- 3. (b) and (c) only
- 4. (a) gf-point(y~x, data = xyPairs) |> gf-lm()
  - (c) The appearance of the residuals -vs.-fitted-values plot is that of a random (unpatterned) scatter of points about the zero line with no tendency to expand/contract in distance from the zero line as X changes. This confirms the independence of residuals, as well as the one uniform T applying at all X, assumed in the SLM.

The appearance of the normal quantile plot of residuals is that of a straight line, as it should be if residuals follow a normal distribution.

- (d) The coefficient of determination ( $R^2$ ) tells what fraction of variability in (observed) y-values is explained by the linear model in x.
- (e)  $r = -\sqrt{0.818} = -0.9044$
- (f) Ho: B = 0 vs. Ha: B, f 0 (p can appear instead of B,)
- (9)  $t = (-0.904)\sqrt{\frac{82}{1-(0.904)^2}} = -16.55$ P-value: 2 \* pt(-16.55, 61)
- (h) The "prediction" one is to locate the likely range of a single y-value at x=27. The "confidence" one is to locate the likely range of the mean y-value at x=27. The "confidence" one is narrower.
- 5. (a) Ho: Variables river and group are independent Ho: The variables have an association

(b) B-Nile is smallest: 
$$\frac{(168)(104)}{577} = 30.28$$

(c) A-A mazon has expected count 
$$\frac{(205)(59)}{577} = 56.49 \qquad \frac{(47-56.49)^2}{56.49} = 1.594$$

- (d) 1 pchisq (9.153, 6)
- (e) It is valid to use pelisq(), since all expected counts are > 5.
- 6. (a) Source df SS MS F
  Group 2 36.793 18.397 3.973
  Error 82 379.753 4.631
  - (b) Ho:  $\mu_A = \mu_B = \mu_C$ Ha: At least two means are different
  - (c) We are told the samples are independent. The populations (each) are normal  $\Rightarrow$  each  $\bar{x}_A, \bar{x}_B, \bar{x}_c$  are normal  $\sqrt{\frac{s_{max}}{s_{min}}} = \frac{2.403}{1.955} < 2$  Yes, it is valid.
  - (d) 1-pf(3.973, 2,82)
  - (e) MA # Mc, significant at the 5% level