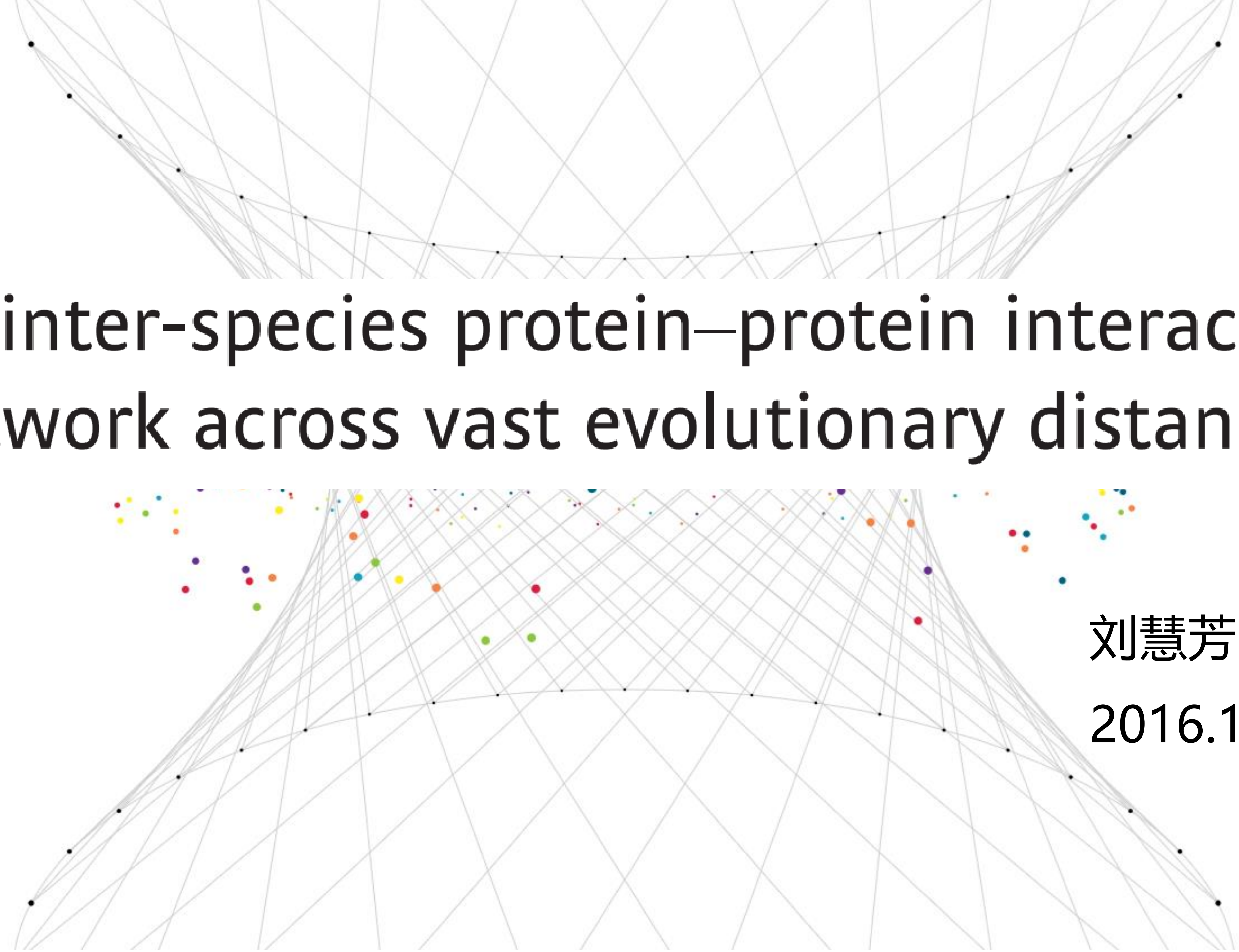

An inter-species protein–protein interaction network across vast evolutionary distance

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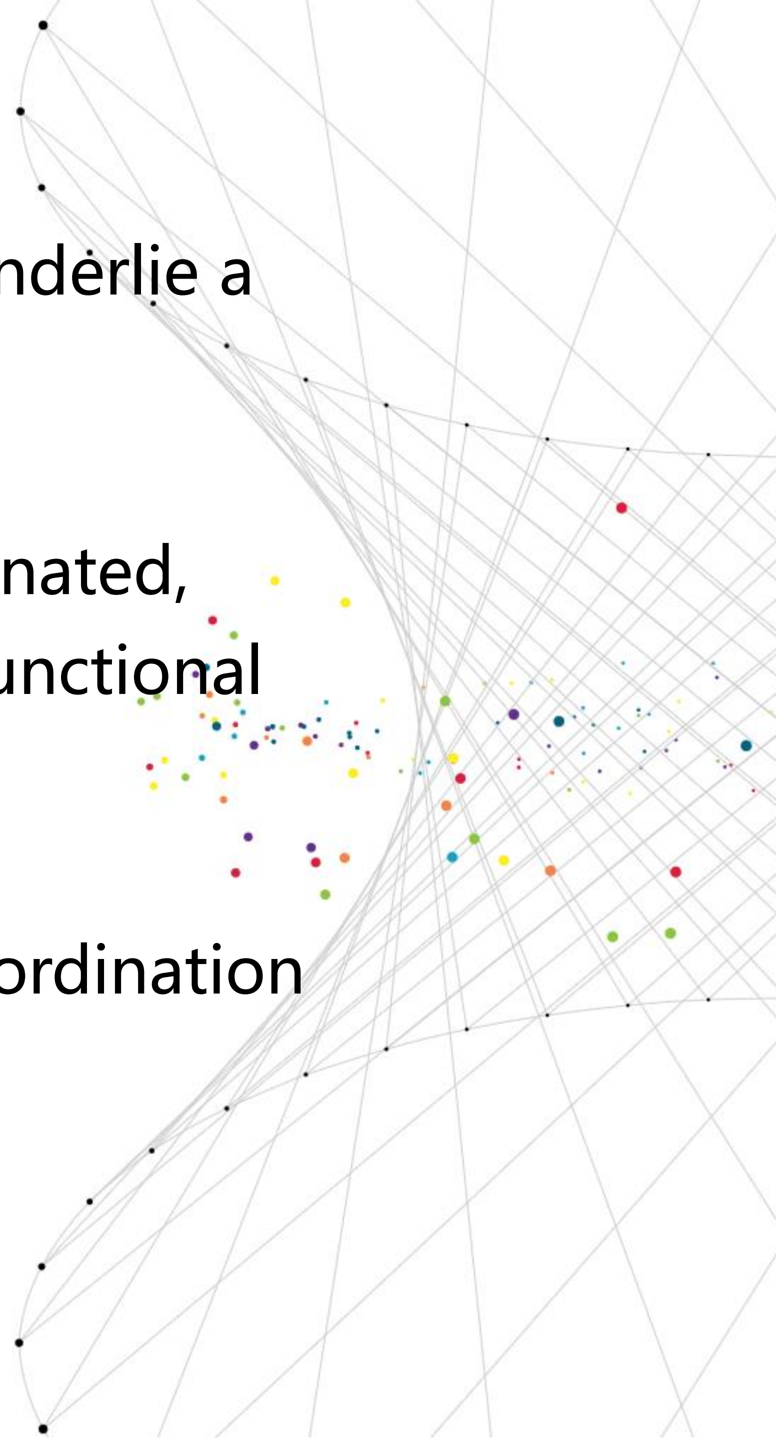
目录

CONTENTS

背景

Background

Background

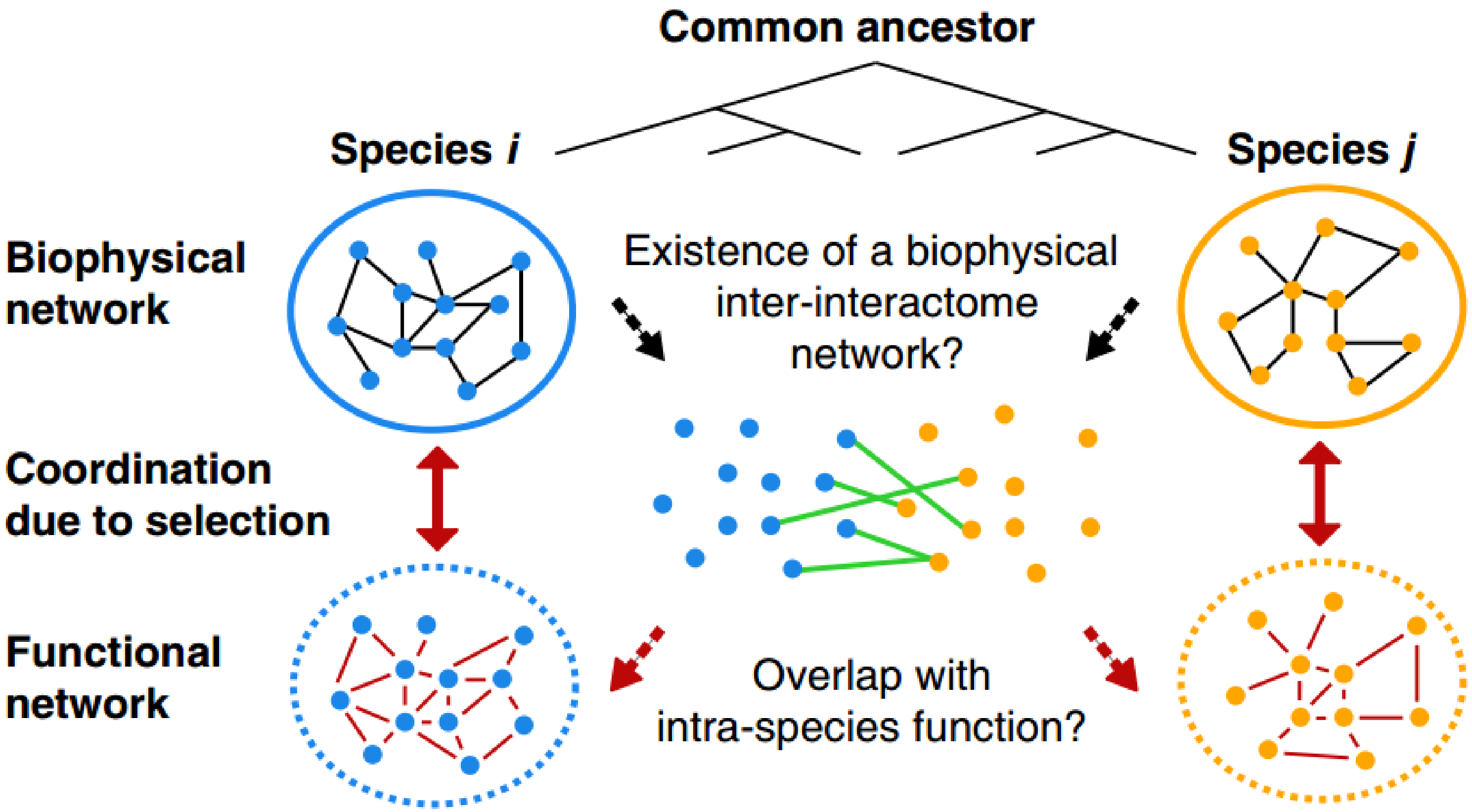


Biophysical interactions between macromolecules underlie a complex web of functional interactions.

How biophysical and functional networks are coordinated, whether all biophysical interactions correspond to functional interactions.

How such biophysical-versus-functional network coordination is shaped by evolutionary forces.

Background



1. To what extent two evolutionarily distant proteomes are capable of forming a biophysical interspecies inter-interactome network?
2. How such an inter-interactome might correlate with intra-species functional relations?

研究方法

Methods

Methods

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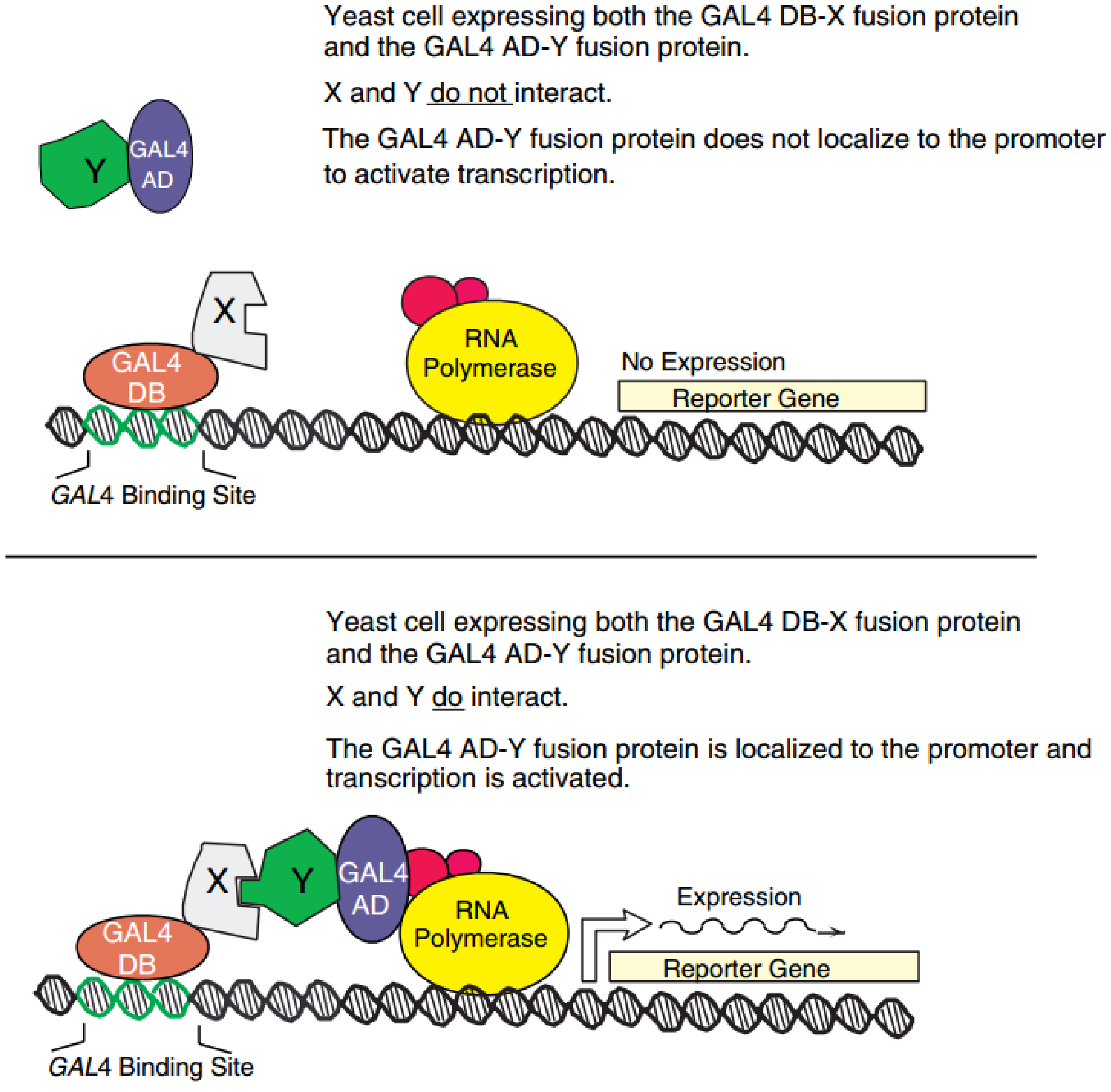


Yeast cell expressing both the GAL4 DB-X fusion protein and the GAL4 AD-Y fusion protein.

X and Y do not interact.

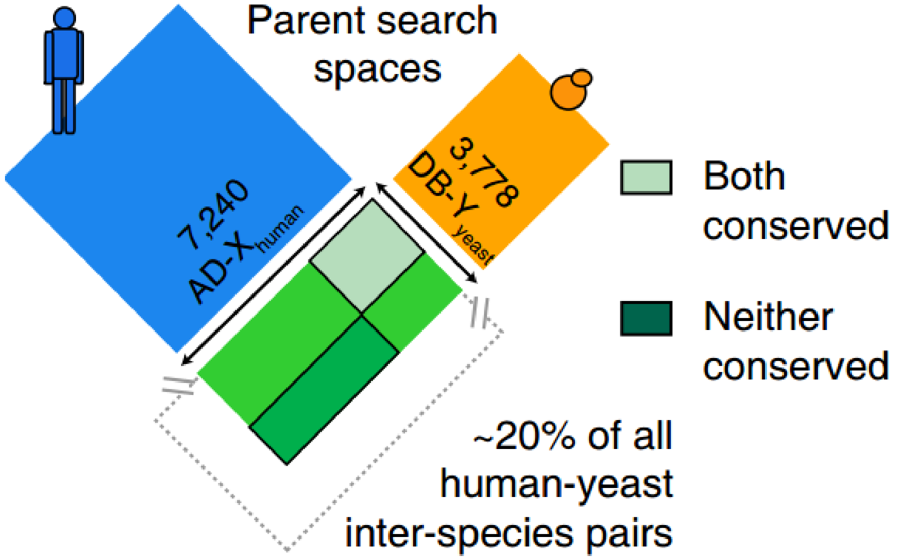
The GAL4 AD-Y fusion protein does not localize to the promoter to activate transcription.

Yeast cell expressing both the GAL4 DB-X fusion protein and the GAL4 AD-Y fusion protein.

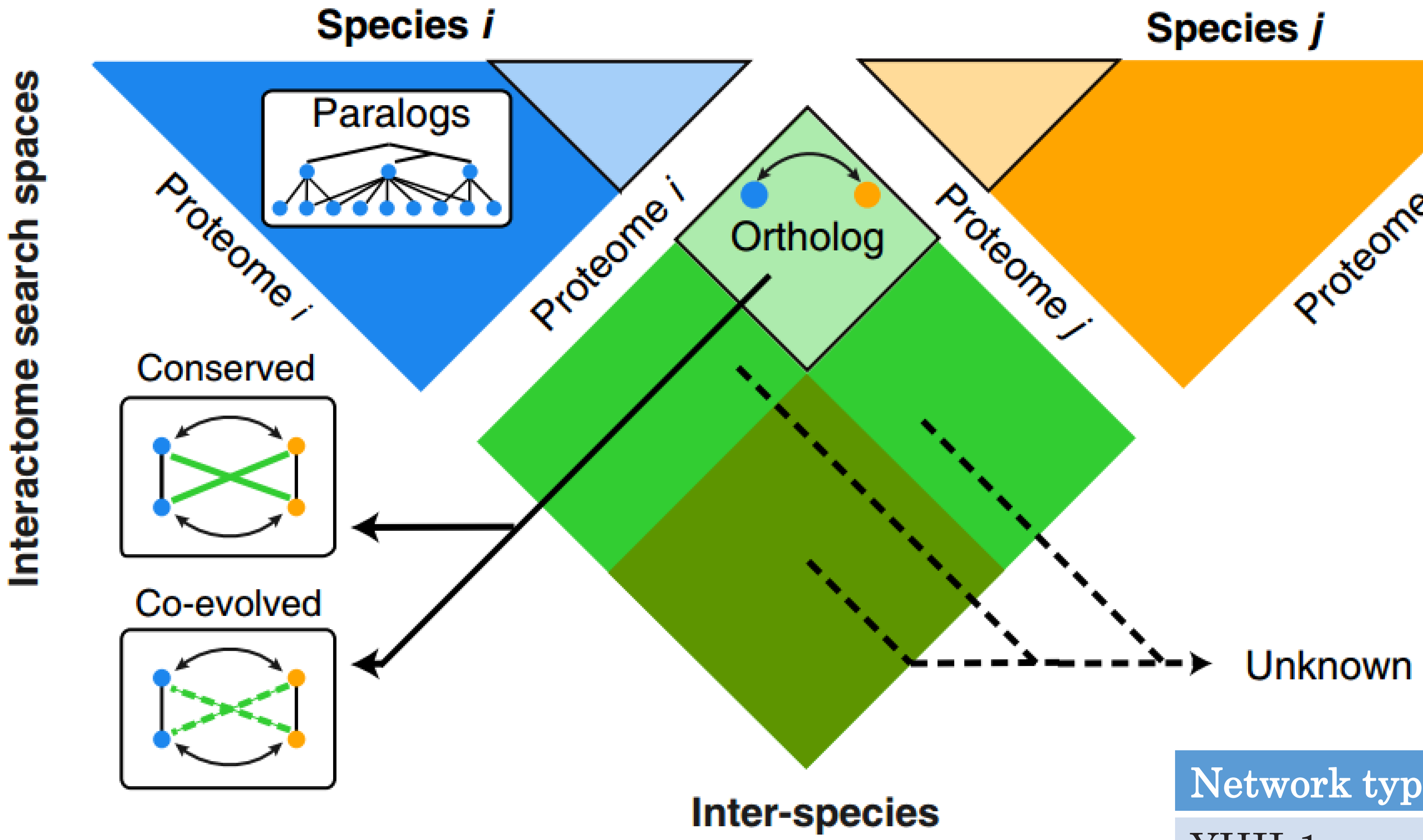
X and Y do interact.

The GAL4 AD-Y fusion protein is localized to the promoter and transcription is activated.

Figure 1. Basis of the Two-Hybrid System.



Methods



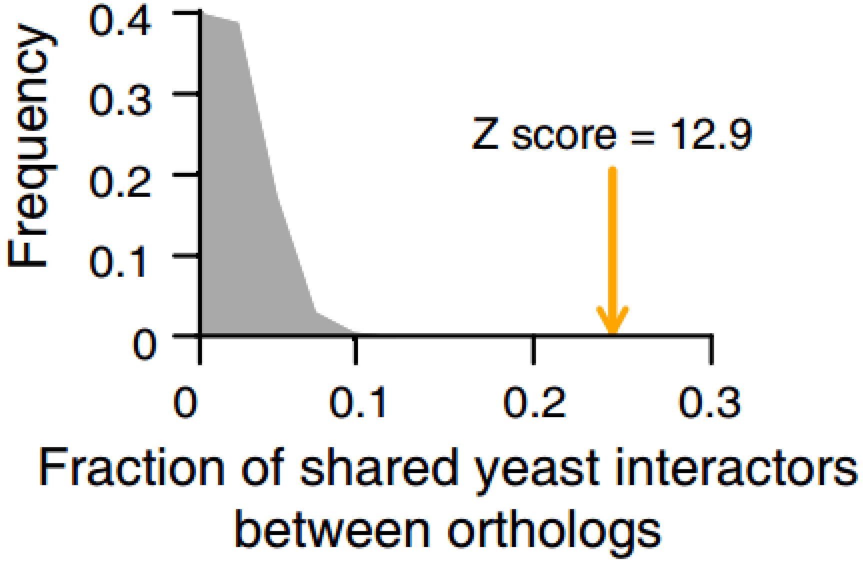
Network type	PPI number
YHII-1	1,583
YI-1	1,690
HI-1	2,750

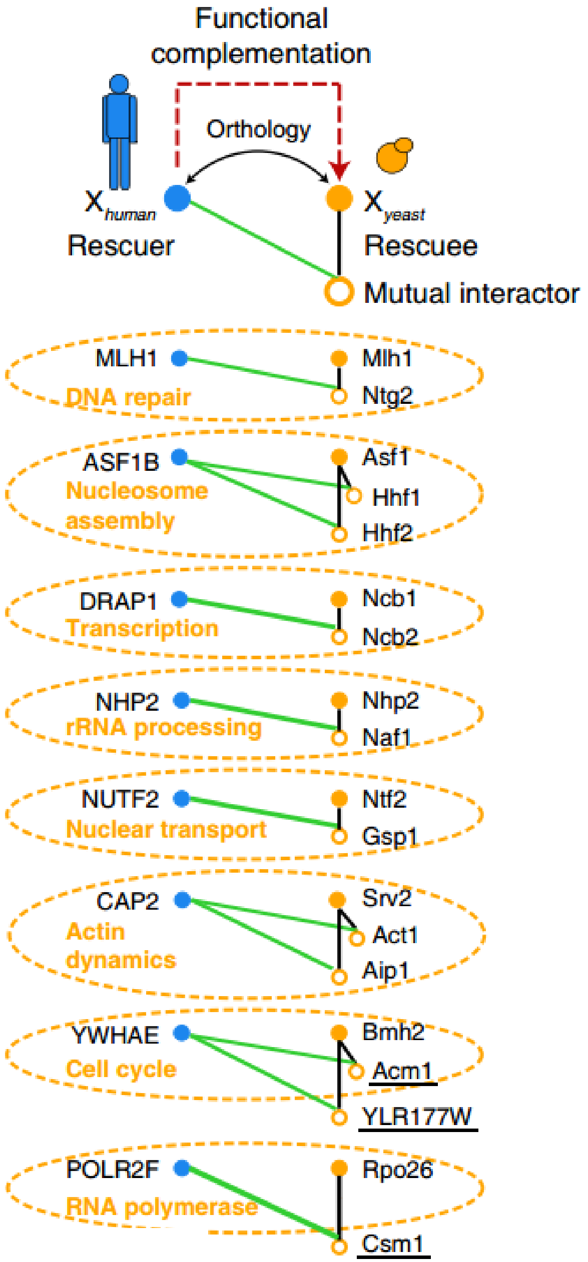
结果

Results

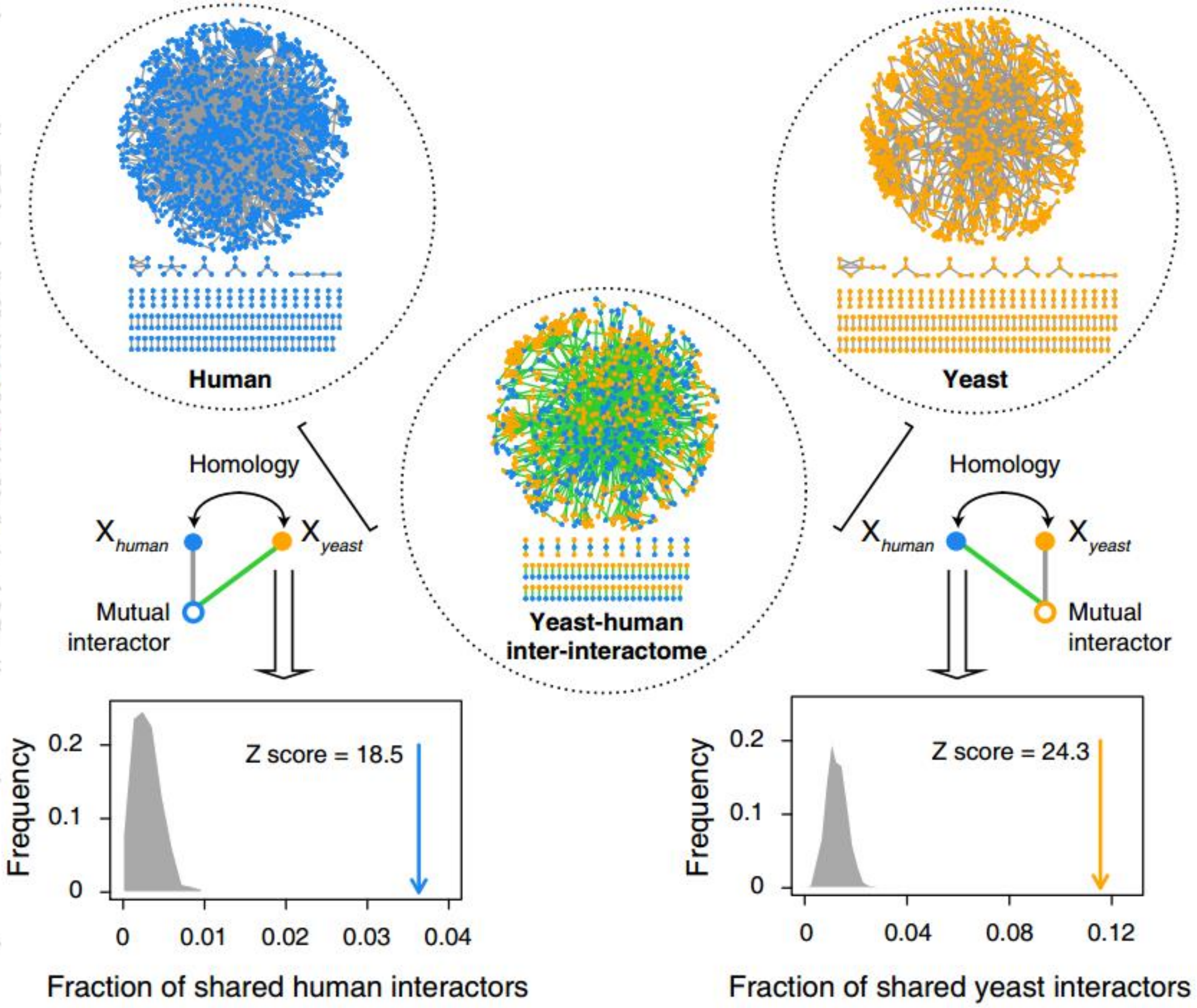
Inter-species interactions of human proteins with conserved functions in yeast

Among 46 human–yeast inter-species interactions identified, ~25% involve an interactor that is shared between rescuers and rescues.





Ancestral origins of inter-species protein–protein interactions

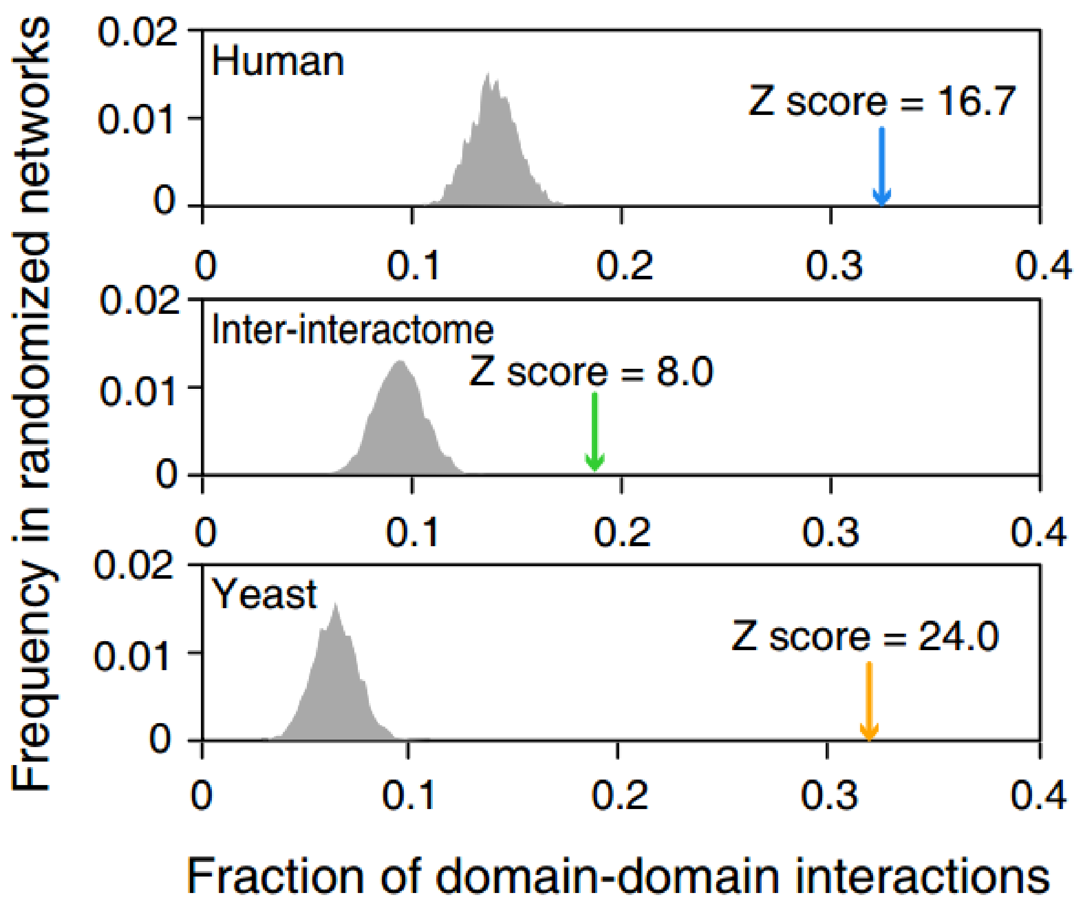


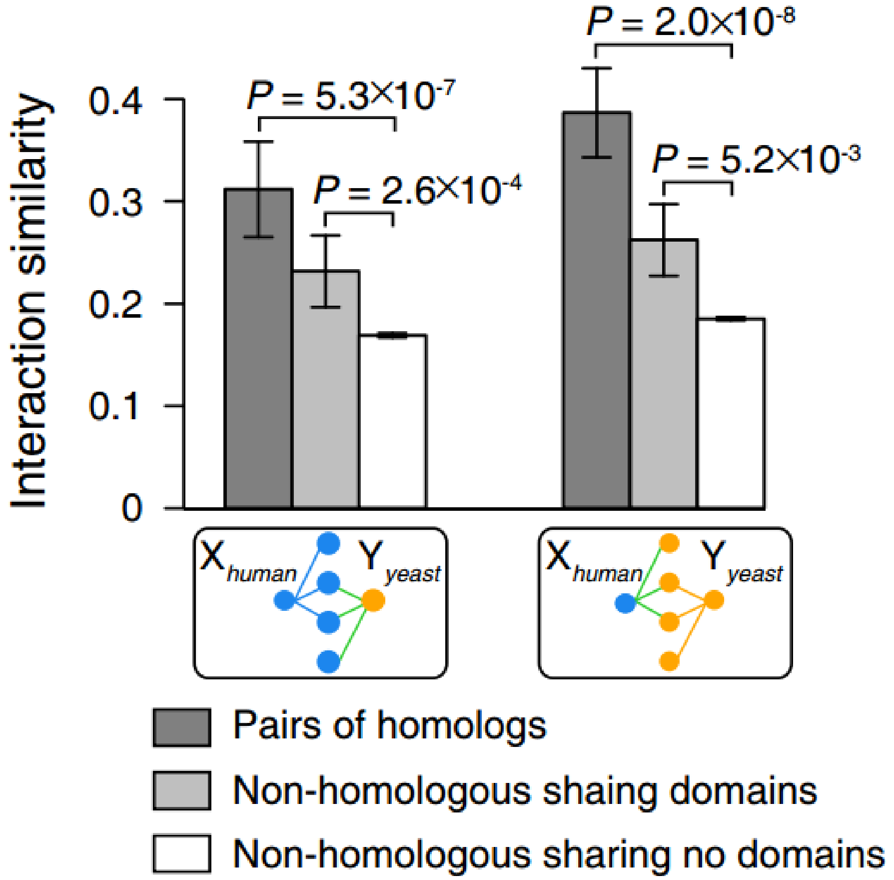
homology relationships

Inter-species interactions likely involve conserved binding properties retained in human–yeast homologs.

Mutual interactors are not conserved, consistent with ancestral protein-binding sites evolving new interactions with non-phylogenetically conserved proteins.

Results





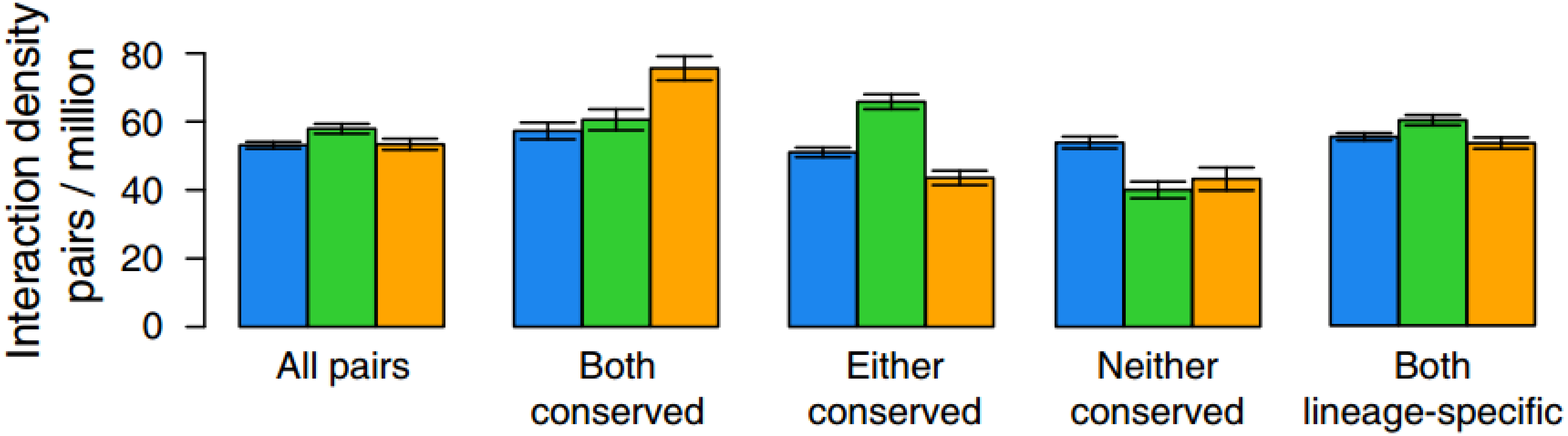
nearly 25% of inter-species interactions of such proteins can be explained by domain–domain interactions.

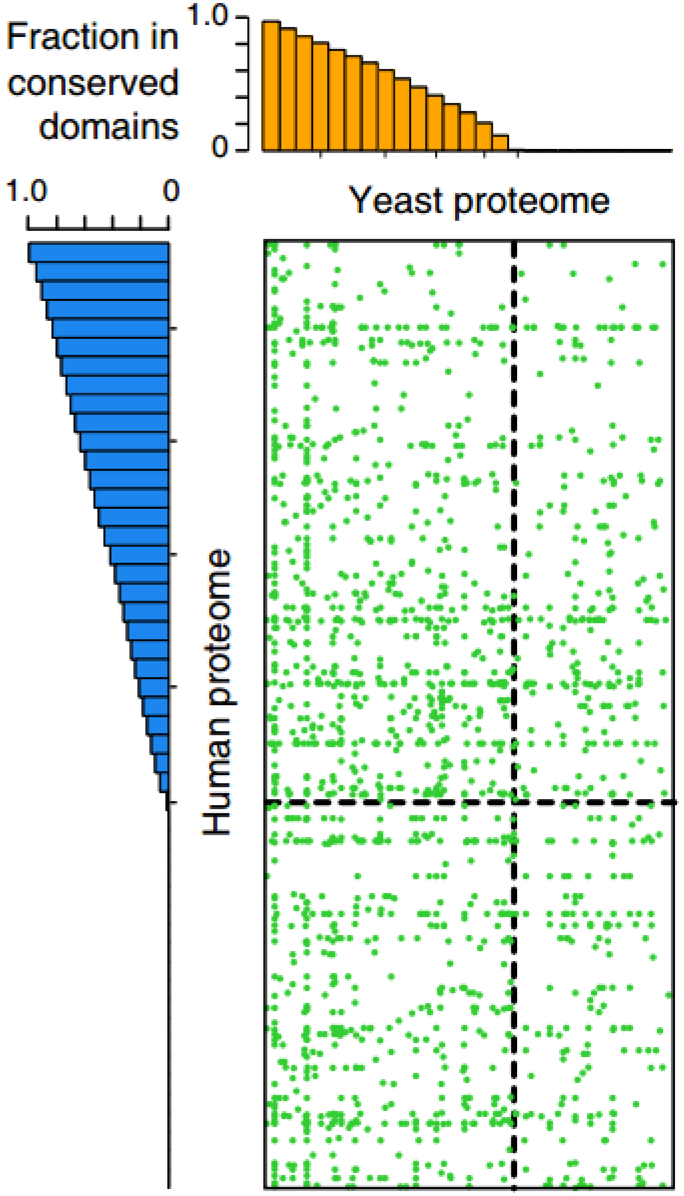
interaction profile similarity indexes between human and yeast homologs measured were significantly.

Proteome-wide distribution of inter-species protein–protein interactions

Results

To explore global patterns of human–yeast inter-species interactions across the two distantly related proteomes.

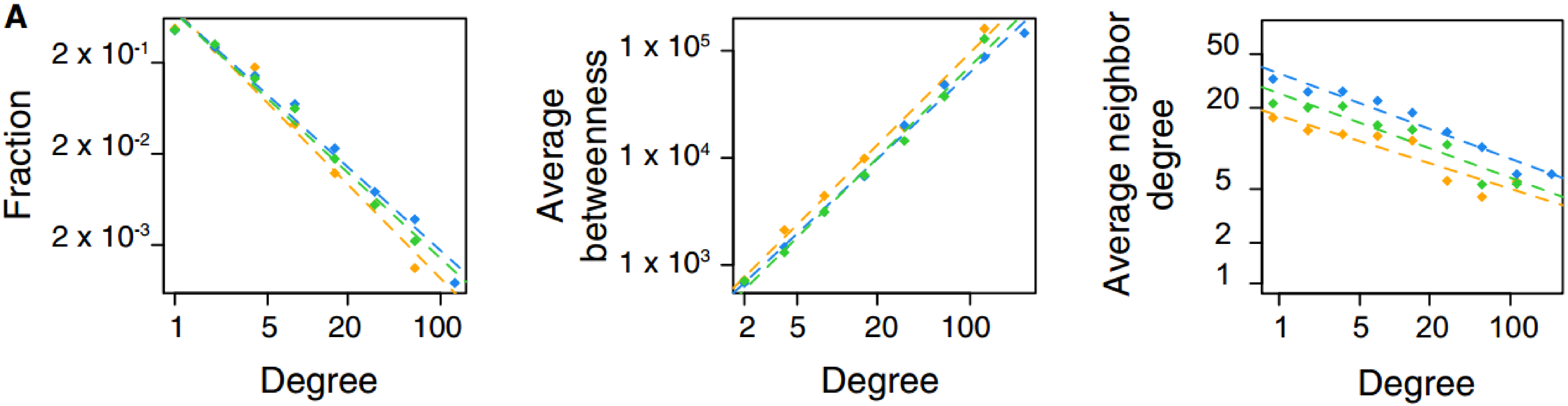




Thus, these observations suggest that equivalent interaction densities of the inter-interactome and its intra-species parent networks are result of opposing evolutionary forces.

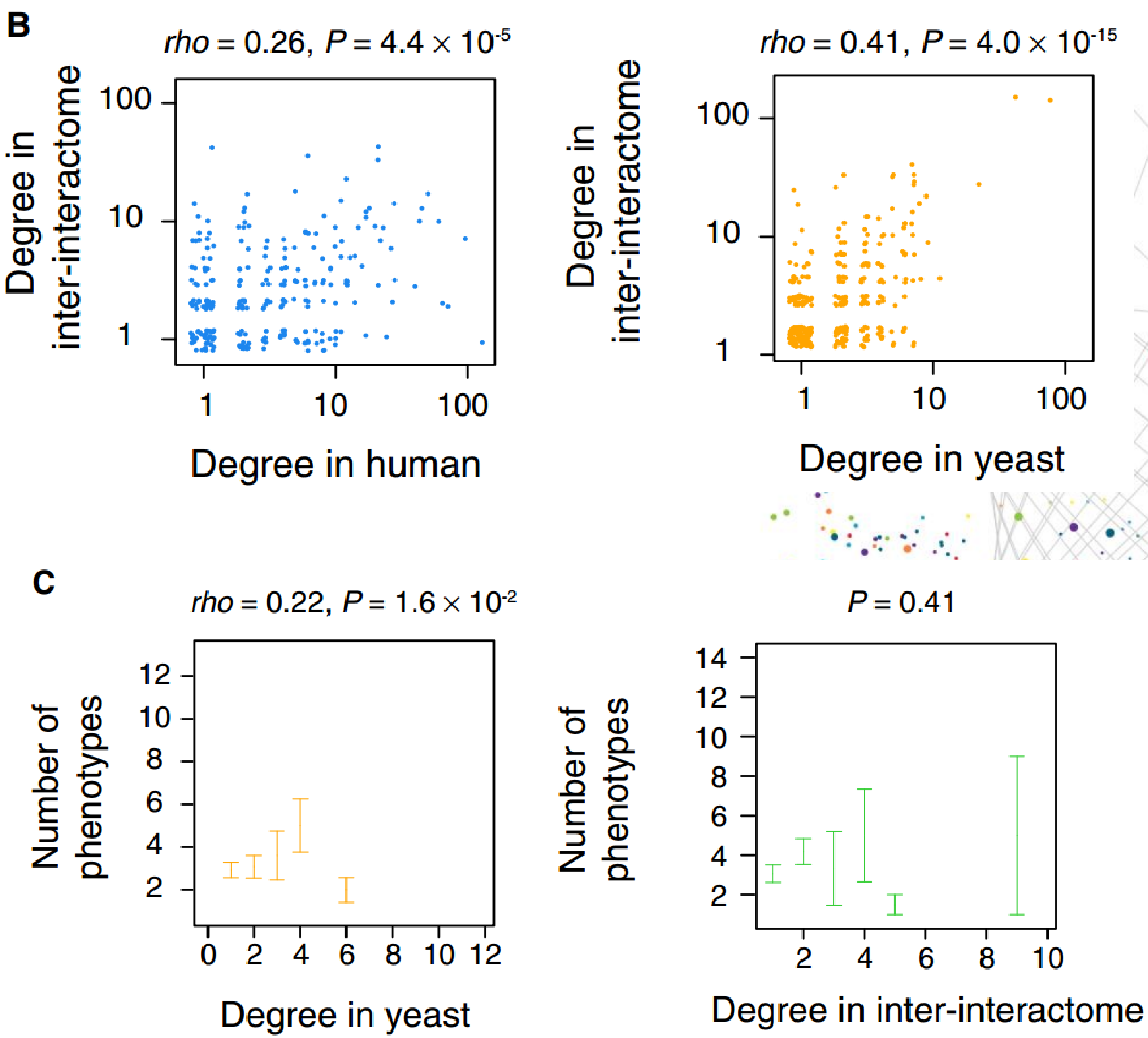
Network properties of the human–yeast inter-interactome

Since inter-species interactions have not been subjected to direct selective pressures, the inter-interactome might exhibit different network features.

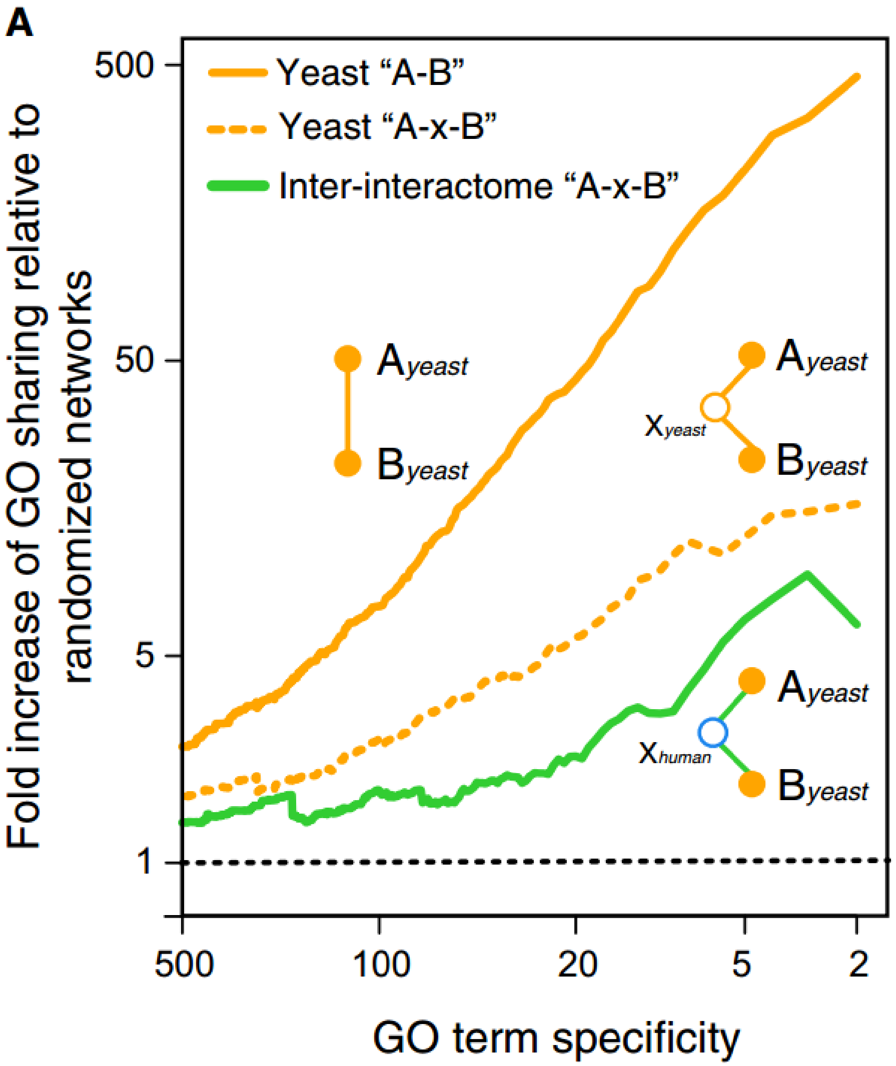


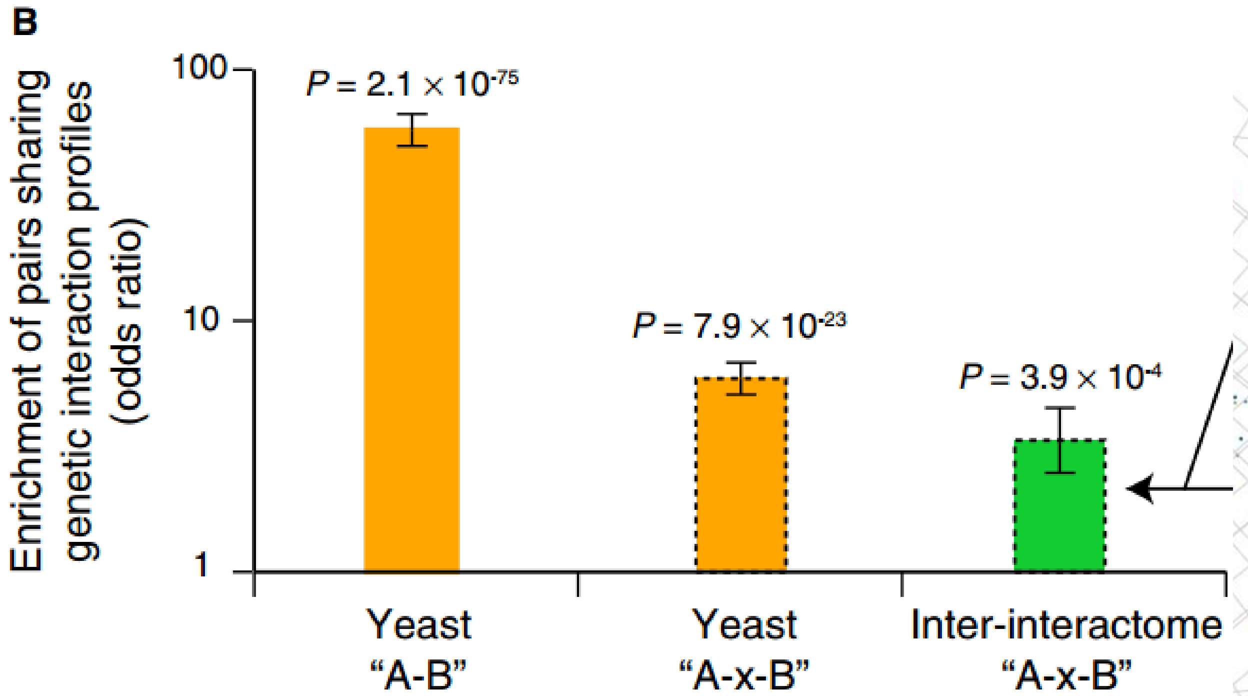
Results

This finding suggests that in spite of common network topological characteristics, coordination between the biophysical interactions and function is fundamentally altered in the inter-interactome.



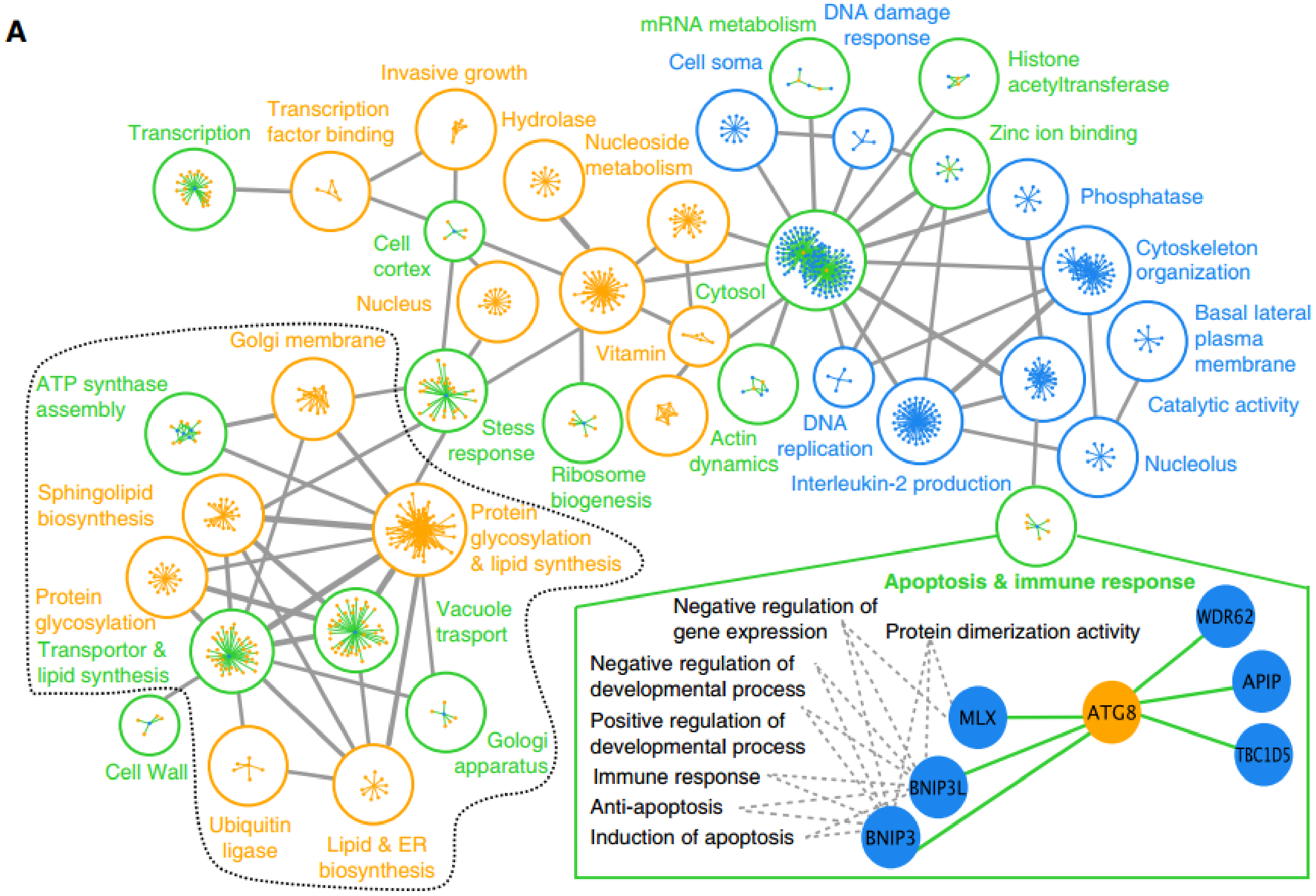
Correspondence between the inter-interactome and intra-species functional networks

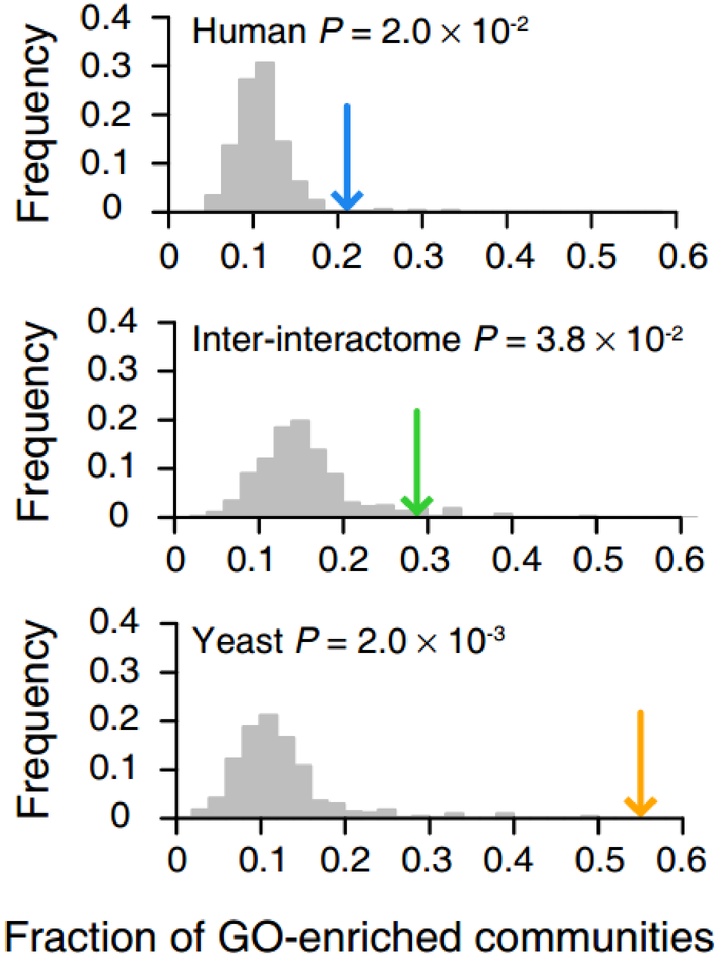




These observations uncover remnants of co-functionality between yeast and human proteomes.

Inter-connected communities in the inter-interactome and the two parent networks





suggesting that remnants of co-functionality and intra-species co-functionality are highly inter-related.

主要结论

Conclusions

Conclusions

1. orthologs tend to interact with their partner's interactors more than expected by chance;
2. interactions between two evolutionarily distant proteomes can derive from ancestral interactions;
3. ancestral protein-binding sites evolve new interactions with non-phylogenetically conserved proteins;
4. inter-species network properties are similar to those of intra-species networks in terms of density and degree distribution;
5. inter-species degree doesn't correlate to gene properties as strongly as intra-species degree does;
6. support evolutionary selection against biophysical interactions between proteins with little or no co-functionality.

总结

Summaries

总结

创新点

方法创新，应用物种之间相互作用组的方法解释生物物理的相互作用和功能上的相互作用是如何协调的等等问题。提供了很多人类和酵母相互作用的数据。

启发

运用生信的分析方法解释生物学问题，考虑问题很全面。

改进

对物种之间网络和物种内部网络的差异分析较多，没有种内和种间特异性的分析。

Thank for attention!