



南京大學
NANJING UNIVERSITY

Complex marine ecological response during the Eocene-Oligocene revealed by global foraminiferal record

First Authors: Zhengbo Lu, Ke Xue, and Yiying Deng.

Corresponding Authors: Junxuan Fan, **Chao Qian**, and Yukun Shi.

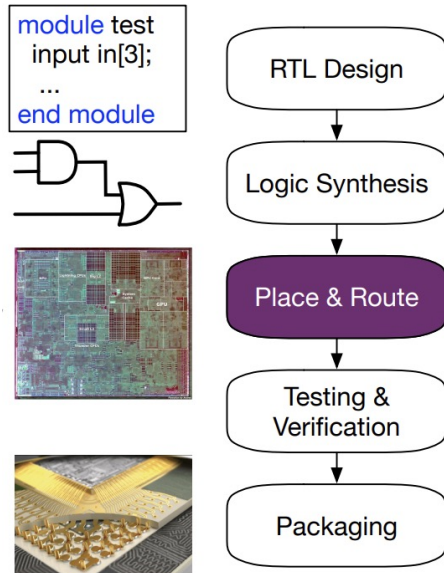
School of Earth Sciences and Engineering, Nanjing University, China

School of Artificial Intelligence, Nanjing University, China

Nature Communications 2026

The 21st Humies Bronze Award (Melbourne, Australia)

The problem we solve



Macro Placement

A vital stage in chip design

The baselines we beat



Significant improvement

(e.g., 80% wirelength improvement
over [Google, Nature'21])

The contributions to community

- **Bring EAs back to the state-of-the-art for macro placement**
- **Reaffirm the potential of EAs for chip design**

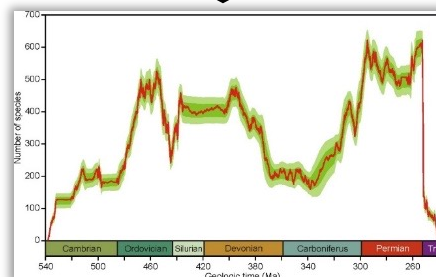


Deep-time life evolution

The problem we solve

Deep-time Life Evolution

Fundamental Question
of Natural Science



The baseline we beat



CONOP.SAGA

[Fan et al., *Science*, 2020]

Science

“New dataset and method, drive the transformation of the entire evolutionary paleontology”

2020 China's

Top 10 Scientific Advances

Computational cost:
“Tianhe II supercomputer”
7,000,000 CPU hours

Methods & Results

Developed CONOP.EA
since our collaboration in 2021

Efficient: nearly 100x speedup, making it possible to use large-scale fossil data

General: can be applied to construct diverse biodiversity change curves

nature communications



Article

<https://doi.org/10.1038/s41467-026-70541-w>

Complex marine ecological response during the Eocene-Oligocene revealed by global foraminiferal record

Received: 8 February 2025

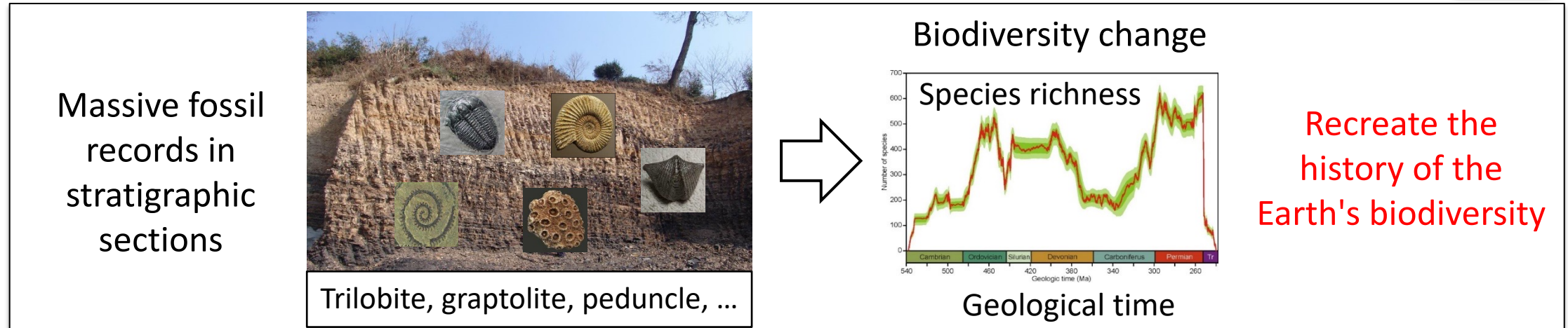
Accepted: 27 February 2026

Published online: 14 March 2026

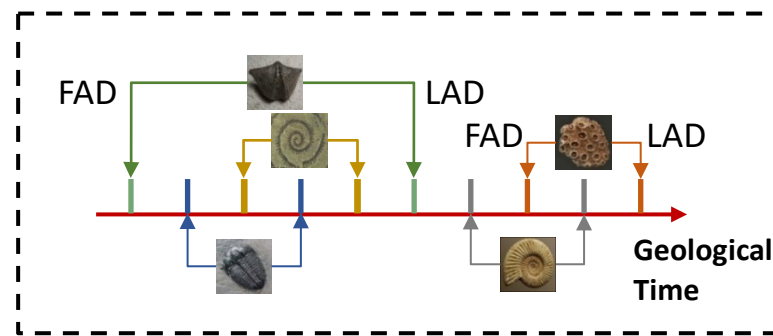
Zhengbo Lu^{1,2,11}, Ke Xue^{3,4,11}, Yiying Deng^{5,11}, Junxuan Fan^{1,2}, Peiyue Fang⁶, Bridget S. Wade⁷, Laia Alegret⁸, Michael J. Benton⁹, Yuchang Wu^{3,4}, Chao Qian^{3,4}, Xudong Hou^{1,2}, Yukun Shi^{1,2}, Peter M. Sadler¹⁰, Huiqing Xu^{1,2}, Zhi-Hua Zhou^{3,4} & Shuzhong Shen^{1,2}

Our problem: Deep-time life evolution

Fundamental Question of Natural Science — Deep-time Life Evolution Core Scientific Content of the International Big Science Program Deep-time Digital Earth



Sort the “First Appearance Datum” (FAD) and “Last Appearance Datum”(LAD) events of different species



Permutation optimization

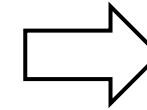
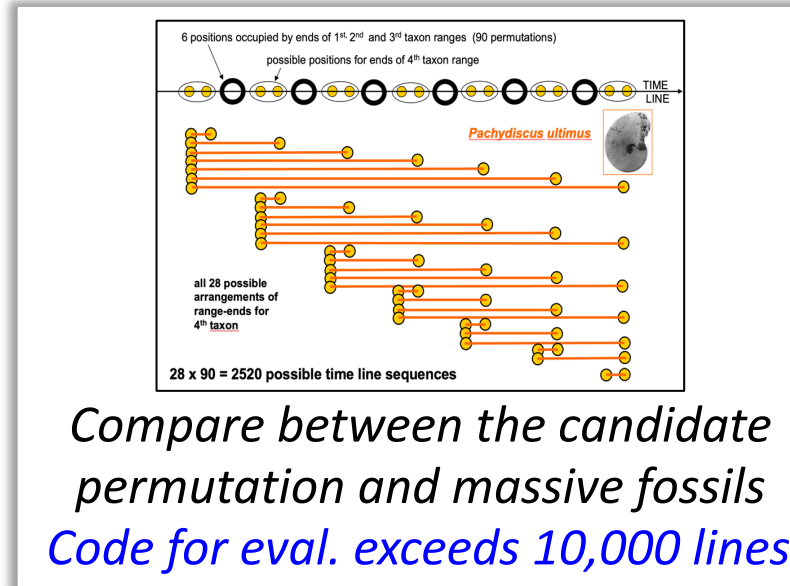
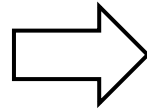
*To align the permutation **as closely as possible** with the fossil records collected from stratigraphic sections*

Problem formulation of deep-time life evolution

The problem formulation of deep-time life evolution: $\max_x f(x)$

Solution x :

The permutation of
LAD and FAD events
of all species



Objective $f(x)$:

The “consistency” of the
permutation and
fossil data

[Hannisdal and Peter, *Science*, 2011;
Fan et al., *Science*, 2020]

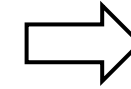
This is a black-box optimization problem

Previous methods of deep-time life evolution

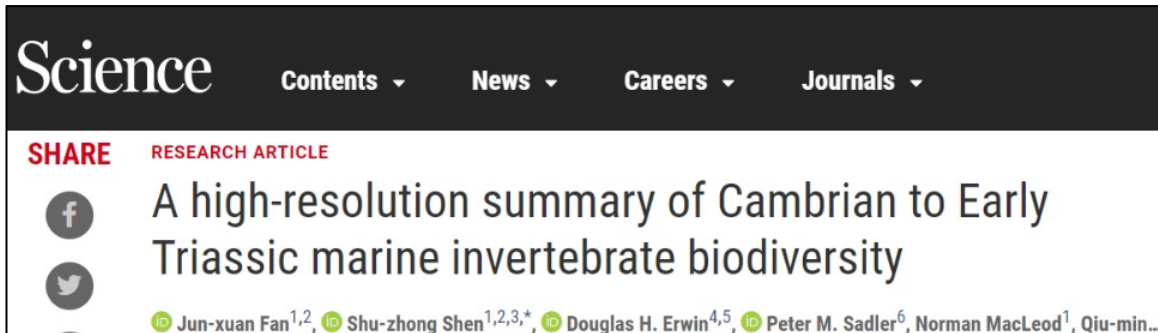
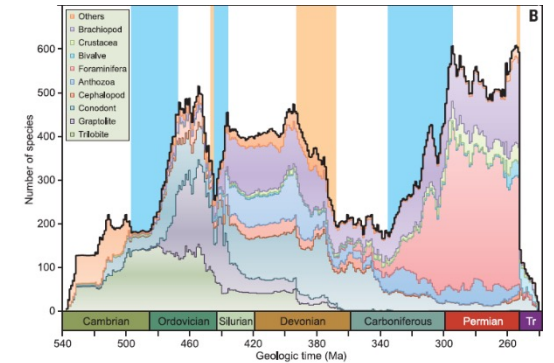
Researchers from School of
Earth Sciences and Engineering,
Nanjing University, China

Developed the *state-of-the-art* method
based on simulated annealing for deep-
time life evolution: **CONOP.SAGA**

Fossil dataset of China
Sections: 3122 Species: 11268



The world's first high-precision
curve of marine biodiversity



Science: “New dataset and method, drive the
transformation of the entire evolutionary paleontology”

Nature: “Palaeontologists have charted 300 million
years of Earth’s history **in breathtaking detail.**”

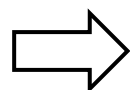
China's Top 10 Scientific Advances in 2020

Challenges of deep-time life evolution

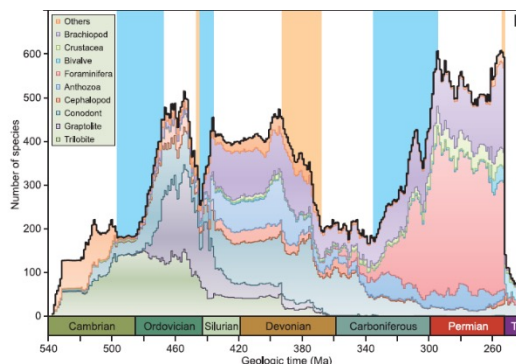
CONOP.SAGA [Fan et al., *Science*, 2020]
based on simulated annealing

Fossil dataset of China
Sections: 3122 Species: 11268

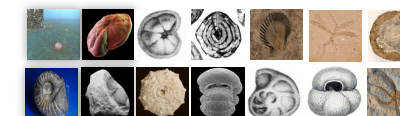
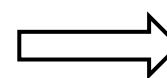
“Tianhe II supercomputer”
7,000,000 CPU hours



The world's first high-precision
curve of marine biodiversity



More
Data



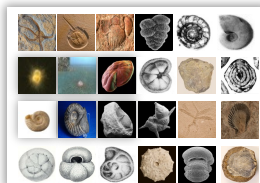
Global stratigraphic
section data

about 8000 sections & 30000 species

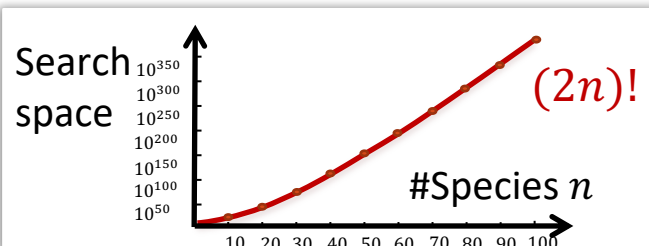
Existing methods:

Computationally Intractable

Large Scale
Optimization

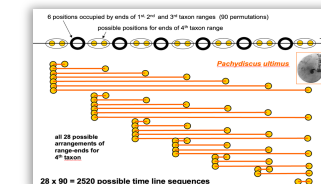


The volume of
collected fossil
keeps growing



*The search space
grows super-
exponentially*

Expensive
Optimization



Evaluation needs
alignment with
massive fossil data

Paleozoic marine invertebrates of China

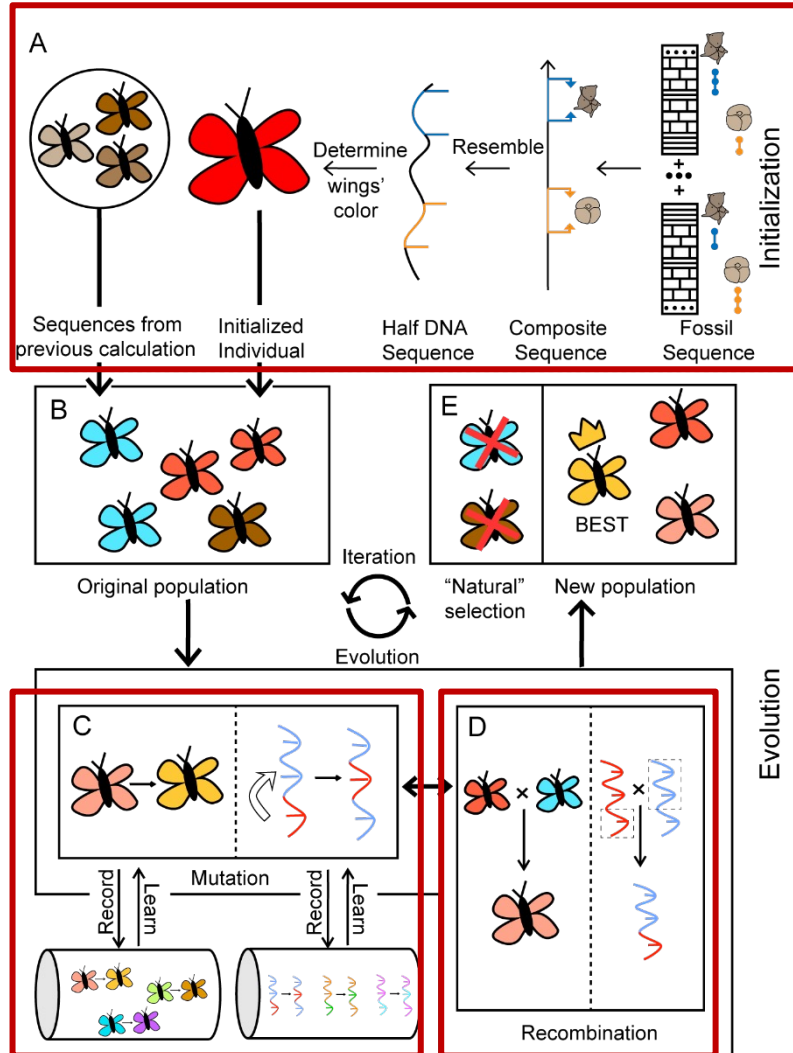
Sections: 3122

Species: 11268

Single evaluation
takes minutes

*The eval. time
increases with
problem size*

Our developed algorithm: CONOP.EA



Since beginning our collaboration in 2021, we have developed **an evolutionary algorithm for deep-time life evolution**

1. Geoscience-Informed Initialization

Statistically analyze and weight the stratigraphic sections in the dataset, prioritizing the critical sections

2. Diversity-aware crossover operator

Select high-quality solutions from the elite diverse archive for crossover

3. Learning-based adaptive mutation operator

Adaptively adjusts the mutation operator types and parameters based on historical information

CONOP.EA - Geoscience-Informed Initialization

Data-driven analysis

Compute event and section weights



$$w(e) = \text{count}(e) \times \text{ratio}(e)$$



$$S_j = \sum w(e)$$

Sec. A		62
Sec. B		92 ✓
Sec. C		55

Geoscience-knowledge-driven analysis

A domain-informed virtual section preserves the relative orders

- superposition
- regional correlation
- biozones
- expert-defined order

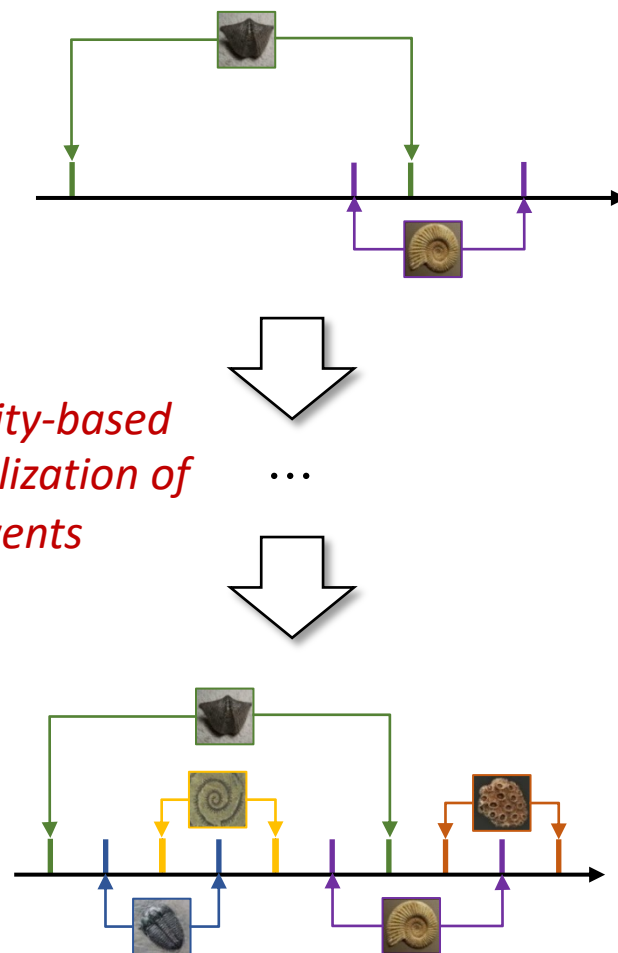


Virtual section



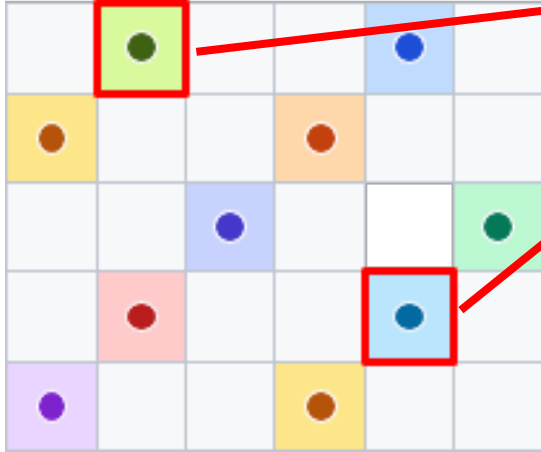
Construct the
"Virtual Section"
from high-weight
expert knowledge

*Priority-based
initialization of
all events*



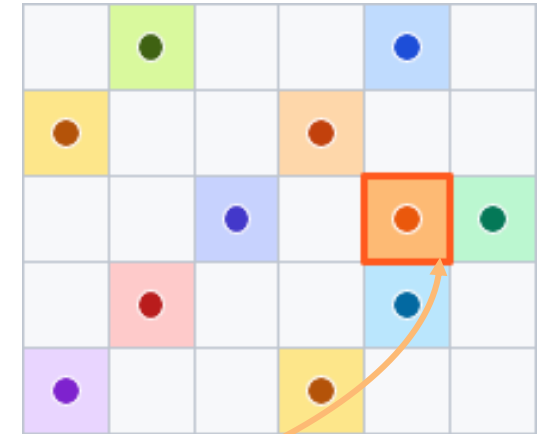
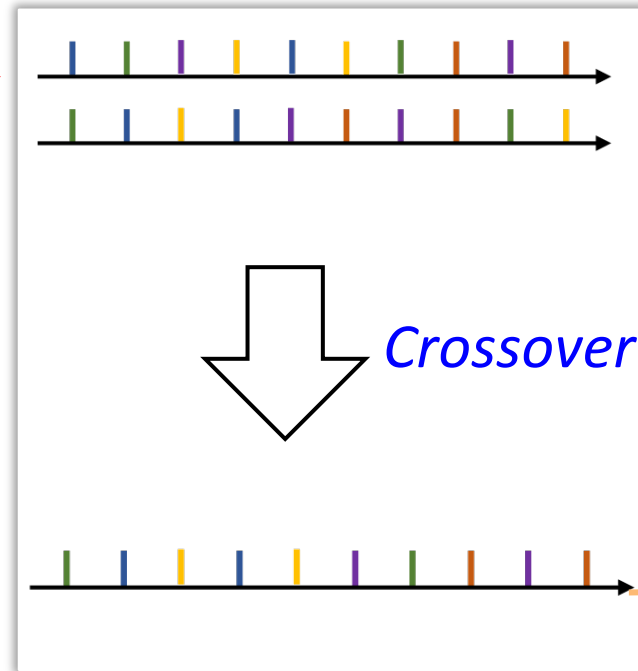
CONOP.EA - Diversity-aware crossover operator

Maintain **an archive** to store good permutations with diverse patterns



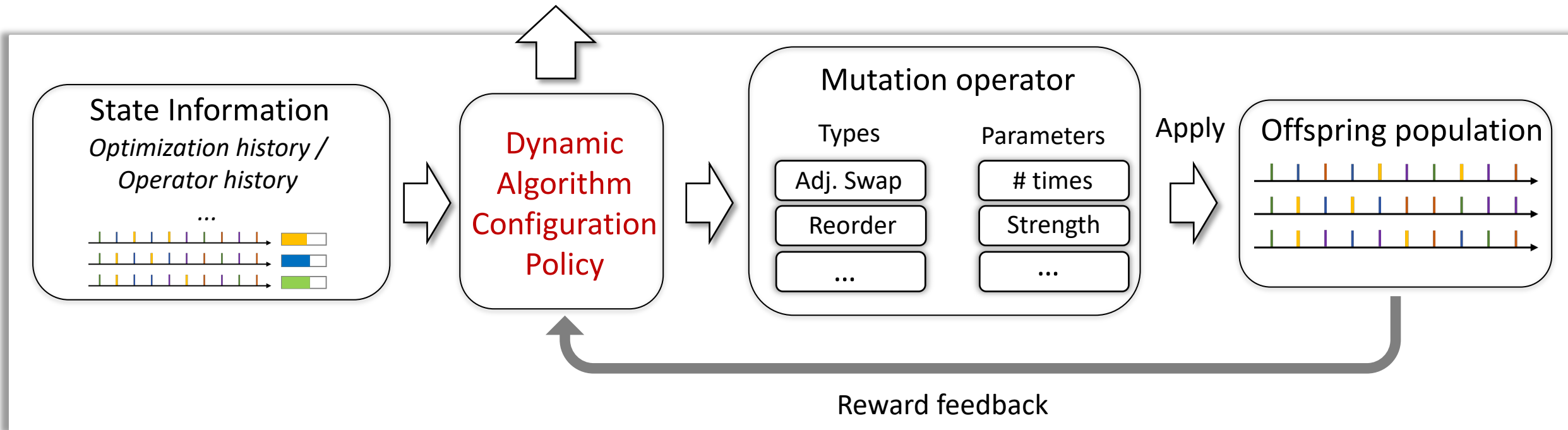
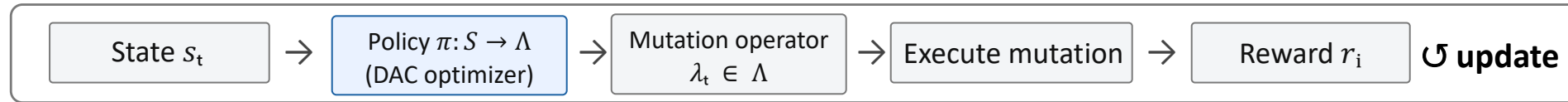
We use **Kendall correlation** to define the similarity between two permutations

$$\tau(x_1, x_2) = \frac{2}{n(n-1)} \sum_{1 \leq i < j \leq n} \text{sgn}(x_1(i) - x_1(j)) \text{sgn}(x_2(i) - x_2(j)).$$



Diversity-aware crossover helps escape local optima

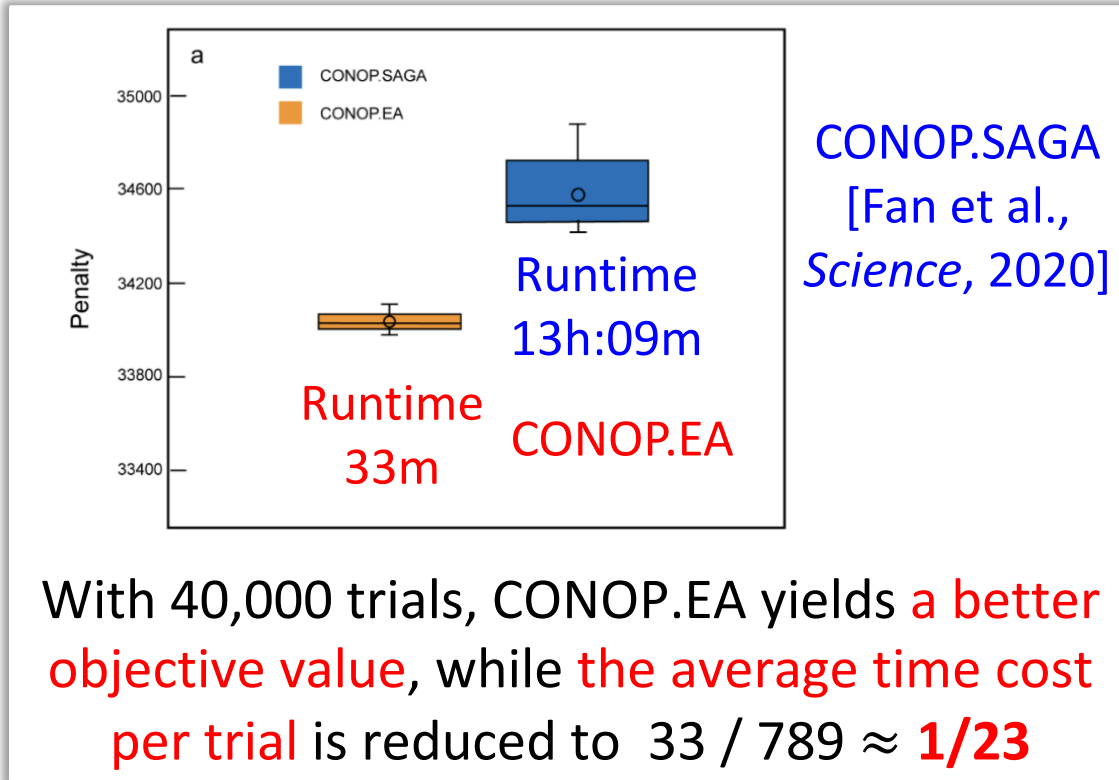
CONOP.EA - Learning-based adaptive mutation operator



Our learned policy: For example, when recent rewards remain low, the policy selects *more global operators* such as Reorder, and *stronger mutations* with larger #times / strength to escape stagnation

Our algorithm CONOP.EA is efficient

Results on the Eocene-Oligocene marine foraminifera (Sections: 161, Species: 1269)



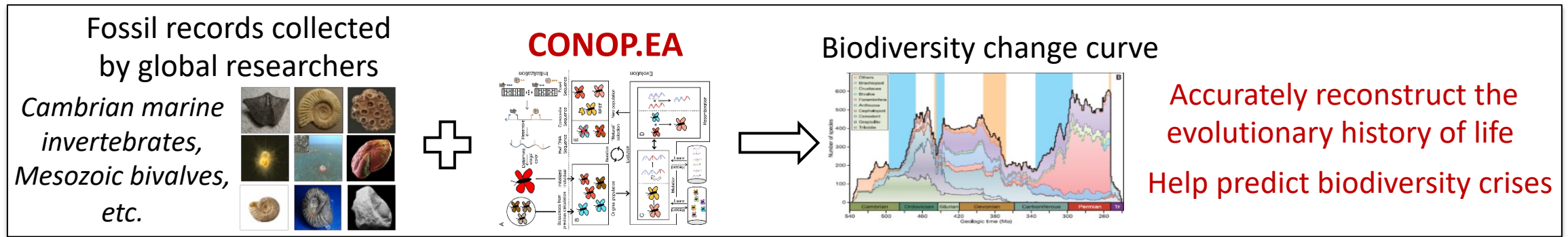
Algorithm	Objective	Trials
CONOP.SAGA [Fan et al., <i>Science</i> , 2020]	34600	40,000
CONOP.EA	< 34600	~9,000

The number of trials to achieve the same objective value is reduced to $9000 / 40000 \approx 1/4.4$

To reach the same objective value, the total runtime of CONOP.EA is reduced to $1 / (23 \times 4.4) = 1/101.2$ of CONOP.SAGA

Our algorithm CONOP.EA is general

CONOP.EA can be applied to construct high-resolution biodiversity change curves
across different geological periods and fossil groups





Science
1 July 2005
Vol. 309 No. 5731
Pages 1-104 \$10

125 Questions: WHAT DON'T WE KNOW?

What Determines Species Diversity?

older rocks suggests that photosynthetic organisms were already well established on Earth by 3.7 billion years ago. Researchers suspect that the organisms that left these traces shared the same basic traits found in all life today. All free-living organisms encode genetic information in DNA and catalyze chemical reactions using proteins. Because DNA and proteins depend so intimately on each other for their survival, it's hard to imagine one of them having evolved first. But it's just as implausible for them to have emerged simultaneously out of a prebiotic soup. Experiments now suggest that earlier forms of life could have been based on a third kind of molecule

shed light on this question. They ran an electric current through a mix of ammonia, methane, and other gases believed at the time to have been present on early Earth. They place, however, although suggestions include tidal pools or oceans covered by glaciers. Research projects now under way may shed more light on how life

How and Where Did Life on Earth Arise?

Cauldron of life? Deep-sea vents are one proposed site for life's start. found that they could

from marine microbes, should improve baseline data, but they will barely scratch the surface. Models that predict when one species will split into two will help. And an emerging discipline called evo-devo is probing how genes involved in development con-

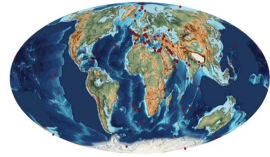
began. Scientists are running experiments in which RNA-based cells may be able to reproduce and evolve. NASA and the European Space Agency have launched

It provides key support for life evolution research, one of the four major directions in the ongoing paradigm shift of geosciences

Application of CONOP.EA

Recreate the history of foraminifera biodiversity during the E-O transition period

The currently largest foraminifera dataset

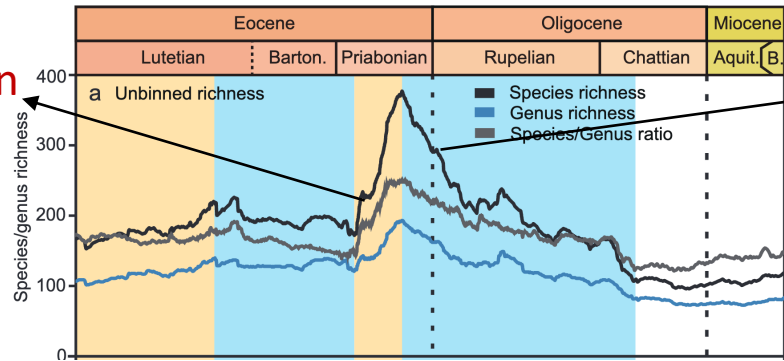


Planktonic fora.



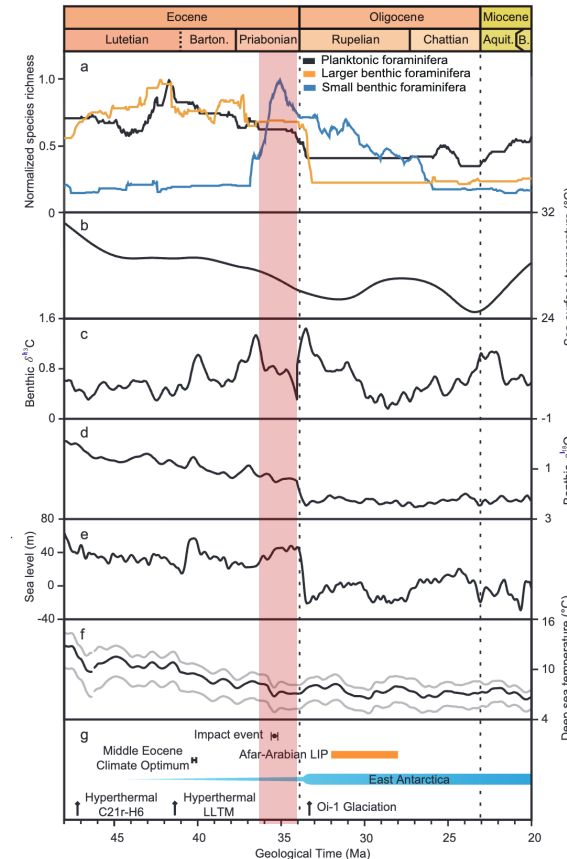
Benthic fora.

Early-
Priabonian
Radiation
~1.9Myr



Eocene-
Oligocene
Extinction
~3.05Myr

Help understand the environmental drivers of the transition of species



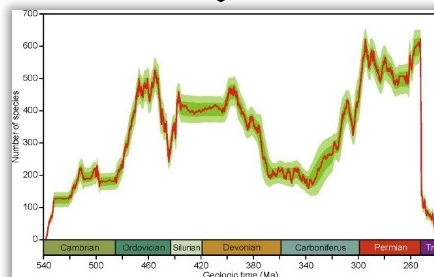
The extinction of planktonic foraminifers and large benthic foraminifers is related to rapid cooling, sea level drop, and positive drift of carbon isotopes

Thanks for listening!

The problem we solve

Deep-time Life Evolution

Fundamental Question
of Natural Science



The baseline we beat



CONOP.SAGA

[Fan et al., *Science*, 2020]

Science

“New dataset and method, drive the transformation of the entire evolutionary paleontology”

2020 China's

Top 10 Scientific Advances

Computational cost:
“Tianhe II supercomputer”
7,000,000 CPU hours

Methods & Results

Developed CONOP.EA
since our collaboration in 2021

Efficient: nearly **100x speedup**, making it possible to use large-scale fossil data

General: can be applied to construct diverse biodiversity change curves

Nature Communications 2026

The contributions to community

- Provide a critical application for EAs
- Show EAs can play a significant role in the current wave of AI for Science