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	RWD1		

a) A centre exists when the Jacobian of the linearized equations describing the dynamical system at an equilibrium has eigenvalues with zero real parts. Such equilibrium points are said to be non-hyperbolic. The Hartman-Grobman theorem has nothing to say about such equilibrium points as the theorem is about the stability properties of hyperbolic equilibrium points being locally identical to the linearized model.

[2]

b) A centre found when linearizing about an equilibrium point is sometimes associated with a limit cycle, where the angular position of the non-linear solution about the centre has simple dynamics that are decoupled from the radial position. If this is the case, then the existence and stability of any putative cycle can be determined by considering the dynamics of the radial component alone. (2 marks for explanation)

Let a 2-D dynamical system be described by the differential equations

$$\dot{x} = f(x,y)$$
$$\dot{y} = g(x,y)$$

Without loss of generality, translate x and y to the equilibrium point in question, so that (0,0) is at the equilibrium point and define the local polar coordinates

$$r^2 = x^2 + y^2$$
$$\theta = \tan^{-1}\frac{y}{x}.$$

Differentiating, we have

$$2r\dot{r} = 2x\dot{x} + 2y\dot{y} \Rightarrow \dot{r} = \frac{x\dot{x} + y\dot{y}}{r}$$

$$\dot{\theta} = \frac{1}{1+\left(\frac{y}{x}\right)^2}\left[\frac{x\dot{y} - y\dot{x}}{x^2}\right]$$
$$= \frac{x\dot{y} - y\dot{x}}{x^2 + y^2}$$
$$= \frac{x\dot{y} - y\dot{x}}{r^2}$$

(5 marks for derivation)

[7]

c)

i) First note that $x_1 = 0$, $x_2 = 0$ substituted into the equations gives

$$\dot{x}_1 = 0$$

$$\dot{x}_2 = 0$$

Thus (0,0) is an equilibrium point.

Differentiating the equations partially with respect to x_1 and x_2 results in the Jacobian J

$$J = \begin{bmatrix} 3\mu x_1^2 + \mu x_2^2 & -1 + 2\mu x_1 x_2 \\ 1 + 2\mu x_1 x_2 & 3\mu x_2^2 + \mu x_1^2 \end{bmatrix}$$

Substituting in (0,0), the A-matrix of the linearized system at the origin is

$$A = \begin{bmatrix} 0 & -1 \\ 1 & 0 \end{bmatrix}$$

The eigenvalues are ±j, i.e. with zero real component, and are independent of μ.
[2]

ii) Changing to polar coordinates as per part (a) we get the dynamical system description

$$\dot{r} = \frac{x_1\left(-x_2 + \mu x_1\left(x_1^2 + x_2^2\right)\right) + x_2\left(x_1 + \mu x_2\left(x_1^2 + x_2^2\right)\right)}{r}$$

$$= \frac{\mu r^4}{r}$$

$$= \mu r^3$$

$$\dot{\theta} = \frac{x_1\left(x_1 + \mu x_2\left(x_1^2 + x_2^2\right)\right) - x_2\left(-x_2 + \mu x_1\left(x_1^2 + x_2^2\right)\right)}{r^2}$$

$$= \frac{r^2}{r^2}$$

$$= 1$$

The non-linear solution thus rotates about the origin counter-clockwise at a constant angular velocity. If μ<0, then r decreases (if r is non-zero) and the solution spirals into the origin, i.e. a stable spiral. If μ>0, then r increases (if r is non-zero) and the solution spirals away from the origin, i.e. an unstable spiral. [4]

iii) If μ=0 then the system is linear and is a centre. Thus the flow is a continuum of circles, rotating counter-clockwise at a constant angular velocity about the origin. [1]

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Question RWD2			

a) A Poincaré Map is constructed by intersecting the solution flow of a dynamical system with a linear subspace that has dimension 1 less than the system dimension, the subspace being orthogonal (or transversal) to the flow. In the case of a 2-D dynamical system, the sub-space is a line. If the flow is a limit cycle, then the flow's intersection with the sub-space is a point that, on its return, will intersect the sub-space (usually) at a different point on the line. The continuous time dynamical system's limit cycle then defines a return or iterative map. The stability of the limit cycle can then be determined by considering the dynamics of this return map.
[2]

b) A cobweb diagram is a mechanism for investigating the global stability properties of a 1-D iterative map. The iterative map is of the form

$$x_{k+1} = f\left(x_k\right)$$

Associating $y=x_{k+1}$ with the vertical axis and $x=x_k$ as the horizontal axis we next plot y=f(x) and y=x. Intersections of this curve with the straight line y=x correspond to possible equilibrium points. Starting at a general value for x we find y=f(x) by drawing a straight line vertically to intersect with the curve y=f(x). We then draw a horizontal straight line to intersect y=x in order to define the next iterate. The cobweb diagram is constructed by repeating this process a large number of times to determine if the solution approaches and stays near an equilibrium point.

Further local investigation of the iterative map can be performed by linearizing the map at the equilibrium points found to see is the magnitude of the linearized map is less than 1.

c)

i) There are two equilibrium points at r=0 and r=1. The equilibrium point at r=1 corresponds to a periodic orbit as the angular velocity is constant. (The equilibrium point at r=0 is unstable, that at r=1 is locally stable – not asked for.)[2]

ii) We generate a Poincaré Map by intersecting the flow with the line θ = constant. From the equations of motion

$$\frac{4dr}{r\left(1-r^2\right)} = dt = d\theta$$

Integrating, we get

$$\int_{r_1}^{r_2} \frac{4dr}{r\left(1-r^2\right)} = \int_{\theta_1}^{\theta_2} d\theta = 2\pi$$

[2]

iii)

The change in radius must satisfy

$$\int_{r_1}^{r_2} \frac{4dr}{r\left(1-r^2\right)} = 4\int_{r_1}^{r_2} \frac{1}{r} - \frac{1}{2(1+r)} + \frac{1}{2(1-r)} dr$$

$$= 4\left[\ln \frac{r}{\sqrt{1-r^2}}\right]_{r_1}^{r_2} = 2\pi$$

Thus

$$\frac{r_2\sqrt{1-r_1^{\,2}}}{r_1\sqrt{1-r_2^{\,2}}} = e^{\frac{\pi}{2}} \Rightarrow \frac{r_2^{\,2}\left(1-r_1^{\,2}\right)}{r_1^{\,2}\left(1-r_2^{\,2}\right)} = e^{\pi}$$

Cross multiplying

$$r_2^{\,2}\left(1-r_1^2\right) = e^{\pi} r_1^2\left(1-r_2^2\right) \Rightarrow r_2^{\,2}\left(1-r_1^2+e^{\pi} r_1^2\right) = e^{\pi} r_1^2$$

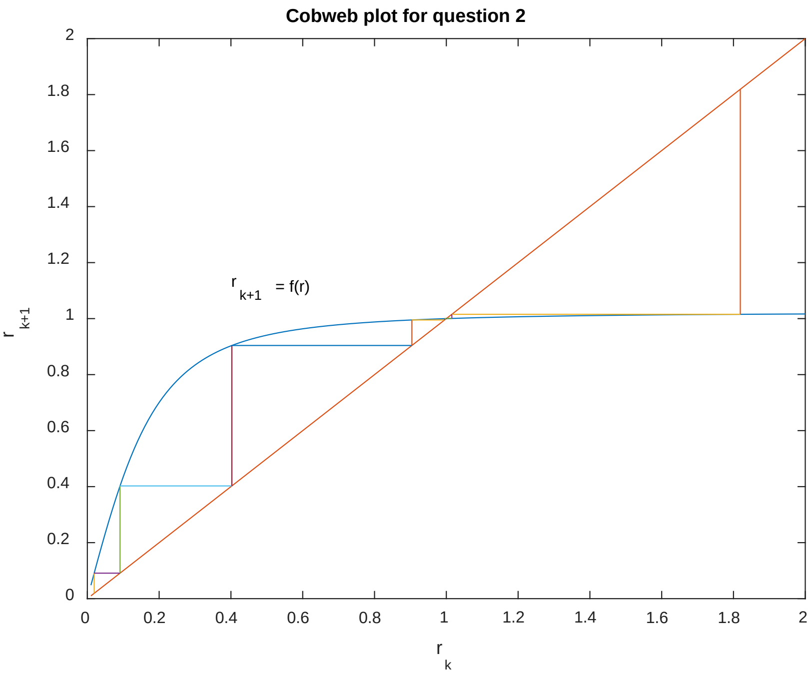
Or

$$r_2^2 = \frac{e^{\pi} r_1^2}{1+r_1^2\left(e^{\pi}-1\right)} = \frac{1}{1+e^{-\pi}\left(r_1^{-2}-1\right)} \Rightarrow r_2 = \frac{1}{\sqrt{1+e^{-\pi}\left(r_1^{-2}-1\right)}}$$

We thus have an iterative function

$$f(r) = \frac{1}{\sqrt{1+e^{-\pi}\left(r^{-2}-1\right)}}$$

that generates the next radius given the current radius. We may thus generate a cobweb function by combining the function above with y=x using the construction described in part (b)



The Matlab generated cobweb plot of the solution is give above, from which it is clear that the equilibrium point is stable.

[8]

The Matlab for part (c)

```
% Generates the cobweb map for Q2 in C24 2017

% Plot the iteration function and y=x
x = [0.01:0.01:2];
```

```
y = x;
for i = 1:length(x)
y(i) = 1/sqrt(1+exp(-pi)*(1/x(i)^2 - 1));
end

figure(1)
clf
plot(x,y,x,x)
title('Cobweb plot for question 2')
ylabel('r_{k+1}')
xlabel('r_k')
text(0.4,1.1,'r_{k+1} = f(r)')

hold on

% Plot the cobweb for two starting points
for z = 0.019:1.8:2
    % Starting point is (x1, y1)
    x1 = z;
    y1 = x1;
    for i = 1:10
        y2 = 1/sqrt(1+exp(-pi)*(1/x1^2 - 1));
        x2 = y2;

        % vertical line
        plot([x1 x1],[y1 y2]);
        % horizontal line
        plot([x1 x2],[y2, y2]);

        %iterate
        x1 = x2;
        y1 = y2;
    end
end
```

C24 Perturbation methods.

(a) $\varepsilon m^2 + (1+\varepsilon)m + 1 = 0$

$(\varepsilon m+1)(m+1)$ are roots so

$m = -1/\varepsilon$ and -1 <u>two roots</u>

In limit $\varepsilon \to 0$, 1st root $\to -\infty$ (ie) disappears.
Original quadratic becomes $m+1=0$
so linear.

So limit as $\varepsilon \to 0$ is <u>singular</u>.

(b) $\varepsilon \frac{d^2y}{dx^2} + \frac{dy}{dx}(1+\varepsilon) + y = 0$ range $0 \le x \le 2$

b.c.s $\left.\begin{aligned} y(0)&=1 \\ y(2)&=1 \end{aligned}\right\}$

(i) lowest order approx: set $\varepsilon = 0$

gives $\frac{dy_0}{dx} + y_0 = 0 \Rightarrow$ soln $y_0 = Ae^{-x}$

Only one constant (A) $\therefore$ can only satisfy one b.c.

(ii) We can see from part (a) that the exact soln. to ODE (obtained by a trial soln of $y \sim e^{mx}$) has one term with $m = -1/\varepsilon$. So this term decays very quickly as x increases in +ve direction
$\therefore$ b.l. must be located at LH end of domain.

<u>Or</u> take 1st 2 terms and look for a balance

$\varepsilon \frac{d^2y_1}{dx^2} + \frac{dy_1}{dx} = 0$ $\left[\text{or } (\varepsilon y_1'' + y_1') + (\varepsilon y_1' + y_1) = 0 \right]$
derivative of same eqn

$\Rightarrow y_1(x) \simeq B + Ce^{-x/\varepsilon}$

and valid close to $x = 0$, so $B + C = 1$, LH b.c.

(iii)

so inner soln :

$$y_1(x) = B + (1-B)\, e^{-x/\varepsilon}$$

outer soln

$$y_0(x) = e^{-(x-2)} = e^2 e^{-x}$$ using RH b.c.

Matched asymptotics

$y_1 \to B$ for x/ε large

$y_0 \to e^2$ for $x \to 0$

$y_{overlap} = B = e^2$

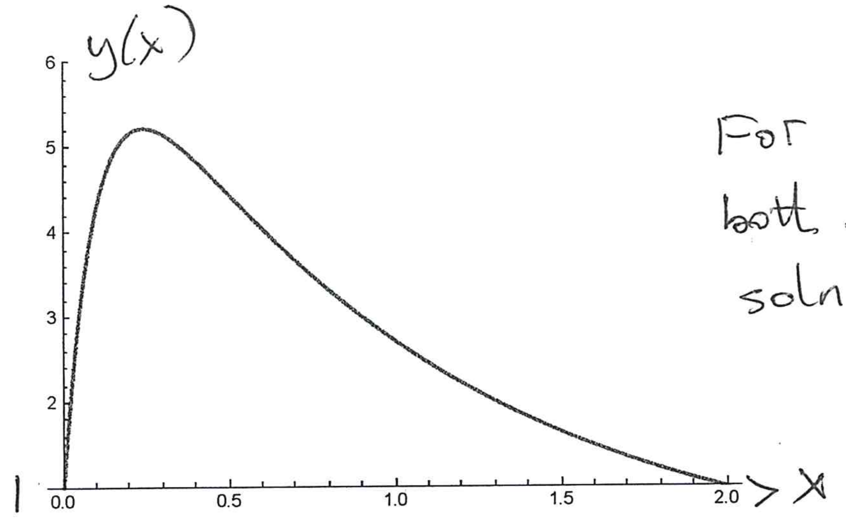
Thus composite solution is

$$y_1 + y_0 - y_{overlap}$$

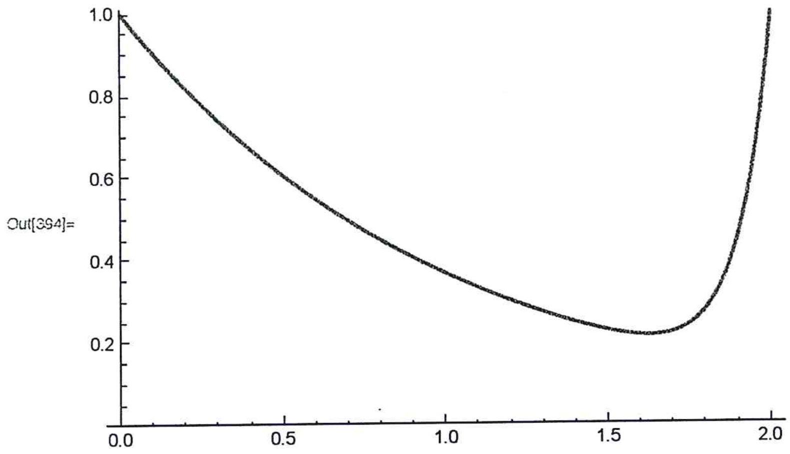
$$= \left[e^2 + (1-e^2)\, e^{-x/\varepsilon}\right] + \left[e^2 e^{-x}\right] - e^2$$

$$= (1-e^2)\, e^{-x/\varepsilon} + e^{-(x-2)}$$

(c) If ε is now negative, the term $e^{-x/\varepsilon}$ now decays only on moving in the $-$ve x direction, so this b.l. must now be located at RH edge.



For $\varepsilon = 1/10$,
both exact and composite
solns.



For $\varepsilon = -1/10$,
note b.l. has now
moved close to $x=2$,
the RH end.

(a) Bayesian model selection aims to identify the model (from a candidate set of models) which best explains the data, and incorporating a prior on what the model might be. It does so by employing Bayes' rule such that

$$p(M \mid \mathcal{D}) = \frac{p(\mathcal{D} \mid M)p(M)}{p(\mathcal{D})},$$

where

- $p(M \mid \mathcal{D})$ is the model posterior we would ideally want;
- $p(\mathcal{D} \mid M)$ is the *evidence* (or model likelihood);
- $p(M)$ is the prior over the space of models;
- $p(\mathcal{D})$ is the probability of the data under all possible models.

The principal advantage of Bayesian model selection lies in it automatically striking a tradeoff between efficacy and complexity, inherently penalising both too simplistic and overly complex models.

Usually, $p(M)$ and $p(\mathcal{D})$ are difficult to specify / compute (the latter, for example, requiring marginalising over all possible models). So in practice we often only use the *evidence* term for Bayesian model selection.

(b) (i) We will arrive at the model evidence by marginalising over the parameter θ such that

$$p(\mathcal{D} \mid M) \quad = \quad \int p(\mathcal{D} \mid \theta, M)p(\theta \mid M)\mathrm{d}\theta.$$

The individual observations are independent and, in principle, would yield a RV follwing a Binomial distribution, which involves a Binomial coefficient accounting for the likelihood of seeing a particular number of heads or tails. However, the question specifically asks for the evidence given a *particular sequence of outcomes* which means the binomial terms can be omitted (this was discussed in the tutorials). Therefore

$$\begin{aligned} p(\mathcal{D} \mid \theta, M) &= \prod_i p(d_i \mid \theta) \\ &= \theta^k (1-\theta)^q. \end{aligned}$$

The prior on θ is given by the Beta distribution as specified in the question such that

$$p(\theta \mid M) \quad = \quad \frac{1}{B(a,b)}\theta^{a-1}(1-\theta)^{b-1}.$$

So, putting it all together we get...

$$\begin{aligned} p(\mathcal{D} \mid M) &= \int p(\mathcal{D} \mid \theta, M)p(\theta \mid M)\mathrm{d}\theta \\ &= \frac{1}{B(a,b)}\int \theta^k\theta^{a-1}(1-\theta)^q(1-\theta)^{b-1}\mathrm{d}\theta \\ &= \frac{1}{B(a,b)}\int \theta^{a-1+k}(1-\theta)^{b-1+q}\mathrm{d}\theta \\ &= \frac{B(a+k, b+q)}{B(a,b)}, \end{aligned}$$

where the last step follows from the *definition* of the Beta function.

(ii) Substituting for the Beta function in the result of part b(i) yields

$$p(\mathcal{D} \mid M) = \frac{\Gamma(a+b)\Gamma(a+k)\Gamma(b+q)}{\Gamma(a)\Gamma(b)\Gamma(a+b+k+q)}.$$

For model M_1: $a = 4, b = 6$, such that

$$p(\mathcal{D} \mid M_1) = \frac{\Gamma(10)\Gamma(4+k)\Gamma(6+q)}{\Gamma(4)\Gamma(6)\Gamma(10+k+q)}.$$

For model M_2: $a = 6, b = 4$, such that

$$p(\mathcal{D} \mid M_2) = \frac{\Gamma(10)\Gamma(6+k)\Gamma(4+q)}{\Gamma(6)\Gamma(4)\Gamma(10+k+q)}.$$

Therefore,

$$\begin{aligned}
\frac{p(\mathcal{D} \mid M_1)}{p(D \mid M_2)} &= \frac{\Gamma(4+k)\Gamma(6+q)}{\Gamma(6+k)\Gamma(4+q)} \\
&= \frac{(k+3)!(q+5)!}{(k+5)!(q+3)!} \\
&= \frac{(k+3)!(q+3)!(q+4)(q+5)}{(k+3)!(k+4)(k+5)(q+3)!} \\
&= \frac{(q+4)(q+5)}{(k+4)(k+5)}.
\end{aligned}$$

(c) From the plots provided in the question, note that M_1 is biased towards *tails* ($\mathbb{E}[\theta] < 0.5$), whereas M_2 is biased towards *heads* ($\mathbb{E}[\theta] > 0.5$).

(i) For a specific sequence of 5 heads and 5 tails, $\frac{p(\mathcal{D}|M_1)}{p(\mathcal{D}|M_2)} = 1$. So both models are equally likely. There is no evidence in favour of either.

(ii) For a specific sequence of 3 heads and 7 tails, $\frac{p(\mathcal{D}|M_1)}{p(\mathcal{D}|M_2)} = 2.36$. Here the data provide more evidence in favour of M_1 which makes sense as it favours a bias towards *tails*.

(iii) For a specific sequence of 7 heads and 3 tails, $\frac{p(\mathcal{D}|M_1)}{p(\mathcal{D}|M_2)} = 0.42$. Here the data provide more evidence in favour of M_2 which makes sense as it favours a bias towards *heads*.