## 1 Introduction

Filamentous fungi are of considerable socioeconomic importance, being both vital as industrial tools of enzyme and antibiotic production ([Santos and Linardi, 2004](#_ENREF_28); [Ward et al., 2004](#_ENREF_35)) and harmful as (food-borne) pathogens ([Goto et al., 1996](#_ENREF_13); [Roze et al., 2007](#_ENREF_27)) and as pests of crops ([Bosmans, 2009](#_ENREF_2)). In addition, fungi are used as model organisms in fundamental research, such as on the effect of sex and recombination ([Bruggeman et al., 2003](#_ENREF_3); [Leslie and Klein, 1996](#_ENREF_16)) and the dynamics of adaptation ([Schoustra et al., 2009](#_ENREF_31)). Despite their significance, we know little about the population biology of individual fungal colonies. Chiefly important for this understanding is the development of population growth models for filamentous fungi ([Nielsen, 1992](#_ENREF_24)). Current models on fungal growth focus on directly describing biomass or product formation involved in particular industrial processes without regard to the underlying population growth driving the system [e.g. ([Mitchell et al., 2004](#_ENREF_22))].

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