Exercise 4.14

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Here we ignore the latently infected cells from 4.13 and examine whether this changes disease dynamics.

We use the following parameter values:

$\Gamma = 1.36$, $\mu = 1.36 \times 10^{-3}$, $\tau = 0.2$, $\delta = 0.33$, $\pi = 100$, $\sigma = 2$, and $\beta = 2.7 \times 10^{-4}$.

In[ ]:= `Quit[]; Clear[];`

In[ ]:=
```
(* define the system of ODEs, where odeCs is the susceptible cells,
    and odeCi is infected cells *)
odeCs = D[Cs[t], t] == (gamma * tau) - (mu * Cs[t]) - ((beta * Cs[t] * pie / sigma) * Ci[t]);
odeCi = D[Ci[t], t] == (beta * Cs[t] * (pie / sigma) * Ci[t]) - (delta * Ci[t]);
sysOde = {odeCs, odeCi};
sysOde /. beta → 0.027 /. t → 0
```

Out[ ]= $\left\{ \text{Cs}'[0] == \text{gamma tau} - \text{mu Cs}[0] - \dfrac{0.027 \, \text{pie Ci}[0] \times \text{Cs}[0]}{\text{sigma}} \right.$,

$\left. \text{Ci}'[0] == -\text{delta Ci}[0] + \dfrac{0.027 \, \text{pie Ci}[0] \times \text{Cs}[0]}{\text{sigma}} \right\}$

```
In[ ]:= (* def function*)
     doSimHiv[CsInit_, CiInit_, gamma0_, tau0_, beta0_, mu0_,
       delta0_, pi0_, sigma0_, maxT_] := Module[{init, sol, params},
       (* def initial conditions*)
       init = {Cs[0] == CsInit, Ci[0] == CiInit};
       (* get numerical solution *)
       sol = NDSolve[{sysOde, init}, {Cs, Ci}, {t, 0, maxT}];

       (* set parameters: gamma = source of new susceptible cells;
       tau = entry rate of susceptible cells;
       mu = non-disease death rate of susceptible cells;
       beta = viral infection probability; pi = rate of production of virions;
       sigma = virion death rate; delta = death rate of actively infected cells *)
       params = {gamma → gamma0, tau → tau0, beta → beta0,
         mu → mu0, delta → delta0, pie → pi0, sigma → sigma0};

       (* make plot *)
       Plot[{Evaluate[Cs[t] /. sol /. params], Evaluate[Ci[t] /. sol /. params]},
        {t, 0, maxT},
        PlotRange → All,
        PlotTheme → "Detailed",
        PlotStyle → {Blue, Red},
        PlotLegends → Placed[{"susceptible", "infected"}, Below],
        PlotLabel → StringForm["β = ``", beta0],
        AxesLabel → {"time", "n cells"}]
      ]

In[ ]:= (* explore two values each of initial number of infected cells and beta *)
     params1 = {200, 1, 1.36, 0.2, 0.000027, 0.00136, 0.33, 100, 2, 120};
     params2 = {200, 1, 1.36, 0.2, 0.00027, 0.00136, 0.33, 100, 2, 120};
     params3 = {200, 1, 1.36, 0.2, 0.0027, 0.00136, 0.33, 100, 2, 120};
     params4 = {200, 1, 1.36, 0.2, 0.000135, 0.00136, 0.33, 100, 2, 120};
     simList = Map[doSimHiv, {params1, params2}, {1}];
     plotList = doSimHiv @@@ {params1, params2, params4, params3};
```

⋯ NDSolve: Encountered non-numerical value for a derivative at t == 0.`.

⋯ NDSolve: Encountered non-numerical value for a derivative at t == 0.`.

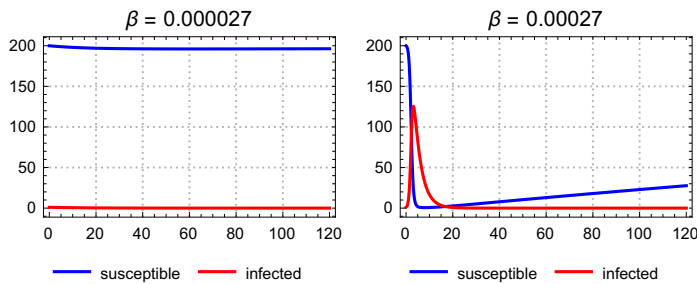⋯ NDSolve: Encountered non-numerical value for a derivative at t == 0.`.

⋯ General: Further output of NDSolve::ndnum will be suppressed during this calculation.

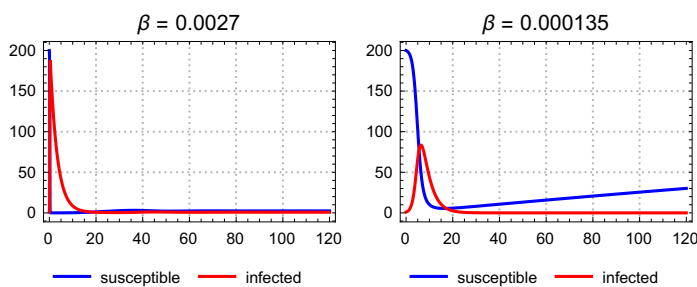*In[ ]:=* `Show[GraphicsGrid[{{plotList[[1]], plotList[[2]]}, {plotList[[4]], plotList[[3]]}}],`
`    PlotLabel → "HIV dynamics with different parameters"]`

HIV dynamics with different parameters

Out[ ]=

Here, we see the effect of latently infected cells on HIV dynamics, which is the rapid elimination of actively infected cells from the population. If these were the only cells serving as sources of new virus, the infection would be eliminated conditional on the value of β, the infection rate. At low values of $\beta = 2.7 \times 10^{-5}$, the infection affects less than 10% of cells. At β values between 5 and 10 times greater ($1.35 10^{-4}$ and 2.7×10^{-4}), the infection rate merely determines the time until peak infection; the population of susceptible cells begins a recovery in both cases. At very high values of β, the infection affects all susceptible cells.