FOUNDATIONS OF SIGNALS AND SYSTEMS 11.3 Homework assignment Prof. T. Erseghe

Exercises 11.3

Solve the following MatLab problems:

- 1. Evaluate numerically the convolution between the signals $x(t) = g(t) = \operatorname{sinc}(t)$ and check that the result is $y(t) = x * g(t) = \operatorname{sinc}(t)$. Choose a very small sampling spacing T to get an accurate result.
- 2. Insuline secretion rates can be measured by the hormone's C-peptide levels. Let x(t) be the C-peptide pancreatic secretion, normalized by volume and measured in [pmol/L/min], and y(t) the plasma C-peptide concentration, measured in [pmol/L]. These can be related through a filter y(t) = x * g(t) with impulse response

$$q(t) = (0.76 e^{-at} + 0.24 e^{-bt}) 1(t) ,$$

where $a = 0.14 \text{ [min}^{-1]}$, and $b = 0.02 \text{ [min}^{-1]}$. Compute numerically the concentration level y(t) when the secretion is the one available in file ex11_3_2.mat, sampled by T = 1 min in the range [0, 420] min. How does the result change for b = 0.2 and b = 0.002? Provide a multiple plot of x, g, and y that compares the three cases.

Solutions.

1. The code can mimic that of Exercise 11.2.2, as follows, where we used the time span [-20, 20] for the sinc.

```
T = 0.01;
tx = -20:T:20;
x = sinc(tx);
tg = -20:T:20;
g = sinc(tg);
y = T*conv(x,g);
ty = tx(1)+tg(1):T:tx(end)+tg(end);
y2 = sinc(ty);
figure
subplot(2,2,1)
plot(tx,x)
grid
xlabel('t')
ylabel('x(t)')
subplot(2,2,2)
plot(tg,g)
grid
xlabel('t')
ylabel('g(t)')
subplot(2,1,2)
plot(ty,y,ty,y2)
grid
xlabel('t')
ylabel('y(t)=x*g(t)')
legend('via MatLab','true signal')
sgtitle('continuous-time convolution')
```

Note how the result is accurate only in the range [-10, 10], due to the fact that, although decaying, the sinc function is a slowly decaying function which is not zero outside the considered interval.



2. This exercise repeats the standard aspects of numerical convolution, with the usual product of conv by T. Note that we selected for g(t) the same interval as x(t), namely [0, 420] min, and that we showed the convolution result only in this range since, outside the range, the convolution values assume x(t) = 0, which is not the case (the ending level of x(t) is about 50, as one can infer from the first plot).

```
load('ex11_3_2.mat') % defines T, x, tx
tg = 0:T:420; % we use the same range of x
g1 = .76 * exp(-.14 * tg) + .24 * exp(-0.2 * tg);
y1 = T*conv(x,g1);
ty = tx(1)+tg(1):T:tx(end)+tg(end);
g2 = .76 * \exp(-.14 * tg) + .24 * \exp(-0.02 * tg);
y2 = T*conv(x,g2);
g3 = .76 * exp(-.14 * tg) + .24 * exp(-0.002 * tg);
y3 = T*conv(x,g3);
figure
subplot(2,2,1)
plot(tx,x)
grid
axis([0 420 ylim])
xlabel('t [min]')
ylabel('x(t) [pmol/L/min]')
title('pancreatic secretion')
subplot(2,2,2)
plot(tg,g1,tg,g2,tg,g3)
grid
axis([0 420 ylim])
xlabel('t')
```

```
ylabel('g(t)')
legend('b=0.2','b=0.02','b=0.002')
title('filter response')
subplot(2,1,2)
plot(ty,y1,ty,y2,ty,y3)
grid
axis([0 420 ylim])
xlabel('t')
ylabel('t')
ylabel('y(t) [pmol/L]')
title('plasma concentration')
sgtitle('hormone C-peptide kinetics')
```

