1 Introduction

The main motivation for the present paper is the study of functional traits in evolutionary biology and quantitative genetics. Evolutionary biology investigates the change of physical traits (phenotypes) across generations. Some traits are univariate or multivariate, but others are functional, like growth curves or thermal performance curves (Kirkpatrick and Heckman, 1989; Heckman, 2003; Kingsolver et al., 2002; Meyer and Kirkpatrick, 2005; Ragland and Carter, 2004). Understanding the modes of variability of these curves is important in order to understand the biological processes behind the trait, and in particular the genetic aspects of it.

Consider for example the flour-beetle growth curves shown in Figure 1(a) (see Irwin and Carter, 2013, for details about these data). They are mass measurements of larvae from hatching to pupation. The dataset consists of 122 half-siblings sired by 29 fathers and different mothers. A distinct characteristic of these curves is an inflection point around day 15; this is the time when larvae stop eating and begin searching for a place to pupate. This process is triggered by hormonal mechanisms whose timing varies from individual to individual; determining what proportion of the time variability can be attributed to genetic factors and what proportion can be attributed to environmental factors is important for understanding the evolution of development and growth. Similarly, in the study of thermal performance curves (which are functions of temperature, not time), the optimal temperature varies from individual to individual and characterizing the sources of this variability is important for understanding thermal adaptations (Huey and Kingsolver, 1989; Izem and Kingsolver, 2005).

We can see, then, that functional samples usually present two types of variability: what we can denominate “horizontal” or “phase” variability (e.g. variability in the location of the mass peaks in Figure 1(a)) and “vertical” or “amplitude” variability (e.g. variability in