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Introduction

Providing valid estimates of a genetic disease with a variable age at onset is essential for preventive strategies. This thesis describes the estimation of breast and ovarian cancer risks conferred by the two high-risk genes BRCA1 and BRCA2 using the maximum likelihood method. The focus of this thesis is to examine the variation in breast and ovarian cancer risks found within and between BRCA1/2 families in the Netherlands (HEBON study), and to examine in an international study whether hormonal risk factors modify these risks among women carrying a mutation in BRCA1 or BRCA2 (IBCCS study).