HIV Mini Project

Based on *Reduction of HIV Concentration During Acute Infection: Independence from a Specific Immune Response* by Andrew N. Phillips

In [1]:
```
# Configure Jupyter so figures appear in the notebook
%matplotlib inline

# import functions from the modsim.py module
from modsim import *
```

In [2]:
```
def make_system(alpha, beta, gamma, delta, mu, pi, rho, sigma, tau):
    """Make a system object for the HIV model.

    alpha: rate of activation of latently infected cells [E/(Lt)]
    beta: rate of infection of uninfected cells per viron [1/(Vt)]
    gamma: rate of production of uninfected cells [R/t]
    delta: rate of removal of actively infected cells [1/t]
    mu: rate of cell death [1/t]
    pi: rate of production of virons by actively infected cells [V/(Et)]
    rho: proportion of cells that become latently infected upon infection [L/R]
    sigma: rate of removal of virons [1/t]
    tau: proportion of uninfected cells activated [1]

    returns: System object
    """
    init = State(R=200, L=0, E=0, V=4 * 10**-7)
    t_0 = 0
    t_end = 120 # days
    dt = 1.0/20.0 # 1.2 hour increments

    return System(init=init, t_0=t_0, t_end=t_end, dt=dt, alpha=alpha, beta=beta,
                  gamma=gamma, delta=delta, mu=mu, pi=pi, rho=rho, sigma=sigma, tau=tau)
```

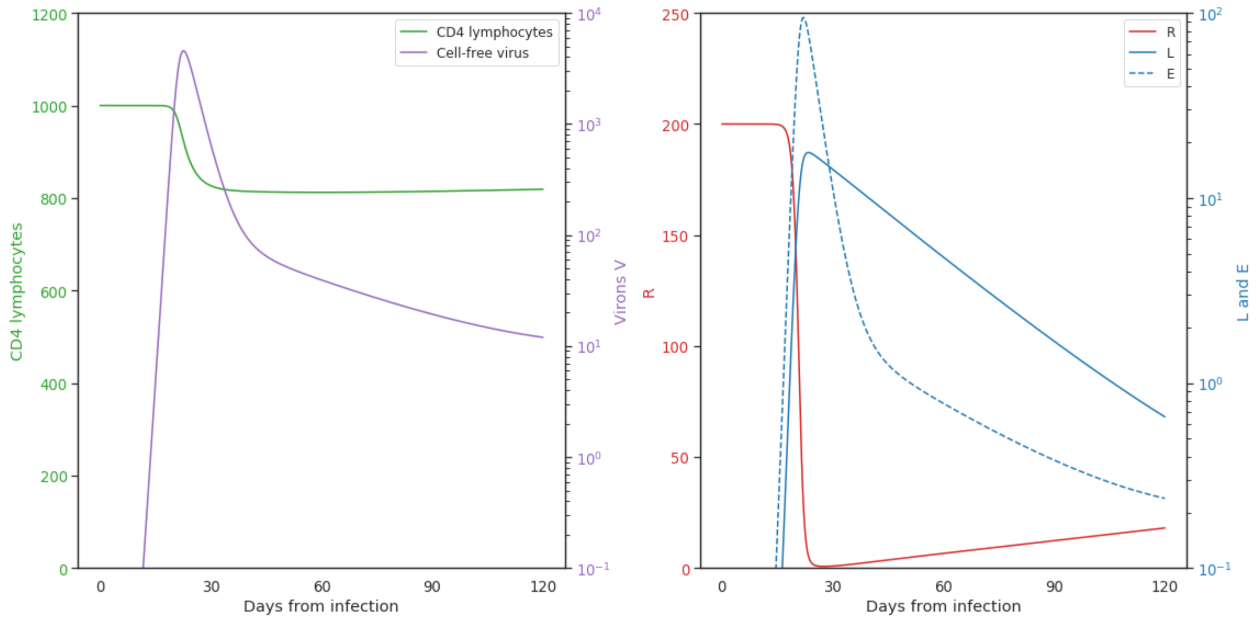
In [3]:
```
def update_func(state, t, system):
    """Update the HIV model.

    state: State with variables R, L, E, V
    t: time step
    system: System with parameters alpha, beta, gamma, delta, mu, pi, rho, sigma, and tau

    returns: State object
    """
    r, l, e, v = state

    # infections/activations
    infected = system.beta * r * v
    latentlyInfected = system.rho * infected
    activelyInfected = infected - latentlyInfected
    latentlyInfectedActivated = system.alpha * l

    # productions
    uninfectedProduction = system.gamma * system.tau
    vironProduction = system.pi * e

    # deaths/removals
    uninfectedDeath = system.mu * r
    latentlyInfectedDeath = system.mu * l
    activelyInfectedDeath = system.delta * e
    vironDeath = system.sigma * v

    dt = system.dt
    r += (uninfectedProduction - infected - uninfectedDeath) *dt
    l += (latentlyInfected - latentlyInfectedActivated - latentlyInfectedDeath) *dt
    e += (activelyInfected + latentlyInfectedActivated - activelyInfectedDeath) *dt
    v += (vironProduction - vironDeath) *dt

    return State(R=r, L=l, E=e, V=v)
```

In [4]:
```
def run_simulation(system, update_func):
    """Runs a simulation of the system.
    Adds a TimeFrame to the System: results

    system: System object
    update_func: function that updates state
    """
    init = system.init
    t_0, t_end, dt = system.t_0, system.t_end, system.dt
    frame = TimeFrame(columns=init.index)
    frame.row[t_0] = init
    ts = linrange(t_0, t_end, dt)

    for t in ts:
        frame.row[t+dt] = update_func(frame.row[t], t, system)

    return frame
```

In [5]:
```
def plot_results(R, L, E, V):
    """Plot the results of the HIV model
    """
    xNums = [0,30,60,90,120]
    fig, (pl1, pl2) = plt.subplots(1, 2, figsize=(16, 8)) # create 2 subplots, right & left

    color = 'tab:green'
    pl1.set_xlabel('Days from infection')
    pl1.set_ylabel('CD4 lymphocytes', color=color)
    cells, = pl1.plot(R + E + L + 800, color=color)
    pl1.tick_params(axis='y', labelcolor=color)
    pl1.set_ylim([0, 1200])
    plt.xticks(xNums)

    ax1 = pl1.twinx()  # instantiate a second axis on pl1 that shares the same x-axis
    color = 'tab:purple'
    ax1.set_ylabel('Virons V', color=color)  # we already handled the x-label with ax1
    v, = ax1.semilogy(V, color=color)
    ax1.tick_params(axis='y', labelcolor=color)
    ax1.set_ylim([0.1, 10000])

    color = 'tab:red'
    pl2.set_xlabel('Days from infection')
    pl2.set_ylabel('R', color=color)
    r, = pl2.plot(R, color=color)
    pl2.tick_params(axis='y', labelcolor=color)
    pl2.set_ylim([0, 250])
    plt.xticks(xNums)

    ax2 = pl2.twinx()  # instantiate a second axis on pl2 that shares the same x-axis
    color = 'tab:blue'
    ax2.set_ylabel('L and E', color=color)  # we already handled the x-label with ax1
    l, = ax2.semilogy(L, color=color)
    e, = ax2.semilogy(E, color=color, linestyle='dashed')
    ax2.tick_params(axis='y', labelcolor=color)
    ax2.set_ylim([0.1, 100])

    pl1.legend((cells, v), ('CD4 lymphocytes', 'Cell-free virus'), fontsize=12, loc='upper right')
    pl2.legend((r, l, e), ('R', 'L', 'E'), fontsize=12, loc='upper right')
    fig.tight_layout()  # otherwise the right y-label is slightly clipped
```

In [6]:
```
alpha = 3.6 * 10**-2 # rate of activation of latently infected cells [E/(Lt)]
beta = 0.00027 # rate of infection of uninfected cells per viron [1/(Vt)]
gamma = 1.36 # rate of production of uninfected cells [R/t]
delta = 0.33 # rate of removal of actively infected cells [1/t]
mu = 1.36 * 10**-3 # rate of cell death [1/t]
pi = 100 # rate of production of virons by actively infected cells [V/(Et)]
rho = 0.1 # proportion of cells that become latently infected upon infection [L/R]
sigma = 2 # rate of removal of virons [1/t]
tau = 0.2 # proportion of uninfected cells activated [1]

system = make_system(alpha, beta, gamma, delta, mu, pi, rho, sigma, tau)
results = run_simulation(system, update_func)
plot_results(results.R, results.L, results.E, results.V)
```

Out[6]:


CD4 lymphocytes
Cell-free virus
CD4 lymphocytes
Virons V
Days from infection
R
L
E
R
L and E
Days from infection