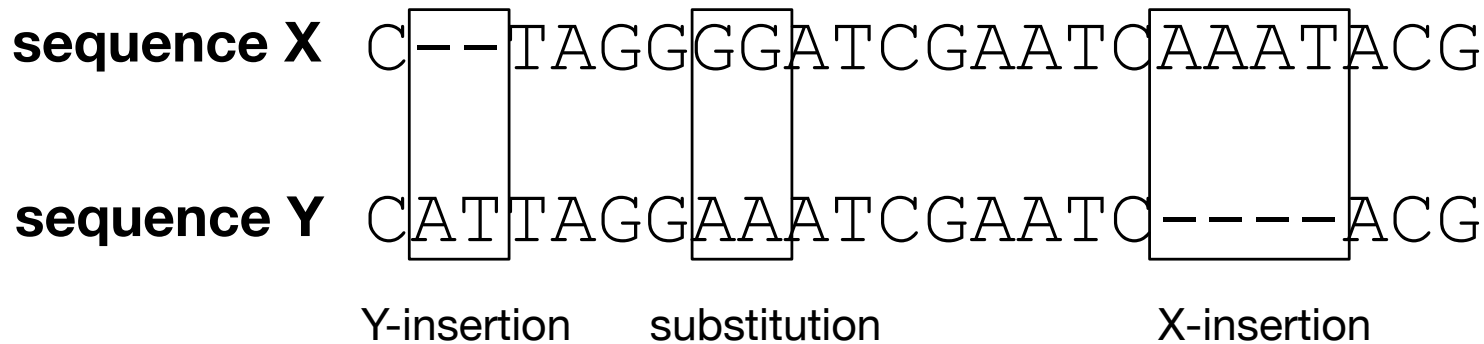


# Model Selection on Pairwise Hidden Markov Models using Factorized Information Criterion

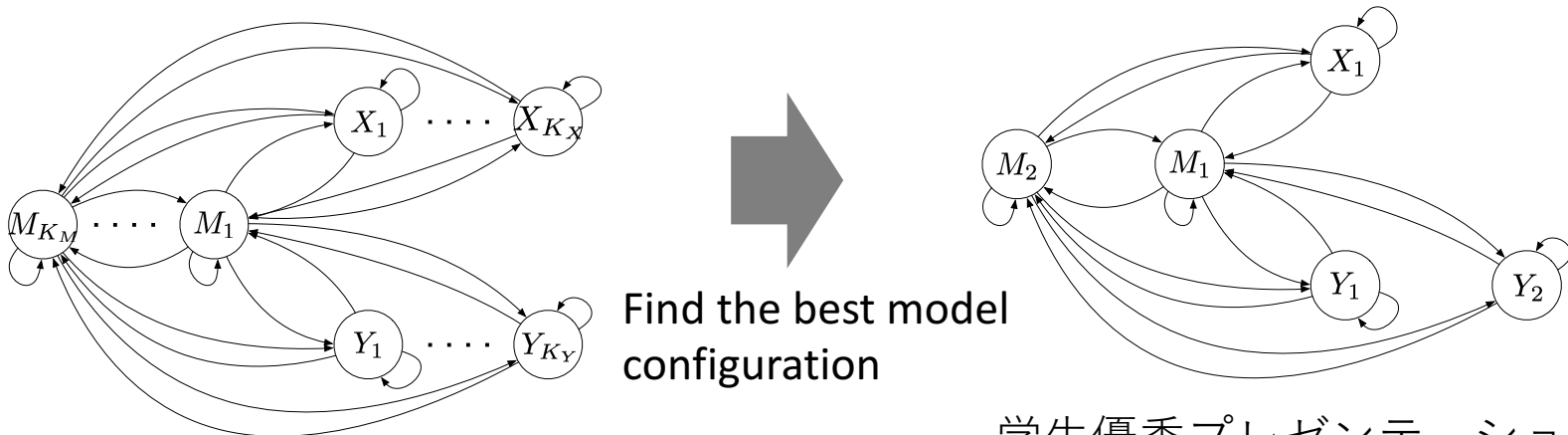
D1-32

Taikai Takeda<sup>1</sup>, Michiaki Hamada<sup>1,2</sup> <sup>1</sup>Waseda University, <sup>2</sup>AIST-Waseda CBBDOIL

**Question - What is the “best” model for biological sequence alignment?**



**How? - Maximization of Factorized Information Criterion (FIC)  
on Pairwise Hidden Markov Models (PHMM)**



学生優秀プレゼンテーション賞対象