VIETNAM NATIONAL UNIVERSITY, HANOI
VNU UNIVERSITY OF ENGINEERING AND TECHNOLOGY

SOCIALIST REPUBLIC OF VIETNAM
Independence – Freedom – Happiness

INFORMATION ON DOCTORAL THESIS

1. Full name: Nguyen Huy Tinh .... 2. Sex: Male...

3. Date of birth: 26/01/1988............................ 4. Place of birth: Ha Noi.......................

5. Admission decision number: 45/QĐ-CTSV. Dated 12/01/2023 ....

6. Changes in academic process: changed the thesis title after seminar..........................

(List the forms of change and corresponding times)

7. Official thesis title: Developing and evaluating estimation methods for amino acid substitution models on large datasets...

8. Major: Computer Science .... 9. Code: 9480101 ....

10. Supervisors: Prof.Dr. Le Sy Vinh
Dr. Dang Cao Cuong ....

(Full name, academic title and degree)

11. Summary of the **new findings** of the thesis:

- The thesis proposed a procedure for evaluating the estimation method of amino acid substitution models from simulated data.
- The thesis proposed a method for estimating amino acid substitution models that utilized multiple matrices along with the property of time non-reversibility. Using multiple matrices with different substitution rates helps make the modeling process more realistic.
- The thesis proposed a method for selecting the best fit model for a given alignment based on deep learning.

12. Practical applicability, if any: Using methods in studying and building phylogenetic trees bases on amino acid alignments ....

13. Further research directions, if any: Applying methods on real datasets......................

14. Thesis-related publications: ....

- N. H. Tinh, C. C. Dang, and L. S. Vinh, “Rooting Phylogenetic Trees from Protein Alignments,” in Proceedings - International Conference on Knowledge and Systems Engineering, KSE, Oct. 2023, pp. 1–5. doi: 10.1109/KSE59128.2023.10299425.

- N. H. Tinh, C. C. Dang, and L. S. Vinh, "Estimating amino acid substitution models from genome datasets: A simulation study on the performance of estimated models," J. Evol. Biol., vol. 37, no. 2, pp. 256–265, 2023, doi: 10.1093/jeb/voad017.
- N. H. Tinh, C. C. Dang, and L. S. Vinh, "QMix: An Efficient Program to Automatically Estimate Multi-Matrix Mixture Models for Amino Acid Substitution Process," J. Comput. Biol., vol. 31, no. 8, pp. 703–707, 2024, doi: 10.1089/cmb.2023.0403.
- N. H. Tinh and L. S. Vinh, "Improving the study of plant evolution with multi-matrix mixture models," Plant Syst. Evol., vol. 310, 2024, doi: 10.1007/s00606-024-01896-0.
- N. H. Tinh and L. S. Vinh, "An efficient deep learning method for amino acid substitution model selection," J. Evol. Biol., vol. 38, no. 1, pp. 129–139, 2024, doi: https://doi.org/10.1093/jeb/voae141.
- N. H. Tinh, C. C. Dang, and L. S. Vinh, "nT4X and nT4M: Novel Time Non-reversible Mixture Amino Acid Substitution Models," J. Mol. Evol., 2025, doi: https://doi.org/10.1007/s00239-024-10230-8.