Curriculum Vitae

Changiz Eslahchi

Date and place of birth :	March 1, 1966, Bam, Iran
Citizenship:	Iran
Current Position:	Professor of Algorithms in Bioinformatics
Current Institution:	Shahid Beheshti University
Current Business address:	Department of Computer Science,
	Shahid Beheshti University,
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RESEARCH INTERESTS

1. Combinatorial algorithms in bioinformatics

2. System biology

3. Phylogenetic networks construction

4. Graph theory.

ACADEMIC BACKGROUND

1. Ph.D. in Mathematics, Department of Mathematical Sciences,
   Sharif University of Technology, Tehran, IRAN, 1998.

Title of Thesis: Hall condition and list coloring of graphs.

Thesis advisor : Professor E. S. Mahmoodian.

2. M.S. in Mathematics, Department of Mathematics, Shiraz University, Shiraz, IRAN, 1990.

3. B.S. in Mathematics, Department of Mathematics, Training Teachers University, Tehran, IRAN, 1987.

Membership of national and international institutions

1. Iranian Mathematical Society.

2. Iranian Bioinformatics Society.

3. International Society for Computational Biology.

Visiting Appointments

1. Visiting Scientist, Department of Mathematics, Reading university, Reading, England, July 1999- September 1999.

2. Visiting Scientist, School of Mathematics, University of Science Malaysia (USM), Pinang, Malaysia, July 2010- August 2010.

3. Visiting Scientist, School of Computing, National University of Singapore(NUS), Singapore, September 2010.

4. Visiting Scientist, School of Computing, National University of Singapore(NUS), Singapore, September 2012.

5. Visiting Scientist, School of Computing, National University of Singapore(NUS), Singapore, September 2013.

JOURNAL PUBLICATIONS

1. PMLPR: A novel method for predicting subcellular localization based on recommender systems, Scientific Reports volume 8, Article number: 12006 (2018), with E.Mirzaei Mehrabad and R. Hassanzadeh.

2. OrthoGNC: A Software for Accurate Identification of Orthologs Based on Gene Neighborhood Conservation, Genomics, proteomics and bioinformatics, (2017):15(6), 361-370, with S. Jahangiri-Tazehkand and L. Wong.

3. Comparison of different approaches for identifying subnetworks in metabolic networks, Journal of bioinformatics and computational biology, (2017): volume 15(6), with A. Rezvan.

4. Dynamical 2-domination in Graphs, ARS COMBINATORIA 134 (2017): 339-350., with H. Meimani, R. Torabi and R. Tuserkani.

5. Gender Classification Based on Eye Movements: A Processing Effect during Passive Face Viewing, Advances in Cognitive Psychology, (2017), volume 13(3) • 232-240, with N. Sammaknejad, H. Pouretemad, A. Salahirad and A. Alinejad.

6. Discovering overlapped protein complexes from weighted PPI networks by removing inter-module hubs, Scientific Reports volume 7, Article number: 3247 (2017), with A. Maddi.

7. Inferring phylogenies from minimal information. Advances in Electrical, Electronics, Information, Communication and Bio-Informatics (AEEICB), 2017 Third International Conference on. IEEE, (2017): 202-206, with R. Tusserkani, H. Poormohammadi and A. Azadi.

8. Screening of autism based on task-free fMRI using graph theoretical approach, Psychiatry Research: Neuroimaging, 48-56 (2017), with R. Khosrowabadi, M. Sadeghi, F. Bakouie, H. Mahdavi, and H. Pouretemad.

9. Inferring gene regulatory networks by PCA-CMI using Hill climbing algorithm based on MIT score and SORDER method, Int. J. Biomathematics, vol.9, no.3, 1650040 (2016), with R. Aghdam, M. Alijanpour, M. Azadi, A. Ebrahimi, A. Rezvan.

10. Inferring gene regulatory networks by an order independent algorithm using incomplete data sets, Journal of Applied Statistics, 1-21 (2016), with R. Aghdam, M. Ganjali and P. Niloofar.

11. Proper Nearly Perfect Sets in Graphs, ARS COMBINATORIA 126 (2016): 143-156., with H.R. Maimani. , R. Torabi. and R. Tuserkani.

12. Some Remarks On Global Total Domination In Graphs, Applied Mathematics E-Notes, 15 (2015): 22-28, with M. Akhbari, N. Jafari Rad, and R. Hasni.

13. CN: A Consensus Algorithm for Inferring Gene Regulatory Networks Using SORDER Algorithm and Conditional Mutual Information Test, Molecular BioSystems, 2015, 11(3):942-949, with R. Aghdam, M. Ganjali and X. Zhang.

14. FCDECOMP: Decomposition of metabolic networks based on flux coupling relations, Journal of bioinformatics and computational biology, 2014, 12(5), with Abolfazl Rezvan and Sayed-Amir Marashi.

15. TripNet: A Method for Constructing Rooted Phylogenetic Networks from Triplets, Plos One, 2014, 9(1-12), with H. Poormohammadi and R. Tusserkani.

16. Applying a Hybrid Method based on PC algorithm-based approach and MIT Score to Infer Gene Regulatory Networks, Iranian Conference on Bioinformatics (Accepted), with R. Aghdam. , M. Alijanpour. , M. Azadi. , A. Ebrahimi.

17. Do Triplets Have Enough Information to Construct the Multi-Labeled Phylogenetic Tree? Plos One, 2014, 9(7): e103622, with R. Hassanzadeh, W-K Sung.

18. IPCA-CMI: An algorithm for Inferring Gene Regulatory Networks Based on a Combination of PCA-CMI and MIT Score, Plos One, 2014, 9(4): e92600, with R. Aghdam and M. Ganjali.

19. ProDomAs; Protein Domain Assignment Algorithm using Centre-Based Clustering and Independent Dominating Set, Proteins: Structure, Function, and Bioinformatics (doi: 10.1002/prot.24547), with E.S.Ansari, H.Pezeshk and M. Sadeghi.

20. A New Protein Domain Assignment Algorithm Based on the Dominating Set of a Graph, MATCH Commun. Math. Comput. Chem., (2014), 71, 445-456, with E. S. Ansari.

21. SSP: An interval integer linear programming for de novo transcriptome assembly and isoform discovery of RNA-Seq read, Genomics, (2013), 102(5-6), 507-514, with Z. Safikhani, M. Sadeghi and H. Pezashk.

22. Two Scenarios for Overcoming Drug Resistance by Co-Targeting, Journal of Bioinformatics Research and Applications, (2013), 198 - 202, with G. Taheri, M. Ayati and L. Wong.

23. Disruption of Protein Complexes, Journal of Bioinformatics and Computational Biology, (2013), 11(3), 1-13, with G. Taheri, M. Habibi and L. Wong.

24. Discovering domain mediating protein interactions, Iran journal of biotechnology, (2013) 1(11). 22-31.

25. Assignment Of Protein Sequences To Protein Family Profiles Using Spatial Statistics, MATCH Communications in Mathematical and Computer Chemistry, (2013) 69(1), 7- 24 with V. Rezaei, H. Pezeshk, and M. Sadeghi.

26. A Clustering Approach for Estimating Parameters of a Profile Hidden Markov Model, International Journal of Data Mining and Bioinformatics, (2013), 8(1), 66-82, with R. Aghdam, H. Pezeshk, A. Malekpour, S.Shemehsavar, and M. Sadeghi.

27. HARARY INDEX OF AN INFINITE FAMILY OF DENDRIMER NANOSTARS, Studia Universitatis Babes-Bolyai, Chemia 58.3 (2013), with S. Alikhani and M. A. Iranmanesh.

28. Constructing Rooted Phylogenetic Networks From Triplets Based On Height Function, International Journal of Emerging Technology and Advanced Engineering, (2012) 2, 7, 389-393, with H. Poormohamadi.

29. Calculation of Transition Probabilities in the Birth and Death Markov process in the epidemic model, Mathematical and Computer Modelling, 2012, 55, 810-815, with F. Movahedi.

30. A note on the total domination supercritical graphs, Transactions on Combinatorics 1.3 (2012): 1-4, with A. Alimadadi and N. Jafari Rad.

31. Erratum to Total domination supercritical graphs with respect to relative complements [Discrete Math. 258 (2002) 361371], Discrete Mathematics Volume 312 (5), 2012, 1076, with Abdollah Alimadadi, Changiz Eslahchi, Teresa W. Haynes, Michael A. Henning, Nader Jafari Radd, Lucas C. van der Merwee.

32. Constructing Circular Phylogenetic Networks from Weighted Quartets Using Simulated Annealing, Mathematical Biosciences 235 (2012) 123127, with R. Hassanzadeha, E. Mottaghib, M. Habibib, H. Pezeshkc, and M. Sadeghi.

33. Outer-k-connected component domination in graphs , AKCE Int. J. Graphs Comb., (2011), 8(2), 131-139, with M.H. Akhbari, N. Jafari Rad and R. Hasni.

34. Generalization of Outer-Connected Domination in Graphs , AKCE International Journal of Graph and Combinatorics, Vol 8 2011, 2, with Akhbari A, Jafri Rad N and Hasni S.

35. A Note On The Total Irredundance In Regular Graphs, Australian Journal of Basic and Applied Sciences, 5(9): 1999-2001, 2011, Changiz Eslahchi, Shahab Haghi and Nader Jafari Rad.

36. Haplotype Block Partitioning and TagSNP Selection Under the Perfect Phylogeny Model, Iranian Journal of Biotechnology, (2011), 9(1), 281- 289 , with Katanforosh A, Pezeshk H and Afzaly N.

37. An Information Theoretic Approach to Secondary Structure Assignment , MATCH Communications in Mathematical and in Computer Chemistry,65 2011, 5-20, with M. Habibi, H. Pezeshk, M. Sadeghi.

38. A Protein Complex Prediction based on k-Connected Sub-graphs in Protein Interaction Network , BMC Systems Biology 2010, 4:129, with Habibi M and Wong L.

39. Overcoming Drug Resistance by Co-Targeting, Proceedings of 4th IEEE International Conference on Bioinformatics and Biomedicine, pages 198-201, Hong Kong, December 2010, with Ayati M, Taheri G, Arab S, Wong L.

40. Construction of Random Perfect Phylogeny Matrix, Advances and Applications in Bioinformatics and Chemistry 2010:3 1-8, with Sadeghi M, Pezeshk H, Ahmadian S, Mah Abadi S.

41. The interpretation of protein structures based on graph theory and contact map, Open Access Bioinformatics 2010:2 127137, with Habibi M, Sadeghi M, Pezeshk H.

42. A Biodirectional Baysian Monte Carlo Approach for Estimating Parameters of a Profile Hidden Markov Model , Applied Science Segment:1(2) APS/1531,2010 1-10, with Aghdam R, Pezeshk H, Malekpour A, Shemehsavar S and Sadeghi M.

43. A Probabilistic Model for the Spread of HIV Infection among Injection Drug Users , Journal of world Academic Press World Journal of Modeling and Simulation, Vol 6 2010 No 4 267-273, with Eslahchi C, Pezeshk H, Sadeghi M, Giabbanelli P. J, Movahedi F. and Dabbaghian V.

44. MC-Net: A method for the construction of phylogenetic networks based on the Monte-Carlo method , BMC Evolutionary Biology, 2010, 10:254, with Changiz Eslahchi, Mahnaz Habibi, Reza Hassanzadeh and Ehsan Mottaghi.

45. A pairwise residue contact area-based mean force potential for discrimination of native protein structure , BMC Bioinformatics, 2010; 11:16 doi:10.1186/1471-2105-11-16, with Arab S, Sadeghi M, Eslahchi C, Pezeshk H.

46. A Segmental Semi Markov Model for Protein Secondary Structure Prediction , Mathematical Biosciences, 2009; 221: 130-135. , with Malekpour S. A., Naghizadeh S., Pezeshk, H., Sadeghi, M., Eslahchi, C.

47. Distance Dependent Atomic Knowledge Based Potential and Force for Discrimination of Native Structures from Decoys PROTEINS, 2009; 77: 454-463, with Mirzaee M., Eslahchi C., Pezeshk H., Sadeghi M.

48. An Algorithm for Construction of all Perfect Phylogeny Matrices , Match, 2009, 62, 2: 251-259, with Mirzaei H., Ahmadian S., Mahabadi S., Sadeghi M., Eslahchi C., Pezeshk H.

49. Enhanced Evolutionary and Heuristic Algorithms for Haplotype Reconstruction Problem Using Minimum Error Correction Model , Match, 2009, 62, 2: 261-274, with Kargar M., Poormohammadi H., Pirhaji L., Sadeghi M., Pezeshk H.

50. Ston: A Novel Method for Protein three-dimensional Structure Comparison , Computers in Biology and Medicine 2009, 39, 2: 166-172, with Eslahchi C., Pezeshk H., Sadeghi M., Rahimi A. M., Maboudi Afkham H., Arab S.

51. Protein Secondary Structure Prediction Using three Neural Networks and a Segmental Semi Markov Model , Mathematical Biosciences 2009, 217, 2: 145-150, with Malekpour S. A., Naghizadeh S., Pezeshk H., Sadeghi M., Eslahchi C.

52. PROSIGN: A Method for Protein Secondary Structure Assignment Based on Three-Dimensional Coordinates of Cosecutive Ca atoms , Computational Biology and

Chemistry 2008, 32, 6: 406-411, with Hosseini S. R., Sadeghi, M., Pezeshk H., Eslahchi C., Habibi M.

53. A Modification on a Left-to-Right and Right-to-Left Dependency Model for Secondary Structure Prediction , Journal of Science, University of Tehran 2008, 34, 3, 61-66, with Naghizadeh S., Pezeshk H., Sadeghi M., Mohammadzadeh M., Eslahchi C.

54. An Information theoritical Approch to Secondary Structure Assignment , Journal of Science, University of Tehran 2008, 34, 3, 41-48, with Habibi M., Eslahchi C., Pezeshk H., Sadeghi M.

55. A Tale of two Symmetrical Tails: Structural and Functional Charateristics of Palindroms in Proteins , BMC Bioinformatics 2008,9:274, with Sheari A, Kargar M, Katanforoush A, Arab S, Sadeghi M, Pezeshk H, Eslahchi C, Marashi S.A.

56. The Performance of chi-square Test and complexity Measures for Signal Recognition in Biological Sequences , Journal of Theoretical Biology. (2008) vol. 251, 380-387, with Pirhaji L, Kargar M, Sheari A, Poormohamadi H, Sadeghi M, Pezeshk H, Eslahchi C.

57. Helix segment assignment in proteins using fuzzy logic , Iranian Journal of Biotechnologhy, 2007, Vol. 5, 93-99, with Shahriar Arab, Farzad Didehvar, Changiz Eslahchi, Mehdi Sadeghi.

58. Impact of RNA structure on the prediction of donor and acceptor splice sites , BMC Bioinformatics. 2006; 7:297, with Marashi SA, Eslahchi C, Pezeshk H, Sadeghi M.

59. Importance of RNA secondary structure information for yeast donor and acceptor splice site predictions by neural networks , Comput Biol Chem. 2006; 30(1):50-7, with Marashi SA, Goodarzi H, Sadeghi M, Eslahchi C, Pezeshk H.

60. Some Properties Of Ordered Hypergraphs , Matematicki Vesnik, 2007, volume 79, 9-13, With A.M. Rahimi.

61. The *k*-Zero-Divisor Hypergraph of A Commutative Ring , International Journal of Mathematics and Mathematical Sciences,2007, vol. 2007, no4, pp. 1-15, With A.M. Rahimi.

62. An Algorithm for Rank Aggregation Problem , Applied mathematics and computation, 2007, volume 189, 2, 1847-1858 , With F. Didehvar

63. c-Perfect k- Uniform Hypergraphs , Journal of Ars Combinatorics, volume 79(2006), 235-244, With A. Rafiey

64. Vertex-Strength of Fuzzy Graphs , International Journal of Mathematics and Mathematical Sciences, 2006, 1-9, With B.N. Onagh

65. Characterization of Graphs with Hall Number 2 , Journal of Graph Theory, 2004, volume 45, 81-101, With M. Johnson

66. Circular Chromatic Number of Hypergraphs , Journal of Ars Combinatorics, volume 73(2004), 239-246, With A. Rafiey

67. Some Concepts in List Coloring , Journal of Combinatorial Mathematics and Combinatorial Computing, 41(2002), 151-160, With M. Ghebleh, and H. Hajiabolhassan.

68. The Hall-Condition Index of a Graph and Overfull Conjecture , Journal of Combinatorial Mathematics and Combinatorial Computing, 35(2000), 197- 216, With A.J.W. Hilton and D. Dugdale

69. Characterization of Graphs with Hall Index 2 , Australasian Journal of Combinatorics, volume 21(2000), 13 21.

70. Progress on the Hall Number Two Problem , Australasian Journal of Combinatorics, volume 21(2000), 211 236, With A.J.W. Hilton, and P.D. Johnson

71. A counterexample for Hilton Johnson s Conjecture on List Coloring of Graphs , Australasian Journal of Combinatorics, volume 18(1998), 127 131, With H. Hajiabolhassan, M.L. Mehrabadi, and R. Tusserkani.

PROCEEDING PUBLICATIONS

1. "A Monte-Carlo Method for the Construction of Phylogenetic Networks from Weighted Quartets", AMIC 2010 and The 6th EAST ASIA SIAM, 2010, 106-109, With R. Hassanzadeh, E. Mottaghi, M. Habibi.

2. MC-Net: A Monte-Carlo Method for the Construction of Phylogenetic Network, Proceeding of the 4th International Conference on Research and Education in Mathematics, UPM, Malaysia, 2009, 563-570, With M. Habibi, R. Hassanzadeh, E. Mottaghi.

3. Pezeshk H, Naghizadeh S, Malekpour S. A, Eslahchi C, Sadeghi M. A Modified Bidirectional Hidden Markov Model and its Application in Protein Secondary Structure Prediction. Proceeding of the Second Interaction Conference on Advanced Computer Control (ICACC 2010), Shenyang, China 27th-29th March 2010, pp 535-538.

4. Eslahchi C., Pezeshk H., Sadeghi M., Sheikh attar A. LIBRA: A de Novo Motif Finding in Promoter Sequences Based on Linear Algebra. Proceedings of world Academy of Science, Engineering and Technology, 2009, 37: 507-512.

5. Haplotyping Problem, A Clustering Approach , AIP Conference Proceedings- Sepember 6, 2007, Volume 936, 185-190, With M. Sadeghi, H. Pezeshk, H. Poormohammadi, and M. Kargar.

HONORS

1. Second Prize Winner in Algebraic Competition for Undergraduate University Students in 1986. This Competition is held annually by the Iranian Mathematical Society, and the Participants are the Distinguished Students from the Universities throughout the Country.

2. Got the First place in the Nationwide Entrance Examination for the MS. degree, 1987.

3. Got the Top Second Place in the Entrance Examination for the Ph.D. degree of the Department of Mathematical Sciences of Sharif University of Technology, 1995.

PROFESSIONAL AFFILIATION

1. Associate Dean for education and graduate studies, faculty of mathematical sciences, Shahid Beheshti University, Tehran, Iran, from 2014 to 2018.

2. Head of Department of Cognitive Modeling, Institute for Brain and Cognitive Science, Shahid Beheshti University, from 2014 to 2016.

3. Senior researcher at School of Biosciences at the Institute for Research in Fundamental Sciences (IPM), Tehran, Iran.

4. Member of the Center of Excellence Discrete Structure, Algebra and Logic at Shahid Beheshti University, Tehran, Iran.

5. Member of the Bioinformatics Group at the Tehran University, Tehran, Iran.

6. Head of Department of Mathematics Faculty of Mathematical Sciences Shahid Beheshti University, Tehran, Iran, from 2006 to 2008.

7. Manager of Computer Center of Shahid Beheshti University, Tehran, Iran, from 2002 to 2004.

CONFERENCE

1. "A Monte-Carlo Method for the Construction of Phylogenetic Networks from Weighted Quartets", AMIC 2010 and The 6th EAST ASIA SIAM, 2010.

2. MC-Net: A Monte-Carlo Method for the Construction of Phylogenetic Network, 4th International Conference on Research and Education in Mathematics, UPM, Malaysia, 21-23 October, 2009.

3. LIBRA: A de Novo Motif Finding in Promoter Sequences Based on Linear Algebra, ICCSB, International Conference on Computational and System Biology, Dubai, United Arab Emirates, January 28-30, 2009.

4. Haplotyping Problem, A Clustering Approach, 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) and 6th European Conference on Computational Biology (ECCB), Vienna, Austria: July 21-25, 2007.

5. Fuzzy Secondary Structure Assignment, Third International conference of Applied Mathematics, Bulgaria, 2006.

6. Fuzzy Helix Assignment, The International conference on 21st Century Graph Theory, Thailand, 2005.

7. C- Perfect k-Uniform Hypergraphs, 19st British Combinatorics Conference (BICC), Bangor University, Walse, England, 2003.

8. Characterization of Graph with Hall Number 2, International Congress of Mathematics, Beijing, China, 2002.

9. Circular Chromatic number of Hypergraphs, 18st British International Combinatorics Conference (BICC), Sussex university, Brigton, England, 2001.

TEACHING EXPERIENCES

1. Undergraduate Courses: Calculus, Number Theory, Algebra I, Linear Algebra I, Engineering Mathematics, Discrete Mathematics, Graph Theory, and Probabilistic Methods in Combinatorics.

2. Graduate Courses: Combinatorics I and II, Graph Theory, Some Concept in Combinatorics, Introduction to Bioinformatics Algorithm, System Biology, Sequene analysis, and Computational Molecular Biology.

Ph.D. Students Under My Supervision

1. M. Mirzaie. Ph.D. Graduated. Recognition of Protein Native Structure Based on Styrategic Form Games.

2. S. Arab. Ph.D.Graduated. Protein 3D Structure Prediction Base on Local Energy Minimization.

3. M. Habibi. Ph.D. Graduated. Prediction the Complexes in Protein-Protein Networks Using Graph Properties.

4. H. Poormohamadi. Ph.D. Graduated. Working on A Heuristic Algorithm for Constructing Phytogenetic Network From a Set of Triplets.

5. F. Movahedi. Ph.D. Graduated, Working on some algorithms to stop epidemic in social networks.

6. Reza Hasanzade, Ph.D. Graduated, Working on constructing phylogenetic network from different data.

7. Elnaz Saberi Ansari Ansari, Ph.D. Graduated, Working on an algorithm for domino assignment of a protein.

8. Soheil Jahangiri, Ph.D. Graduated, Working on a Software for Accurate Identification of Orthologs Based on Gene Neighborhood Conservation.

9. Abolfazl Rezvan, Ph.D. Graduated, Working on Comparison of different approaches for identifying subnetworks in metabolic networks.

REFERENCES

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   National University of Singapore,

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3. Professor H. Pezeshk,

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