In response to the imperfections of current sequence alignment methods, originated from the inherent serialism within their corresponding electrical systems, a few optical approaches for biological data comparison have been proposed recently. However, due to their low performance, raised from their inefficient coding scheme, this paper presents a novel all-optical high-throughput method for aligning DNA, RNA, and protein sequences, named HELIOS. The HELIOS method employs highly sophisticated operations to locate character matches, single or multiple mutations, and single or multiple indels within various biological sequences. On the other hand, the HELIOS optical architecture exploits high-speed processing and operational parallelism in optics, by adopting wavelength and polarization of optical beams. For evaluation, the functionality and accuracy of the HELIOS method are approved through behavioral and optical simulation studies, while its complexity and performance are estimated through analytical computation. The accuracy evaluations indicate that the HELIOS method achieves a precise pairwise alignment of two sequences, highly similar to those of Smith-Waterman, Needleman-Wunsch, BLAST, MUSCLE, ClustalW, ClustalΩ, T-Coffee, Kalign, and MAFFT. According to our performance evaluations, the HELIOS optical architecture outperforms all alternative electrical and optical algorithms in terms of processing time and memory requirement, relying on its highly sophisticated method and optical architecture. Moreover, the employed compact coding scheme highly escalates the number of input characters, and hence, it offers reduced time and space complexities, compared to the electrical and optical alternatives. It makes the HELIOS method and optical architecture highly applicable for biomedical applications.

1. ACCURACY EVALUATION

In order to comprehensively assess the accuracy of the HELIOS method, two statistical analyses are performed through simulation studies: 1) Quantitative measurement of homology [1], and 2) Accuracy measurement of classification output [2], compared to the well-known algorithms, briefly reported in Tables A1 and A2, respectively. In this manner, the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, API52 Gene Set [3] is assumed in this study, as represented in Table A3.

A. Quantitative measurement of homology

To perform quantitative measurement of homology [1], the parameters Identity, Similarity, and Alignment Score of the HELIOS outputs are calculated through simulation studies, as reported in Tables A4-A6, respectively, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, API52 Gene Set [3]. While the Identity reports the number of exactly matched characters of two sequences (in percentage), the Similarity measures the resemblance of two compared sequences. Specifically, regarding the physicochemical properties, the amino acids are categorized into six groups with different Similarity values; including GAVLI, FYW, STCM, KRH, DENQ, and P. As the third metric, the BLOSUM62 [4] substitution scoring matrix [4] is adopted to calculate the Alignment Score, with gap opening and extension penalties equal to -10 and -0.5, respectively.

Table A1. A brief report of the quantitative measurement of homology of the HELIOS method, compared to nine well-known algorithms, including SW, NW, BLAST, ClustalW, Clustal Omega, Muscle, T-Coffee, Kalign, and MAFFT. The parameters Identity, Similarity, and Alignment score are averaged and reported. The dataset used in this study is the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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<tr>
<th>HELIOS</th>
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<th>MUSCLE</th>
<th>ClustalW</th>
<th>ClustalΩ</th>
<th>T-Coffee</th>
<th>Kalign</th>
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<td>745.7</td>
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<td>746.2</td>
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Table A2. A brief report of the accuracy measurement of classification output of the HELIOS method with referencing well-known algorithms, including SW, NW, BLAST, ClustalW, Clustal Omega, Muscle, T-Coffee, Kalign, and MAFFT. The parameters SEN, Spec, Acc, PPV, NPV, MCC, and F-Score are averaged and reported. The dataset used in this study is the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

<table>
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<th>SW</th>
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<th>ClustalW</th>
<th>ClustalΩ</th>
<th>T-Coffee</th>
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B. Accuracy measurement of classification output

Afterward, the accuracy measurement of the classification output [2] of the HELIOS method is addressed by calculating the values of Sensitivity (SEN), Specificity (Spec), Accuracy (ACC), Positive Predictive Value (PPV), Negative Predictive Value (NPV), Matthew’s Coefficient Correlation (MCC), and Test’s Accuracy (F-Score) in the simulation studies, according to Eq 5 to Eq 11, respectively.


B. Accuracy measurement of classification output

Afterward, the accuracy measurement of the classification output [2] of the HELIOS method is addressed by calculating the values of Sensitivity (SEN), Specificity (Spec), Accuracy (ACC), Positive Predictive Value (PPV), Negative Predictive Value (NPV), Matthew’s Coefficient Correlation (MCC), and Test’s Accuracy (F-Score) in the simulation studies, according to Eq 5 to Eq 11, respectively.


REFERENCES

**Table A3.** The list of input sequences, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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</tr>
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<td>MQFML LFSRQ GKLRQ QKWVY PLSDK EKKKI TRELQ QTULRA KPKRM CSFLR WSRLK IVYKR YASLY FCCAI EDQDN ELITL EIHIY YVELL DKYFG SVCEL DIIFN FEKAY FILDE FLGGE EVQET SKKNV LKAIE QADLL QERAQ EATTP RSVLE EIGLT</td>
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<td>MQFML LFSRQ GKLRQ QKWVY PLSDK EKKKI TRELQ QTULRA KPKRM CSFLR WSRLK IVYKR YASLY FCCAI EDQDN ELITL EIHIY YVELL DKYFG SVCEL DIIFN FEKAY FILDE FLGGE EVQET SKKNV LKAIE QADLL QERAQ EATTP RSVLE EIGLT</td>
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**Table A4.** The parameter Identity of the HELIOS method in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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**Table A5.** The parameter Similarity of the HELIOS method in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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**Table A6.** The parameter Alignment Score of the HELIOS method in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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**Table A7.** The parameter Identity of the Smith-Waterman algorithm in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A8. The parameter Similarity of the Smith-Waterman algorithm in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A9. The parameter Alignment Score of the Smith-Waterman algorithm in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A10. The parameter Identity of the Needleman-Wunsch algorithm in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A11. The parameter Similarity of the Needleman-Wunsch algorithm in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A12. The parameter Alignment Score of the Needleman-Wunsch algorithm in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A13. The parameter Identity of the BLAST in the quantitative measurement of homology, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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### Table A14. The parameter Similarity of the BLAST in the quantitative measurement of homology, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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Table A26. The parameter Similarity of the T-Coffee in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A29. The parameter Similarity of the Kalign in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A30. The parameter Alignment Score of the Kalign in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A31. The parameter Identity of the MAFFT in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A32. The parameter Similarity of the MAFFT in the quantitative measurement of homology, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A34. The parameter Sensitivity (SEN) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A35. The parameter Specification (Spec) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A36. The parameter Accuracy (Acc) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A37. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A38. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A39. The parameter Matthew's Coefficient Correlation (MCC) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A40. The parameter Test's Accuracy (F-Score) of the HELIOS method with referencing the Smith-Waterman algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A41. The parameter Sensitivity (SEN) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A42. The parameter Specification (Spec) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A43. The parameter Accuracy (Acc) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A44. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A45. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A46. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A47. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the Needleman-Wunsch algorithm in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A48. The parameter Sensitivity (SEN) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A49. The parameter Specification (Spec) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A50. The parameter Accuracy (Acc) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A51. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A52. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A53. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A54. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the BLAST in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A55. The parameter Sensitivity (SEN) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A56. The parameter Specification (Spec) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A57. The parameter Accuracy (Acc) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A58. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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Table A59. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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Table A60. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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Table A61. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the ClustalW in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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Table A62. The parameter Sensitivity (SEN) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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Table A63. The parameter Specification (Spec) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A64. The parameter Accuracy (Acc) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A65. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A66. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A67. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A68. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the ClustalΩ in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A69. The parameter Sensitivity (SEN) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A70. The parameter Specification (Spec) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A71. The parameter Accuracy (Acc) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A72. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A73. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A74. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A75. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the MUSCLE in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A76. The parameter Sensitivity (SEN) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A77. The parameter Specification (Spec) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A78. The parameter Accuracy (Acc) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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### Table A79. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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### Table A80. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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### Table A81. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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### Table A82. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the T-Coffee in the accuracy measurement of classification output, assuming the *ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set* [3].

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### Table A83.
The parameter Sensitivity (SEN) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A84.
The parameter Specification (Spec) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A85.
The parameter Accuracy (Acc) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A86.
The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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### Table A87.
The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A88. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A89. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the Kalign in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A90. The parameter Sensitivity (SEN) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A91. The parameter Specification (Spec) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A92. The parameter Accuracy (Acc) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the Chip-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A93. The parameter Positive Predictive Value (PPV) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A94. The parameter Negative Predictive Value (NPV) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A95. The parameter Matthew’s Coefficient Correlation (MCC) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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Table A96. The parameter Test’s Accuracy (F-Score) of the HELIOS method with referencing the MAFFT in the accuracy measurement of classification output, assuming the ChIP-X Enrichment Analysis Resource, CHEA Transcription Factor Targets Dataset, AP1S2 Gene Set [3].

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