Chapter 1

Introduction

I begin with an extended example to motivate both the basic ideas behind generalized linear mixed models (GLMMs) and the variety of inferences possible within the context of such models. The example concerns chestnut trees and leaf blight.

1.1   Example: Chestnut leaf blight

The American chestnut tree was a predominant hardwood in the forests of the eastern United States, reaching 80–100 feet in height at maturity and providing timber and low-fat, high-protein nutrition for animals and humans in the form of chestnuts. In the early 1900s an imported fungal pathogen, which causes chestnut leaf blight, was introduced into the United States. The pathogen spread from infected trees in the New York City area and, by 1950, had killed over 3 billion trees and virtually eliminated the chestnut tree in the United States (Woods and Shanks, 1959). Economic losses in both timber and nut production have been estimated in the hundreds of billions of dollars. As well, there are the ecological impacts of eliminating a dominant species.

   Attempts to restore this tree to the U.S. forests include development of blight resistant varieties of chestnuts and weakening of the fungus by infecting it with a virus which reduces the fungus' virulence (hypovirulence). I will describe the latter in more detail. The basic idea is to release isolates (genetically identical individuals) of chestnut blight fungus that are hypovirulent and let the viruses infect the natural populations of the fungus, thereby allowing chestnuts trees to survive.

   Viruses spread between fungal individuals when they come in contact and fuse together. A major obstacle in spreading this virus and thus controlling the disease is that different isolates of the fungus cannot necessarily transfer the virus to one another.

   Michael Milgroom (Cornell Plant Pathology) and his colleague, Paolo Cortesi (University of Milan) have described (Cortesi and Milgroom, 1998) the effect of genes that govern whether or not transmission of this virus is possible between isolates of the fungus. Mismatches on one or more of these so-called "incompatibility genes" decrease the probability of transmission.

   To estimate the effects of these genes, they have paired numerous isolates which