attendees engage with local law enforcement or to otherwise help those experiencing unacceptable behaviour feel safe. In the context of in-person events, organizers will also provide escorts as desired by the person experiencing distress.

7. Scope

We expect all participants (contributors, paid or otherwise, and other guests) to abide by this Code of Conduct in all community venues - online and in-person - as well as in all one-on-one communications pertaining to community business.

This code of conduct and its related procedures also applies to unacceptable behaviour occurring outside the scope of community activities when such behaviour has the potential to adversely affect the safety and well-being of community members.

8. Contact info

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Megan Michel (megan_michel@eva.mpg.de)
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To report any violation during the SPAAM5 meeting you can contact an organizer, the SPAAM Safety Office or fill out the anonymous report form at https://forms.gle/9RqKZL8hXBxMvFLs6