



FIGURE 1.1. Scatterplot matrix of the prostate cancer data. The first row shows the response against each of the predictors in turn. Two of the predictors, svi and gleason, are categorical.

For this problem not all errors are equal; we want to avoid filtering out good email, while letting spam get through is not desirable but less serious in its consequences. We discuss a number of different methods for tackling this learning problem in the book.

### Example 2: Prostate Cancer

The data for this example, displayed in Figure 1.1, come from a study by Stamey et al. (1989) that examined the correlation between the level of prostate specific antigen (PSA) and a number of clinical measures, in 97 men who were about to receive a radical prostatectomy.

The goal is to predict the log of PSA (lpsa) from a number of measurements including log-cancer-volume (lcavol), log prostate weight lweight,

age, log of benign prostatic hyperplasia amount (lbp), seminal vesicle invasion (svi), log of capsular penetration (lcp), Gleason score (gleason), and percent of Gleason scores 4 or 5 (pgg45). Figure 1.1 is a scatterplot matrix of the variables. Some correlations with lpsa are evident, but a good predictive model is difficult to construct by eye.

This is a supervised learning problem, known as a *regression problem*, because the outcome measurement is quantitative.

### 3.2.1 Example: Prostate Cancer

The data for this example come from a study by Stamey et al. (1989). They examined the correlation between the level of prostate-specific antigen and a number of clinical measures in men who were about to receive a radical prostatectomy. The variables are log cancer volume (lcavol), log prostate weight (lweight), age, log of the amount of benign prostatic hyperplasia (lbp), seminal vesicle invasion (svi), log of capsular penetration (lcp), Gleason score (gleason), and percent of Gleason scores 4 or 5 (pgg45). The correlation matrix of the predictors given in Table 3.1 shows many strong correlations. Figure 1.1 (page 3) of Chapter 1 is a scatterplot matrix showing every pairwise plot between the variables. We see that svi is a

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