CASE STUDY 3 (Stekel, 2003)

EXAMPLE 10.3 B-CELL LYMPHOMAS

Samples are taken from 60 patients suffering from B-cell lymphomas and are hybridised to microarrays. The aim of the experiment is to identify clinically relevant subgroups of patients using a cluster analysis and then to build a classification model to differentiate between the subgroups.

Experimental Design 1

Thirty patient samples are prepared and labelled with Cy3, and 30 patient samples are prepared and labelled with Cy5. These are hybridised to 30 different two-colour arrays (Figure 10.3a).

Experimental Design 2

The samples from each patient are prepared and labelled with Cy3 and hybridised to 60 different two-colour arrays; a universal reference sample is hybridised in Cy5 to each array (Figure 10.3b).

Experimental Design 3

The samples from each patient are prepared and hybridised to 60 different Affymetrix arrays (Figure 10.3c).

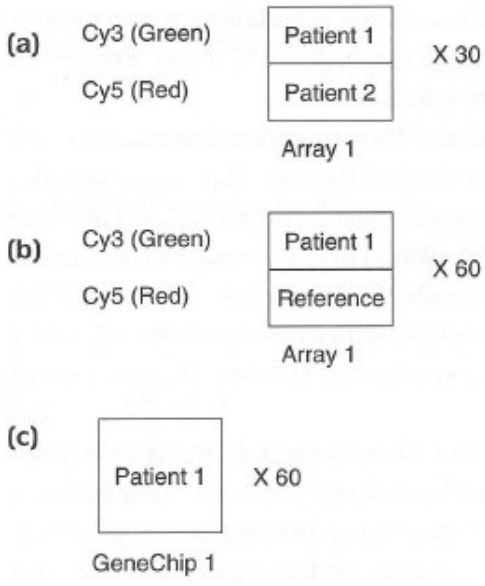

Figure 10.3: Experimental design for lymphoma study. Samples are taken from 60 patients suffering from diffuse large B-cell lymphomas. The aim is to identify clinically relevant subgroups of patients using cluster analysis and then to build a predictor to differentiate between the classes. There are three possible experimental designs: **(a)** Samples from 30 patients are labelled with Cy3, and samples from the other 30 patients are labelled with Cy5. These are hybridised to 30 different two-colour arrays. **(b)** Samples from all 60 patients are labelled with Cy3. These are hybridised with Cy3 and hybridised to 60 separate arrays. A universal reference sample is hybridised in Cy5 to each of the arrays. **(c)** Samples from each patient are hybridised to 60 Affymetrix GeneChips.