ABSTRAK

Dalam pengembangan bahan obat diperlukan uji praklinik yang membutuhkan hewan percobaan bergalur murni. Penelitian ini membangun suatu sistem indentifikasi secara otomatis tikus dan mencit bergalur murni menggunakan pendekatan *Dynamic Programming*. Penelitian ini menggunakan data *sequence* DNA 3 mencit dengan berbeda galur, tikus, dan tikus Lemur, dengan jumlah total 300 *sequence* DNA mencit dan tikus. Berdasarkan hasil penelitian yang dilakukan dengan kombinasi dari 3 metode *multiple sequence alignment* dan 2 metode *consensus*, diperoleh akurasi bervariasi dari yang terendah yaitu 38,000 % sampai dengan yang tertinggi 81,667 % .

Kata kunci : *sequence* DNA, Bioinformatika, galur mencit, *Dynamic Programming*, *sequence alignment*, *sequence consensus*, *multiple sequence alignment*.

ABSTRACT

In the development of pharmaceuticals needed preclinic trials that require animal experiments fluted pure. This research builds a system to automatically identify rats and mice using fluted pure Dynamic Programming approach. This research uses DNA sequence of data with three different strains of mice, rats, and Lemurs, with a total of 300 sequence the DNA of mice and rats. Based on the results of the research conducted with combination of three multiple sequence alignment method and two method sequence consensus, obtained accuracy varies from the lowest i.e. 38,000% up to the highest 81,667%.

Keywords : DNA sequence, Bioinformatics, a strain of mice, Dynamic Programming, sequence alignment, sequence consensus, multiple sequence alignment.