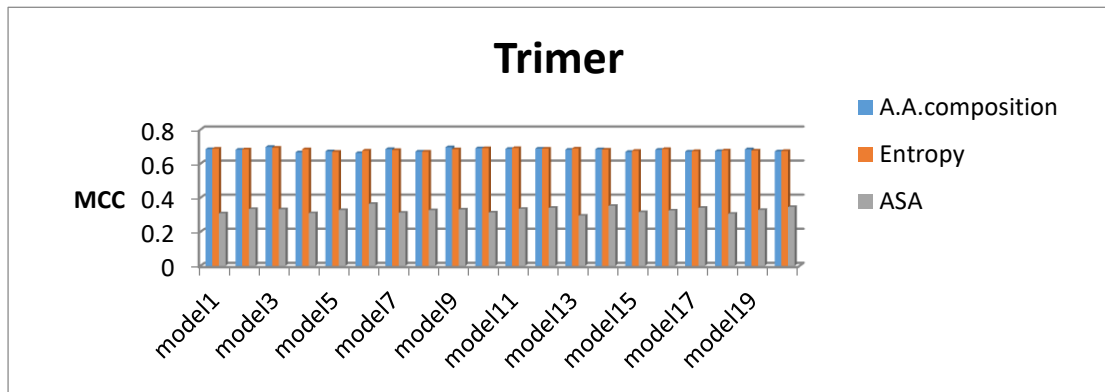
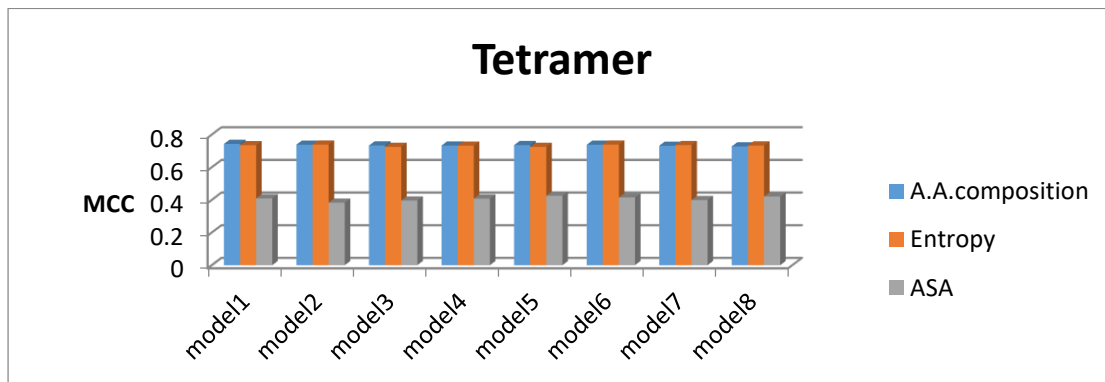


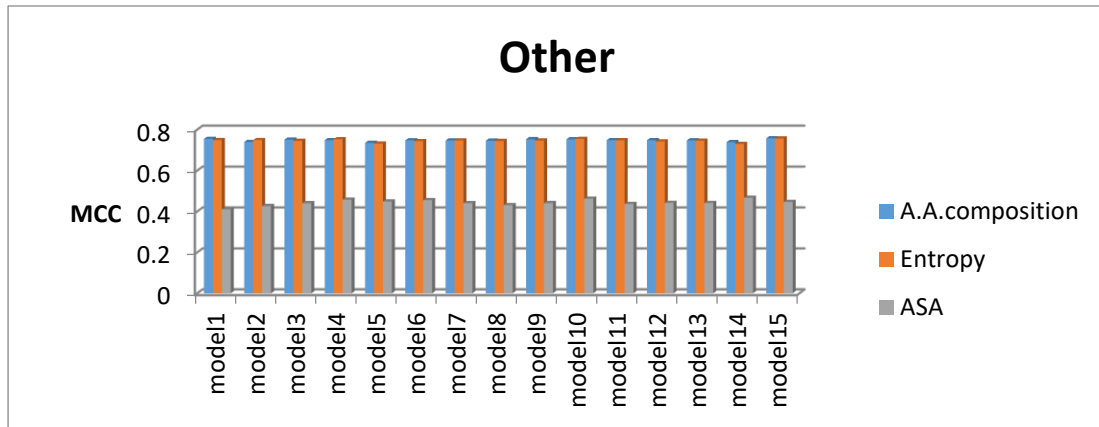
Supplementary data



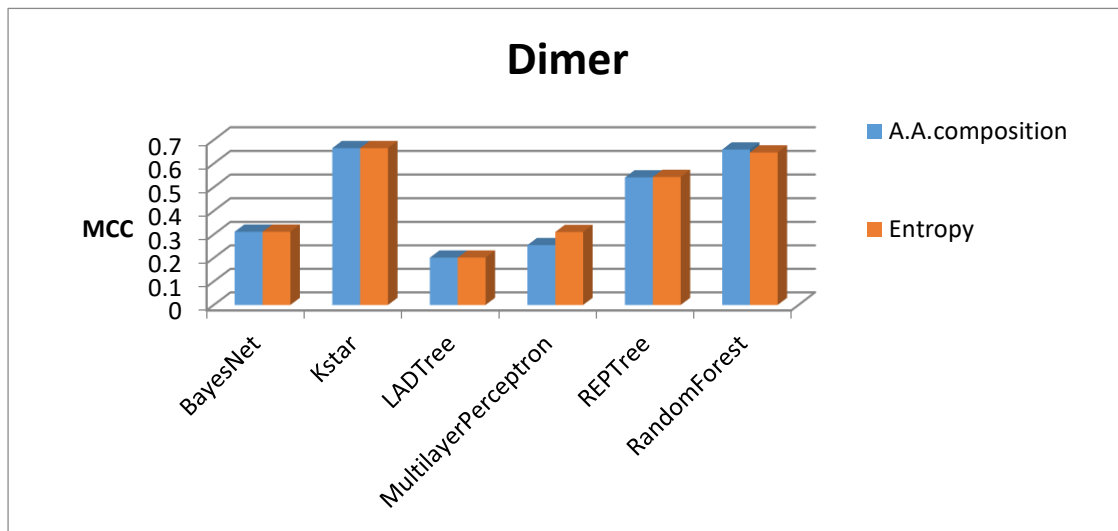
Supplementary figure 1: Prediction performance of amino acid composition and entropy are above 70% in trimer.



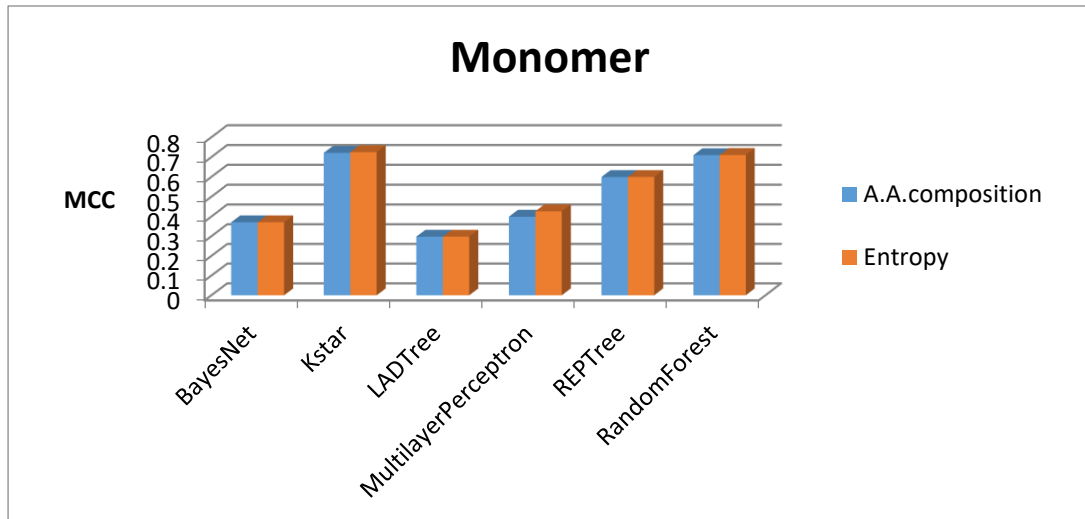
Supplementary figure 2: Prediction performance of amino acid composition and entropy are above 70% in tetramer.



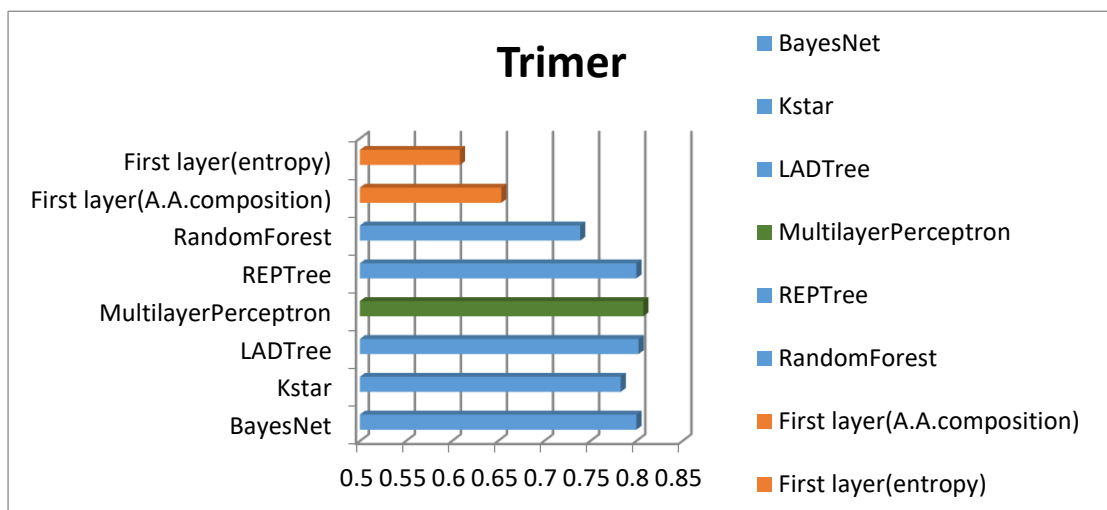
Supplementary figure 3: Prediction performance of amino acid composition and entropy are above 70% in other subunits class.



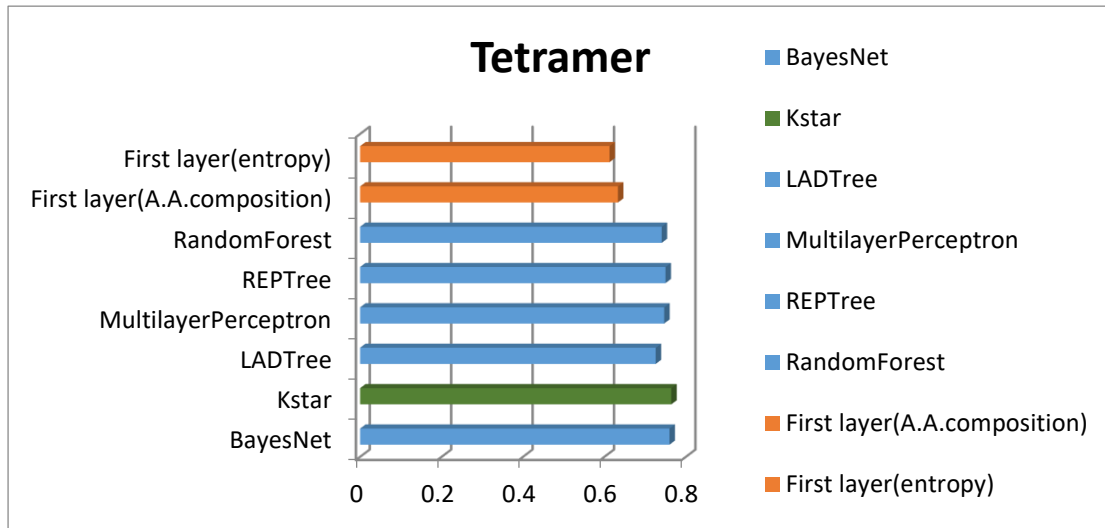
Supplementary figure 4: The prediction accuracy of dimer by KStar and Random Forest can reach above 60%.



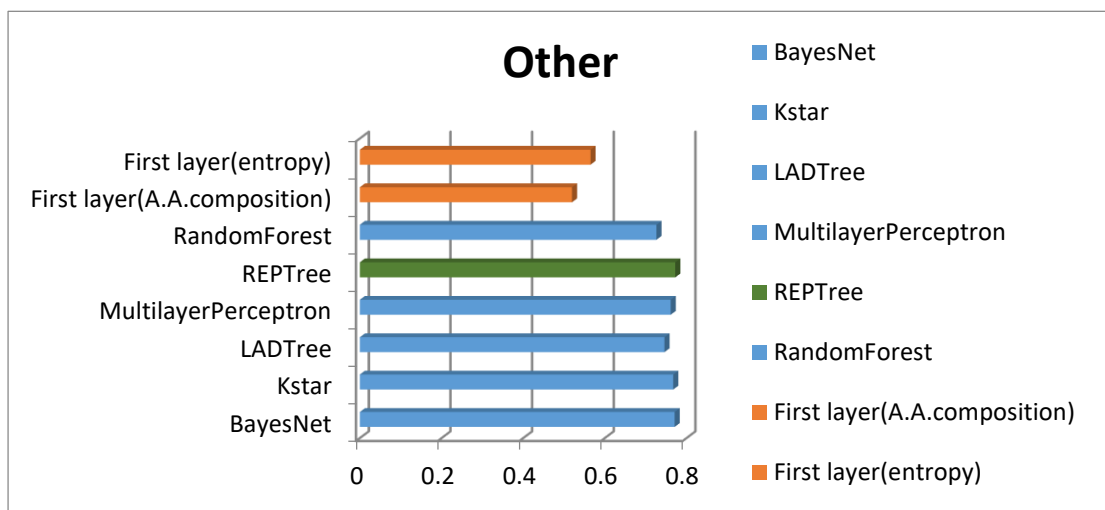
Supplementary figure 5: The prediction accuracy of monomer by KStar and Random Forest can reach above 70%.



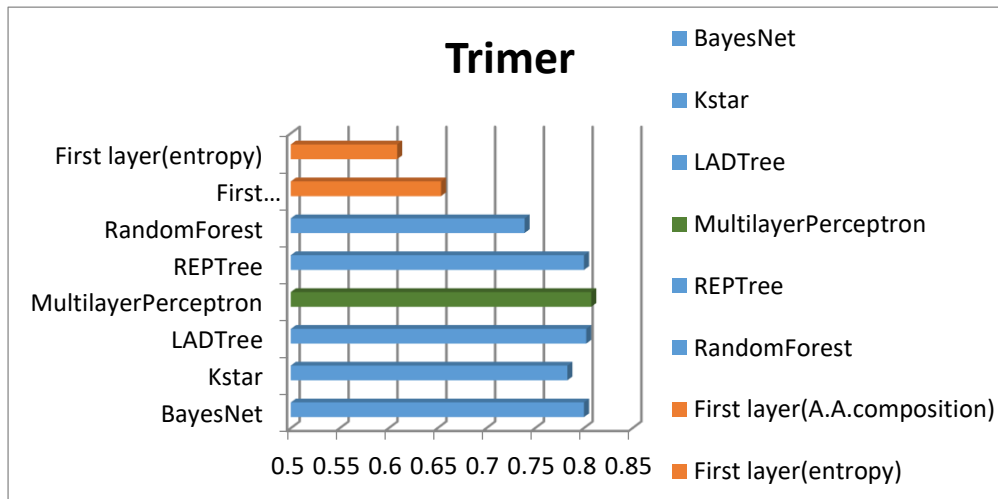
Supplementary figure 6: To compare different machine learning algorithms by amino acid composition and entropy in the second layer of PClass in trimer.



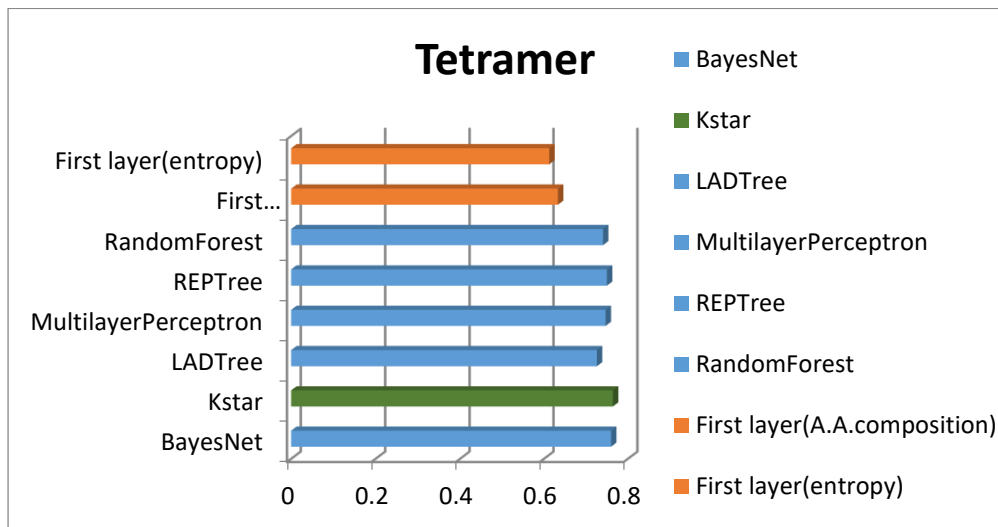
Supplementary figure 7: To compare different machine learning algorithms by amino acid composition and entropy in the second layer of PClass in tetramer.



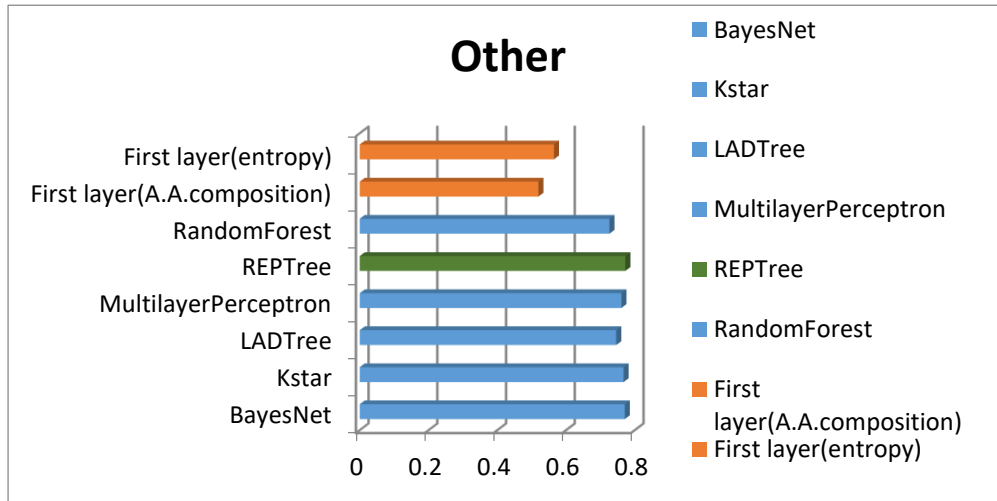
Supplementary figure 8: To compare different machine learning algorithms by amino acid composition and entropy in the second layer of PClass in other subunits class.



Supplementary figure 9: To compare different machine learning algorithms in the first layer of PClass in trimer.



Supplementary figure 10: To compare different machine learning algorithms in the first layer of PClass in tetramer.



Supplementary figure 11: Other first layer compare with machine learning methods.

Home Link About Contact

PClass

Protein Quaternary Structure Classification:
Using Bootstrapping for Model Selection

Sequence

Submit Reset Example

What we do
PClass

Protein quaternary structure complex is also known as multimer, which plays an important role in the cell and based on the subunits number to describe two or more complex could be formed by the monomers.

How to do
Using Bootstrapping for Model Selection

- Integrated Classification
- Bootstrap method
- Amino acid composition
- Entropy
- Accessible Surface area (ASA)

Related research
SCORER 2.0 & Multicoil 2

"Scorer 2.0"
C.T. Armstrong, T.L. Vincent, P.J. Green and D.N. Woolfson

"Multicoil 2"
Ethan Wolf, Peter S. Kim, and Bonnie Berger

Supplementary figure 12: The homepage of PClass.

PDB_ID : 1i7a
SEQUENCE : MGEQPIFTTRAHVFDIPSTKKNWVPAKQAVTVSYFYDVTNRSYRIISVDGAKVIINSTITPNMTFTKTSQKFGQWADSRANTVFLGLFSSSELQTKFAEKFAQEVREAAR
RESULT : monomer

What we do

PClass

Protein quaternary structure complex is also known as multimer or polymer, which plays an important role in the cell and based on the subunits number to describe two or more complex could be formed by the monomers.

How to do

Using Bootstrapping for Model Selection

Intrgrated Classification

Bootstrap method

Amino acid composition

Entropy

Accessible Surface area (ASA)

Related research

SCORER 2.0 & Multicoil 2

"scorer 2.0"

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Supplementary figure 13: The result of PClass.