A look at enzyme kinetics

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Here we do a phase plane analysis of the system of biochemical kinetics, taken from Lin & Segel ch. 10.

```
> restart;
> values:=kappa=1,lambda=0.375: values;
```

$$\kappa = 1, \lambda = .375$$

```
> dynamics:=D(s)=-s+(s+kappa-lambda)*c,
  D(c)=(s-(s+kappa)*c)/epsilon:
  dynamics[1]; dynamics[2];
```

$$\mathrm{D}(s) = -s + (s + \kappa - \lambda)\, c$$

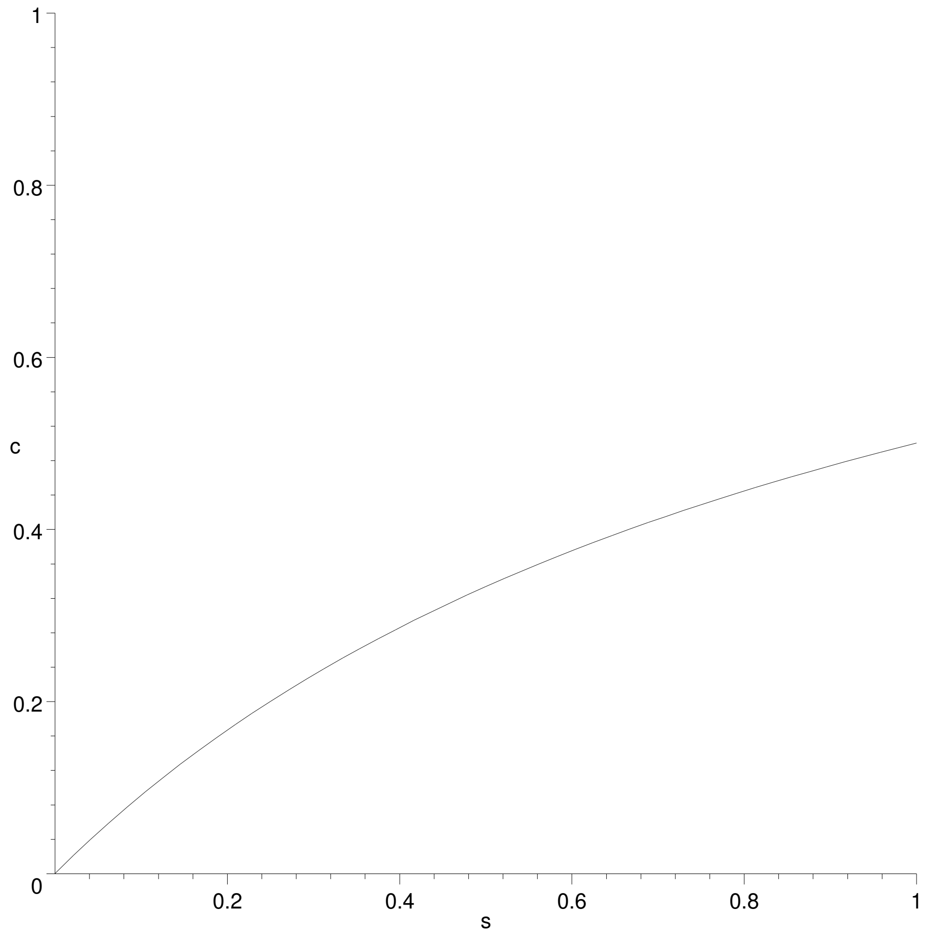
$$\mathrm{D}(c) = \frac{s - (s + \kappa)\, c}{\varepsilon}$$

The dynamics is comparatively slow when the term multiplying ε is set equal to zero. We compute and plot this set, which we may call the *slow manifold*:

```
> slow:=subs(dynamics,epsilon*D(c)=0): slow;
```

$$s - (s + \kappa)\, c = 0$$

```
> slowplot:=plot(subs(values,solve(slow,c)),s=0..1,c=0..1,
                 color=blue): slowplot;
```

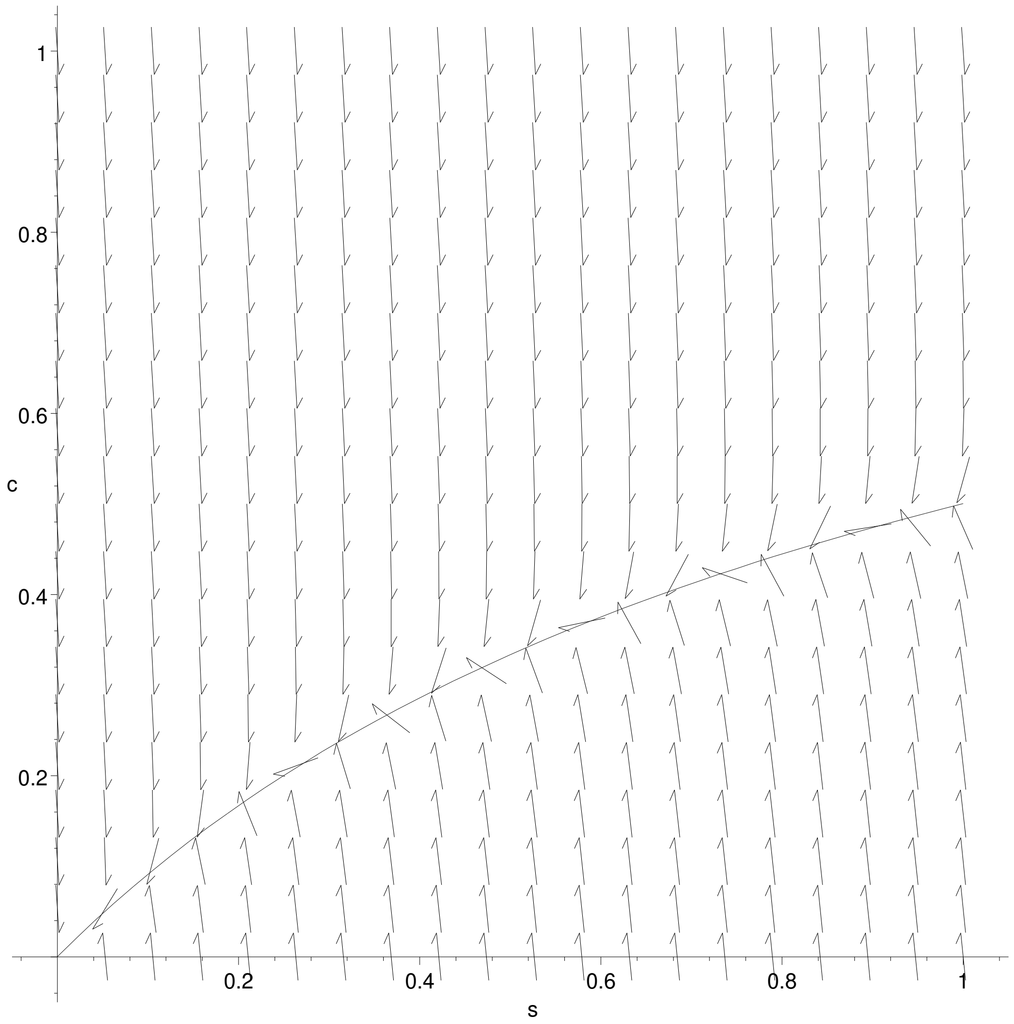


Maple technicality: need to convert our differential equations into a form acceptable to DEplot. Then we make a direction field plot, and superimpose it on the slow manifold plot:

```
> dynamicx:=subs({D(s)=D(s)(t),s=s(t),D(c)=D(c)(t),c=c(t)},
            [dynamics]);
```

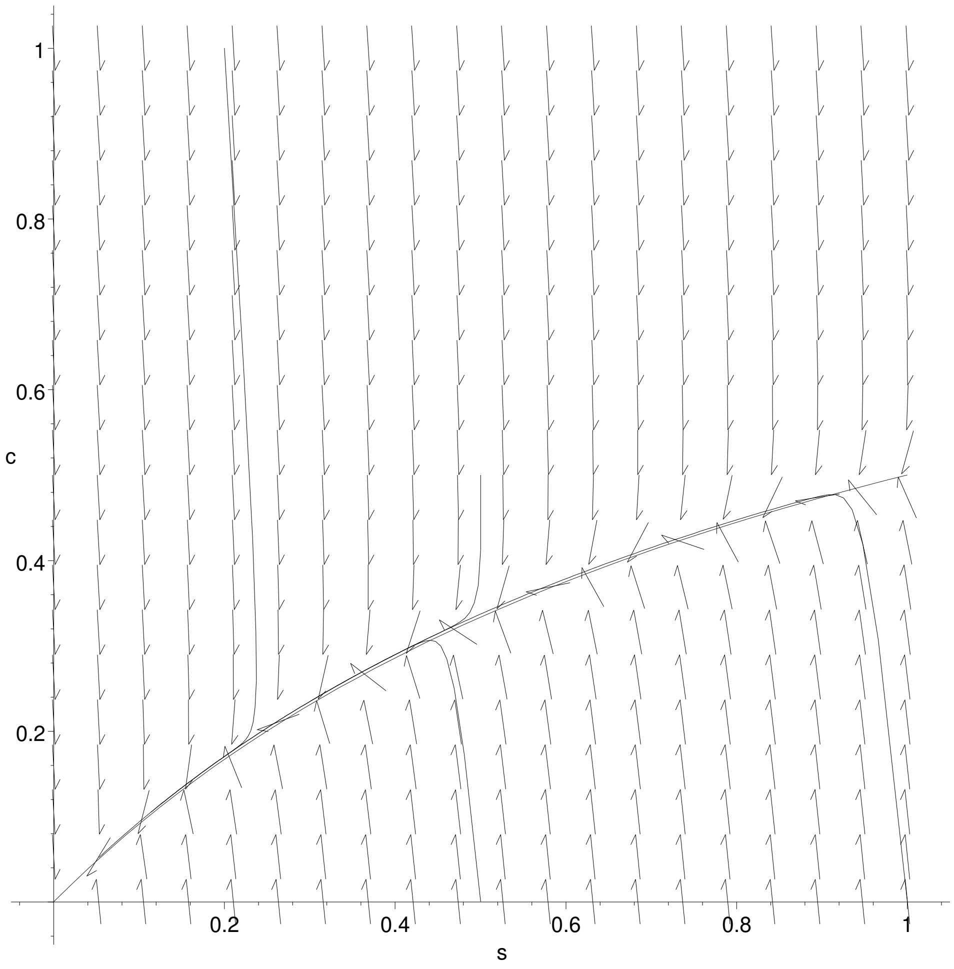
$$dynamicx := \left[\mathrm{D}(s)(t) = -\mathrm{s}(t) + (\mathrm{s}(t) + \kappa - \lambda)\,\mathrm{c}(t),\ \mathrm{D}(c)(t) = \frac{\mathrm{s}(t) - (\mathrm{s}(t) + \kappa)\,\mathrm{c}(t)}{\varepsilon} \right]$$

```
> dfplot:=DEtools[DEplot](subs(values,epsilon=0.1,dynamicx),
            [s,c],t=0..5,s=0..1,c=0..1,colour=black):
  plots[display](slowplot,dfplot,scaling=CONSTRAINED);
```



Even better: We can plot a few trajectories of the system in addition.

```
> initials:=[[s(0)=1,c(0)=0],[s(0)=0.5,c(0)=0],[s(0)=0.2,c(0)=1],
             [s(0)=0.5,c(0)=0.5]]:
  deplot:=DEtools[DEplot](subs(values,epsilon=0.1,dynamicx),
            [s,c],t=0..5,initials,s=0..1,c=0..1,stepsize=0.05,
            colour=black,linecolour=black):
  plots[display](slowplot,deplot,scaling=CONSTRAINED);
```


1
0.8
0.6
0.4
0.2
c
0.2
0.4
0.6
0.8
1
s

>