Visualization tool for comparison of amino acids in protein simulations

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Fig. 1. Teasing result of our method: from this data input (left), the relevant feature are extracted using our technique (middle), producing effective result (right).

***Abstract*—**

***Keywords*-one or two words; separated by semicolon; from specific; to generic fields;**

I. Introduction

A. Related work

(a) First step (b) Second step (c) Result

Fig. 2. Technique overview

II. Data characterization

A. Data dimensions

DSSP:
SASA:
GYRATE:
ENERGY:
RMSF:

III. Technical background

In this section, we detail this classical technique. The reader can find a more complete exposition in the work of Paul [**?**].

IV. Technique overview

In order to produce this application, we start with this processing, followed by this technique. In order to cope with this challenge, we introduce this formulation to produce this intermediate result. The formulation leads to this type of system, which is efficiently solved by adapting this technique. The final result is produced by this transform. The whole process is schematized in Fig. 2.

A. Grid

Item highlighting:
Item selection:

B. Parallel Coordinates

Axis brushing:
Axis sorting:
Axis reordering:
Recoloring by axis selection:

C. Radar Plot

Item highlighting:

D. Slider

V. Experiments

VI. Results and Discussion

A. Future work

VII. Conclusion

Acknowledgment

The authors would like to thank this colleague and this financing institute.

References