Proceedings of the
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"Meeting Challenges of Global Research and Education in Mathematical Sciences"

Renaissance Hotel Kuala Lumpur, Malaysia
21st - 23rd October 2009

Jointly Organized by:

Institute for Mathematical Research,
Universiti Putra Malaysia (INSPEM)

Institute of Mathematics,
Vietnam Academy of Science & Technology (IMVAST)

Faculty of Mathematics & Natural Sciences,
Bandung Institute of Technology, Indonesia (ITB)

Malaysian Mathematical Sciences Society (PERSAMA)

Malaysian Society for Cryptology Research (MSCR)
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Editors
Mohamad Rushdan Md. Said, Hishamuddin Zainuddin, Noor Akma Ibrahim,
Rohani Ahmad Tarmizi and Habshah Midi

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PREFACE

The International Conference on Research and Education in Mathematics (ICREM) is a biennial conference organized by the Institute for Mathematical Research, Universiti Putra Malaysia. The fourth conference (ICREM4) differs from the earlier ones by having joint organizers from abroad namely Institute of Mathematics, Vietnam Academy of Science and Technology and the faculty of mathematics and natural Sciences, Bandung Institute of Technology, Indonesia as well as local ones i.e. Malaysian Society Mathematical Sciences and Malaysian Society for Cryptology Research. The conference is also supported by Abdus Salam International Centre for Theoretical Physics, Trieste, Italy and United Nations Educational, Scientific and Cultural Organization (UNESCO).

The present proceedings capture part of the excitement of the conference documenting well over one hundred papers contributed by participants from more than twenty countries. They cover all four main areas in mathematical sciences i.e. pure mathematics, Applied Mathematics and Theoretical Sciences, Statistics and Mathematics Education but ones that mirror the interests of the regional community of mathematical scientist and practitioners.

The Organizers would like to thank all the invited speakers and participants for their contributions in making this conference a success and hence brought forth this valuable proceedings.

We would like to express our deepest appreciation to all sponsors of the conference, without which the conference may not be realized. Specifically, we would like to mention Abdus Salam International Centre for Theoretical Physics UNESCO, Ministry of Higher Education and Ministry of Science, Technology and Innovations, Malaysia. Last, but not least, our utmost thanks to the management of the University for their unfailing support towards our activities.
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WATTERTON'S SIMULATION METHOD IN THE STUDY OF THE NUMBER OF ALLELES IN COMMON

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Abstract

In this paper we recall the results of Watterson's simulation method and theoretical study concerning the number of allele in common between three populations that undergone two times of genetic divergence are compared. We found the agreement between these two results are quite satisfactory. The results are found using a n-coalescent approach of Kingman.

Keywords: coalescent process, infinite allele model, genetic divergence, um model

1 Introduction

Genealogical process found a large number of applications within population genetics. Kingman (1982a, b, c) introduced the n-coalescent process as a method of describing the genealogy of a sample of fixed size, n, taken from a large haploid population evolving according to one of a wide class of reproductive models. It also provides an exact description of the genealogy of the Moran model. This process was extended by Watterson (1984a) in the infinitely many neutral allele setting, to a process with two type of equivalence class, "old" and "new". Donnelly and Tavare (1986) studied a coalescent akin to that of Watterson which also takes account of the age-ordering of alleles present in the sample.

Consider a population of fixed size M haploid individuals (or genes). This population evolves through discrete time $m = \ldots, -2, -1, 0, 1, 2, \ldots$. At each time point m, one individual is chosen at random to produce a single offspring and one individual (possibly the same one) is chosen to die. The offspring and the $M - 1$ survivors form the population of the next integer time, $m + 1$. The offspring may, with probability $u$, be a new mutant of an allelic type never before seen, or with probability $1 - u$, be of the same allelic type as its parent. This process is a discrete time version of the infinitely many neutral alleles evolution of Kimura and Crow (1964) with Moran type reproduction (Moran (1958)).

Suppose we take a sample of n genes without replacement from the population at time 0, and trace back their ancestry. At some time, two of these genes will have a most recent common ancestor. We may say that their ancestral lines have coalesced at this ancestor. Further back in time a second coalescence will occur, and so on. Figure 1 shows a possible composition of a sample of size n with respect to an ancestral population at time -m, say. As can be seen from Figure 1, the coalescent process partitions the sample into some subsets. Some of them are descended, without intervening mutation, from a gene at time $m$ ago, whereas the rest are descended from mutants which arose more recently than time $m$ ago. Watterson (1984) classified the former as "old" equivalence class and the latter as "new" equivalence classes. Because of the model, each individual in a particular new class will share the same genetic type, and different new classes correspond to different types.

![Figure 1: Lines of descent and coalescent](image)

With respect to time -$m$, denote the number of old equivalence classes, which is the number of "founders" in Watterson's (1984) terminology or "lines of descent" (Griffiths (1980)), by $D_m$ and the $p^{th}$ old equivalence class

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