EECS 16A Designing Information Devices and Systems I

Spring 2015 Midterm II Sample Problems

1. **Bio-Molecule Detector**

One application for electronics that has gained a lot of attention over the past several years is in so-called "bio-molecule" detection. The idea is to build a system that detects the presence of specific molecules and/or cells (e.g., specific viruses, proteins, etc.) in a biological sample; if this detection can be performed automatically and using relatively low-cost components, it can have a dramatic impact on a number of areas such as medical diagnosis, drug development, DNA sequencing, etc.

In this problem we'll look at how some of the techniques we learned about in the touchscreen module can be applied to realize a hypothetical bio-molecule detector. (Real bio-molecule detection systems involve quite a bit more complexity than what we'll include here, but in many designs the same basic principles apply.)

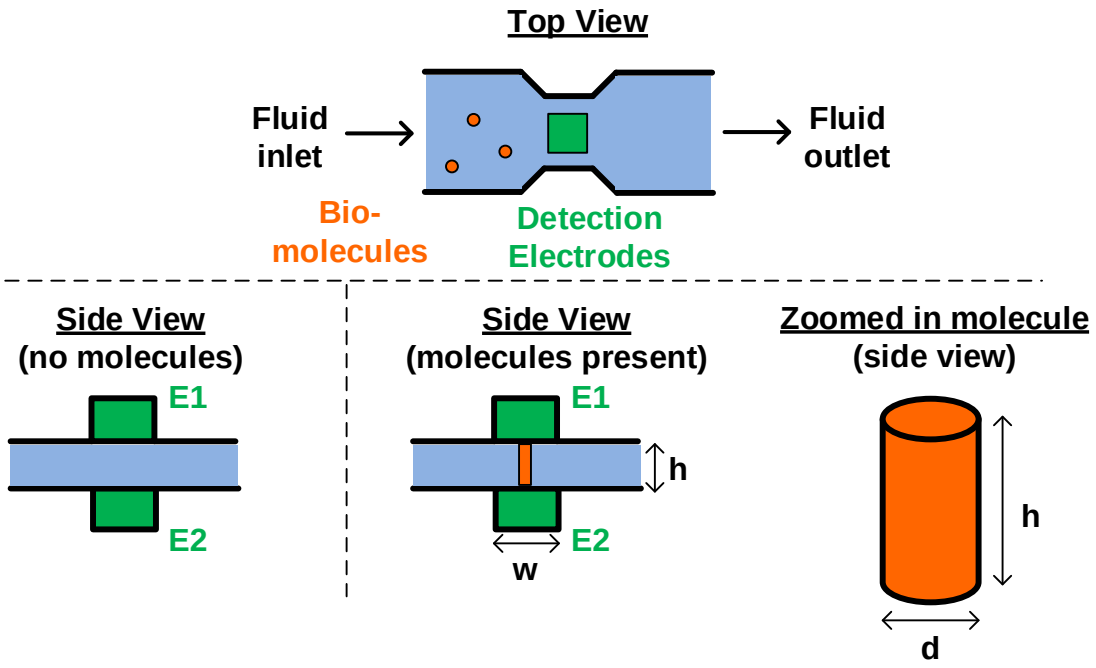


Fig. 1: Cartoon of our simplified bio-molecule detector system.

As shown in Fig. 1 above, the detector works by flowing a liquid that may or may not contain the biomolecules through a region in the device that has electrodes on the top and bottom of the liquid channel. The electrodes (E1/E2 in Fig. 1) are chemically "functionalized" (using e.g. some appropriately designed antibodies) so that if the specific bio-molecule of interest is present in the fluid sample, one or more of the molecules will get physically trapped between the two electrodes

(bottom right of Fig. 1). After all of the fluid has been cleared out of the device (i.e., so that if there are bio-molecules present, there is only air in between the two electrodes E1/E2), we can then figure out whether or not one or more bio-molecules were trapped by measuring the resistance between the two electrodes, the capacitance between the two electrodes, or both.

(a) Let's first assume that we want to detect the presence of a bio-molecule by measuring resistance. If no bio-molecule is present, what should be the resistance between E1/E2? As shown in Fig. 1, if each bio-molecule is a cylinder with diameter d = 10nm, height h = 100nm, and has a resistivity ρ = 100 Ω*m, what would be the resistance between E1 and E2 if only a single bio-molecule has been trapped? Note that you can assume that the trapped molecule is exactly vertically oriented when it is trapped – i.e., the top and bottom faces of the molecule are both aligned with surfaces of the electrodes.

Solution:

If no bio-molecule is present between E1/E2 we are left with just air between the electrodes, and so for all intents and purposes the resistance between them should be **infinite**.

If there is a bio-molecule trapped between E1/E2, the resistance R should be:

$R = \rho * L/A = 100\ \Omega*m * 100e\text{-}9\ m / (\pi * (1/2 * 10e\text{-}9\ m)^2) =$ **127.3 GΩ**

(b) Using the same numbers for d, h, and ρ as part a), as a function of the number of trapped bio-molecules $N_{molcules}$, what is the resistance between E1 and E2? (Note that you can assume that $N_{molecules}$ is small enough that all of the molecules fit within the electrode area, and that all of the molecules are still trapped in an exactly vertical orientation.)

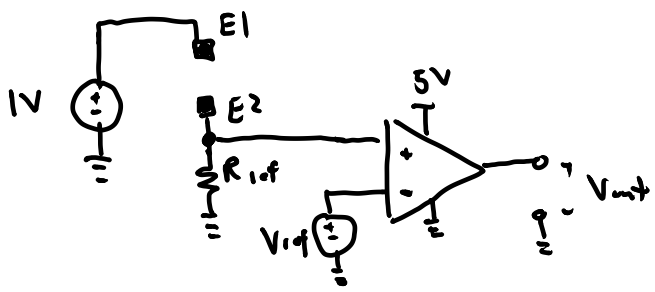
Solution:

The bio-molecules effectively all end up being in parallel with each other – or, equivalently, their cross-sectional areas end up. Therefore, the net resistance between E1/E2 is:

$R = 127.3G\Omega / N_{molecules}$

(c) Given your answers to parts (a) and (b), design a circuit that will output a +5V voltage if more than 5 molecules are trapped, and 0V if 4 or fewer molecules are trapped.

Solution:



$R_{ref} = \frac{127.3\ G\Omega}{5}$

$0.444V < V_{ref} < 0.5V$

(d) Now let's assume that the bio-molecules aren't conductive at all (i.e., $\rho = \infty\ \Omega$*m), and so we will instead try and detect the change in capacitance caused by the presence of trapped bio-molecules. Assuming that the electrodes are square (from the top view) and have a side length w = 10μm, that h is still 100nm, and that the permittivity of the bio-molecule is $\varepsilon = \varepsilon_r * \varepsilon_0 = 10 * 8.85\text{e-}12$ F/m, what is the capacitance between E1 and E2 if no bio-molecules are present?

Solution:

$C_{E1\text{-}E2} = \varepsilon_0 * A / d = 8.85\text{e-}12\ \text{F/m} * (10\text{e-}6\ \text{m})^2 / (100\text{e-}9\ \text{m}) =$ **8.85 fF**

(e) Using the same parameters as part (c), what is the capacitance between E1 and E2 if a single bio-molecule is trapped? How about if $N_{molecules}$ are trapped?

Solution:

What we need to do is figure out how much the capacitance of the region that contains the bio-molecule changed by due to the presence of the molecule. This is equivalent to thinking of the molecule as adding another capacitor in parallel with the capacitance of the electrodes – it's just that we need to keep track of the fact that some of the area that made up the electrode capacitance is now occupied by the bio-molecule.

If no molecule was present, that small section of the electrode would have a capacitance of:

$C_{no\_molecule} = \varepsilon_0 * A_{molecule} / d = 8.85\text{e-}12\ \text{F/m} * (\pi * (1/2 * 10\text{e-}9\ \text{m})^2) / (100\text{e-}9\ \text{m}) = 6.95$ zF

(A "zF" is 1e-21 F)

$C_{with\_molecule} = \varepsilon_r * \varepsilon_0 * A_{molecule} / d = 10 * C_{no\_molecule}$

So, the change in capacitance for each molecule is:

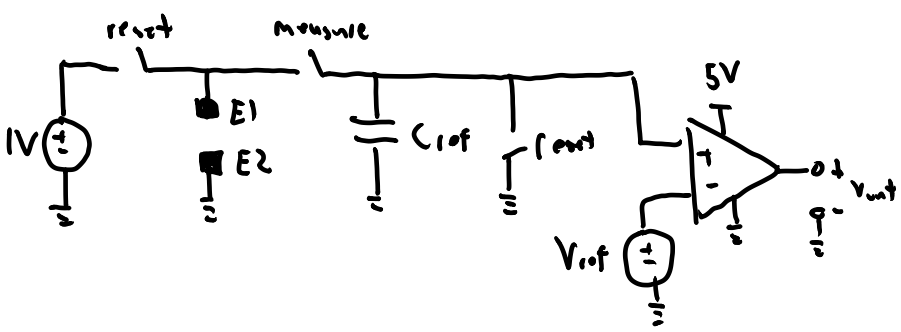
$\Delta C = C_{molecule} - C_{no\_molecule} = 9 * C_{no\_molecule} = 62.6$ zF

Therefore, the total capacitance between E1 and E2 as a function of $N_{molecules}$ is:

$\mathbf{C_{E1\text{-}E2} = 8.85fF + 62.6zF * N_{molecules}}$

(f) Given your answers to parts (d) and (e), design a circuit that will output a +5V voltage if more than 5 molecules are tapped, and 0V if 4 or fewer molecules are trapped.

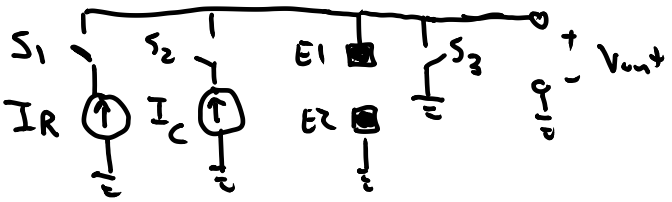
Solution:



(Note that the ΔC is extremely small and would require a very precise circuit design)

(g) We may not know in advance whether the bio-molecule will be conductive, and so we might want to build our detector circuit so that it is capable of measuring either the resistance or the capacitance between E1/E2. Design a circuit that will output a voltage that is proportional to the resistance between E1/E2 (if measuring resistance), or output a voltage that is inversely proportional to the capacitance between E1/E2 (if measuring capacitance). Note that you can assume that if your circuit is configured to measure capacitance, the resistivity of the bio-molecule is infinite (i.e., you will always be measuring either purely resistance or purely capacitance).

Solution:



If measuring resistance, then switch S_1 would always be on and switches S_2 and S_3 would always be off.

If measuring capacitance, then switch S_1 should always be off, and switches S_2 and S_3 will alternate between being on and off; the output voltage should be measured after having switch S2 on for some period of time T_{on}.

(h) Because the bio-molecules are small and the binding process that traps them isn't perfect, the measurements we get from any real detector can be quite noisy. Because of this, one of your colleagues suggests to use the circuit you designed in part (g) to measure both the capacitance and the resistance of a sample, and to then somehow use that information to get a more noise tolerant estimate of $N_{molecules}$. Calling the measured resistance R_{meas} and the measured capacitance C_{meas}, using the tools we've learned in EE16A, formulate and describe a strategy that may achieve this goal.

Solution:

Using our results from parts (a), (b), and (e), we can use the following equations to model the ideal relationships between R_{meas}/C_{meas} and $N_{molecules}$:

$R_{meas} = R_{mol} / N_{molecules}$

$C_{meas} = C_0 + C_{mol}*N_{molecules}$

As you might have imagined, we would like to formulate some kind of least squares problem to estimate $N_{molecules}$ given noisy measurements of R_{meas} and C_{meas}. Least squares only works with linear equations however, so we'll need to do some massaging of the models to get it in to a format we know how to deal with.

First, let's deal with R_{meas}, which depends upon $N_{molecules}^{-1}$. The simplest thing to do is simply work with conductance instead of resistance – i.e., take the inverse of our measured resistance so that we get a quantity that is linearly proportional to $N_{molecules}$. In other words, we can write the following equation:

$R_{mol}^{-1} * N_{molecules} = R_{meas}^{-1} + \varepsilon_R^{-1}$

$\rightarrow G_{mol} * N_{molecules} = G_{meas} + \varepsilon_G$

(Note we introduced an error term to capture the noise in our measurement.)

Now let's look at C_{meas}. In this case, all we need to do is subtract off C_0 from C_{meas} to get a linear relationship:

$C_{mol} * N_{molecules} = (C_{meas} - C_0) + \varepsilon_C$

It should now hopefully be obvious how to convert this to a least squares problem in the traditional form:

$$\begin{bmatrix} G_{mol} \\ C_{mol} \end{bmatrix} N_{molecules} = \begin{bmatrix} G_{meas} \\ (C_{meas} - C_0) \end{bmatrix} + \begin{bmatrix} \varepsilon_G \\ \varepsilon_C \end{bmatrix}$$

Therefore, the best estimate (in the least squared error sense) for $N_{molecules}$ would be:

$$N_{molecules} = \frac{G_{mol}G_{meas} + C_{mol}(C_{meas} - C_0)}{G_{mol}^{\ 2} + C_{mol}^{\ 2}}$$

2. Digital-to-Analog Converter

As we saw in homework 6, one device that finds a lot of usage is a "digital-to-analog converter" (DAC) that allows us to translate signals from the digital representation we use in e.g. our computers to an analog quantity we can use in the "real" world. In this problem we'll look at one implementation of such a DAC that converts the digital codes into an analog voltage. The DAC design we'll be working with is shown below in Fig. 2, and is known as an "R-2R" DAC.

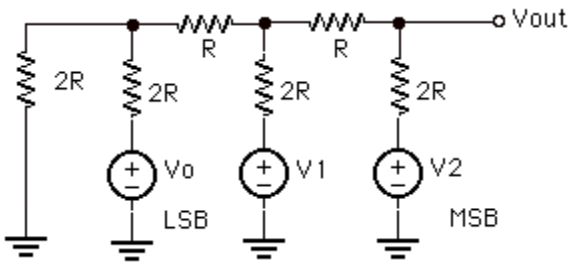
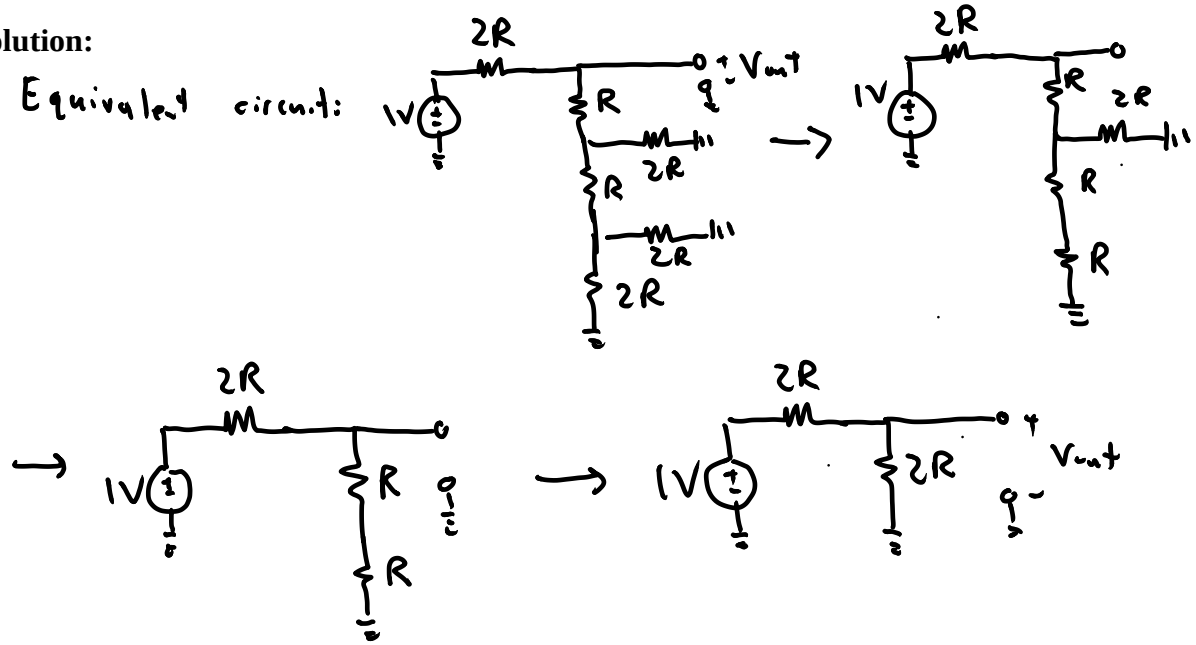


Fig. 2: Digital-to-analog converter circuit.

Note that throughout this problem, we will assume that a digital "1" translates in to a voltage of 1V, and a digital "0" translates in to a voltage of 0V.

(a) For a digital input of 100 (i.e., V2 = 1V, V1 = 0V, and V0 = 0V), what is the output voltage V_{out}?

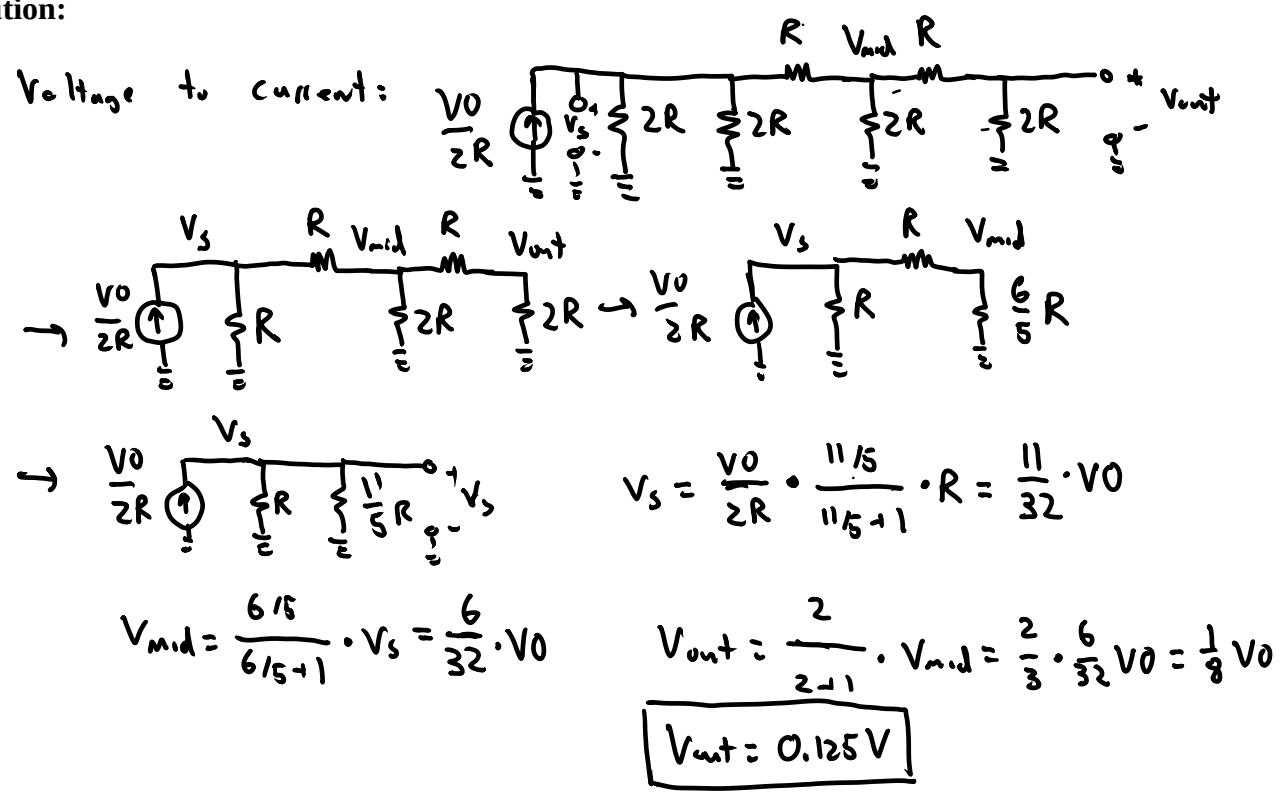
Solution:



So, $\mathbf{V_{out} = V_{digital} / 2 = 0.5V}$

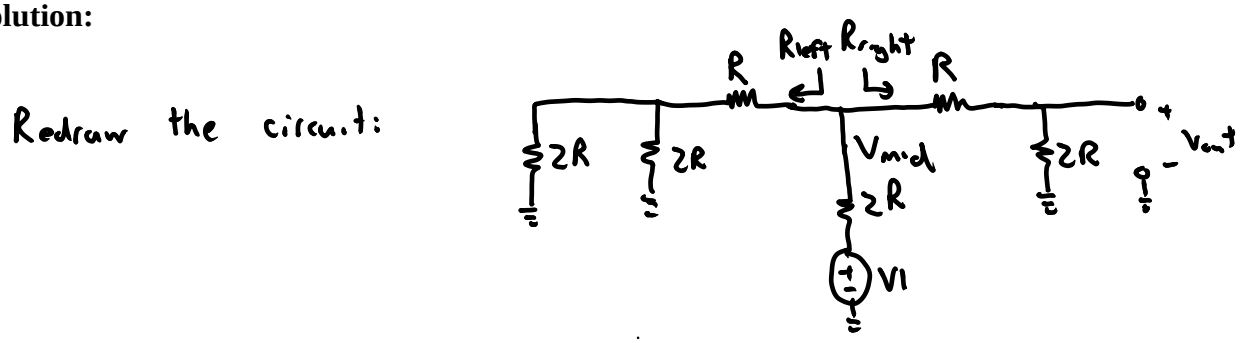
(b) For a digital input of 001 (i.e., V2 = 0V, V1 = 0V, and V0 = 1V), what is the output voltage V_{out}? (Hint: you may find it easier to solve this problem by remembering that you can "transform" between voltage and current sources.)

Solution:



(c) For a digital input of 010, what is the output voltage V_{out}?

Solution:



R_{left} = 2R (like we saw in part a)
Rr_{ight} = 3R (like we saw in part b)

So, $V_{mid} = (R_{left} \parallel R_{right}) / (R_{left} \parallel R_{right} + 2R)*V1 = (6/5)/(6/5+2)*V1 = (3/8)*V1$

Finally, $V_{out} = 2/3*V_{mid}$, so $V_{out} = ¼*V1$

→ **V_{out} = 0.25V**

(d) It turns out that by combining the results of parts (a), (b), and (c), it can be shown that the circuit in Fig. 2 can be modeled as the circuit shown below in Fig. 3, where RT = R, and VT = V2/2 + V1/4 + V0/8.

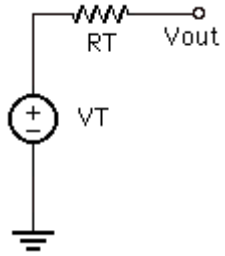
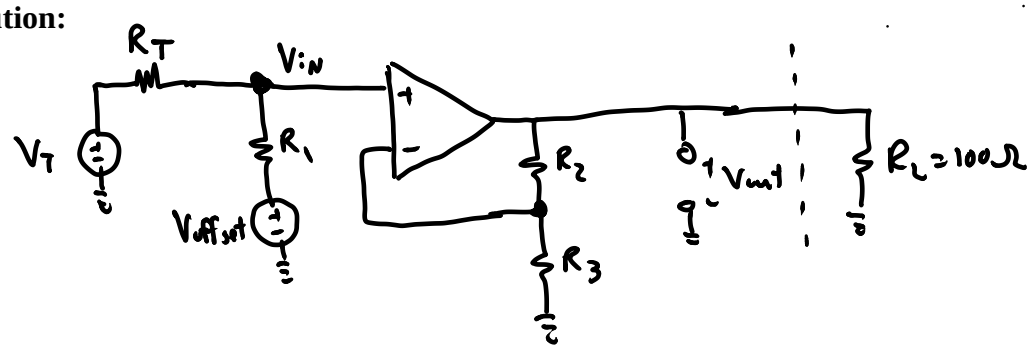


Fig. 3: R-2R DAC equivalent circuit.

Using this model for the R-2R DAC circuit and assuming that RT = 1kΩ, design a circuit that would provide an output voltage that swings from -1.75V (corresponding to 000) to 1.75V (corresponding to 111) while driving a 100Ω load resistance.

Solution:



VT swings between 0V and 0.875V, so to get V_{out} between -1.75V and 1.75V we need to shift the middle level and apply gain (as done in the circuit above).

Let's choose R_1 = RT, so V_{offset} = - (0.875V – 0V)/2 = -7/16 V.

The summer circuit has a gain of ½ - i.e., V_{in} = ½ (VT + V_{offset}), so we need to compensate for that plus the difference in the original swing of the DAC signal using the non-inverting amplifier:

1.75V / (7/16V * ½) = (7/4) / (7/32) = 8

Hence, we should choose $R_2 = 7*R_3$. For example, we could choose R_2 = 7kΩ and R_3 = 1kΩ.

3. "Timer" Circuit

As we saw in the locationing module, keeping track of the amount of that has elapsed between the occurrence of two events (e.g., receiving a signal from one satellite vs. another) can be extremely useful. Therefore, in this problem we will explore the design of a circuit that can produce a periodic voltage waveform, where the period of that waveform will be set by the values we choose for our components. In particular, we want to design a circuit that will output +5V for half of the period, and -5V for the other half of the period – i.e., your circuit should output a square wave with a 50% duty cycle.

In order to realize this circuit, you are allowed to use any combination of the following components:

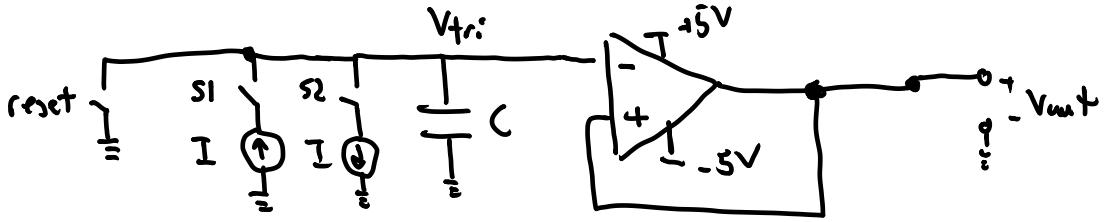
- Ideal op-amps
- Resistors
- Capacitors
- Switches
- Batteries (i.e., voltage sources)

If you need some control signals (like those we used in the touchscreen module from the Arduino) that drive some switches in order to reset and/or initialize some voltages within your circuit, please feel free to utilize those as well.

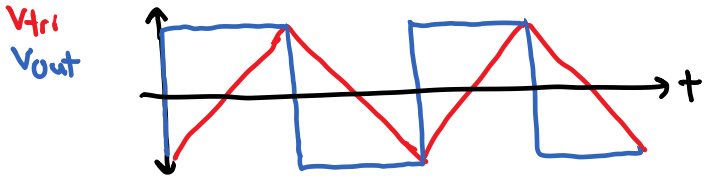
(a) Sketch a design for a circuit that achieves the timer functionality described above. Don't worry about setting the value of the period yet or the values of the any of the components yet – just show a schematic for the circuit. (Hint: If driven by a fixed current, how does the voltage across a capacitor change over time?)

Solution:

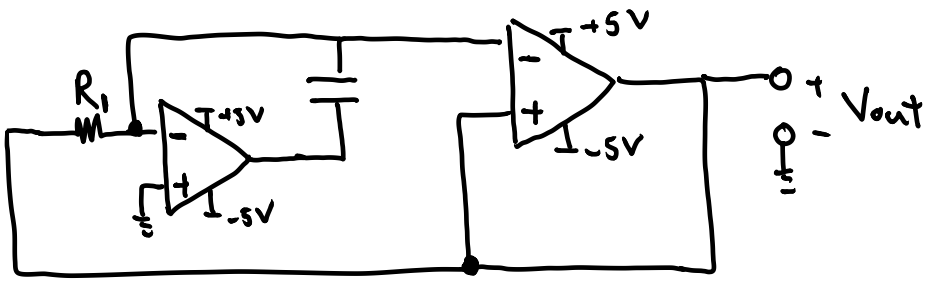
Conceptually, if we could make a triangle wave, we can get a square wave out of it by using a comparator. Recalling that a constant current in to a capacitor gives a ramp voltage (i.e., one side of a triangle wave), we can start with the following initial implementation:



As shown below, the idea in this circuit is that we use the current sources plus the capacitor to generate a triangle wave on V_{tri} that swings between -5V and +5V; when V_{tri} hits one of the two limits, we want the sign of both the current flowing in to the capacitor and the voltage at V_{out} to flip. Thus, the switch S1 should be on when V_{out} = +5V (to drive V_{tri} towards 5V) and switch S2 should be on when V_{out} = -5V (to drive V_{tri} back towards -5V).



We weren't actually given current sources however, so we'll need to build at least one out of an op-amp. Fortunately, it turns out that when we do this we can also get rid of the switches since we can then control the sign of the current directly by using V_{out}.



(b) Now select component values for your design such that the period of your timer circuit is 100μs.

Solution:

In order to select the component values, we first need to figure out what sets the period of oscillation in our circuit. As described above, what we are looking for then is how long it takes for the triangle wave to swing all the way from one of the rails (e.g., +5V) to the other rail (e.g., -5V) – the period is then just twice of this time (since we need to go from e.g. +5V to -5V and back to +5V).

Recalling that the magnitude of current created by the op-amp that has the capacitor C in its feedback loop is $|I| = |V_{out}| / R_1$, we therefore just need to know how long it takes for that current I to change the voltage on the capacitor by 10V (i.e., +5V – (-5V)).

$I*T/C = \Delta V$
$\rightarrow T = 10V*C/I = 10V * C * R1 / V_{out}$

Thus:

T = 2*R1*C

Now we can finally choose some specific values. Arbitrarily choosing **C = 100pF**, then **R1 = 500Ω**.

4. Estimating Friends

You've recently been hired at a new and growing social-network startup, and you want to develop a model that can predict the number of friends new users on the network will have.

(a) You collect a bunch of data regarding the age of the current users and the number of friends they have. Using this data, you'd like to develop a predictive model for the number of friends a new user will have. The data you have collected looks like the data in Fig. 4.

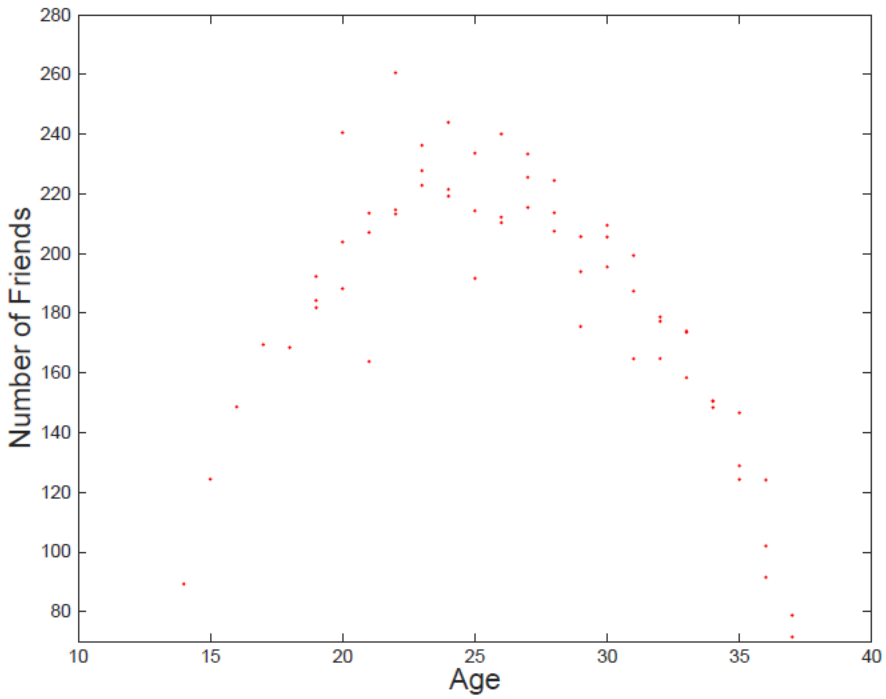


Fig. 4: Number of friends vs. age

If the points you have are of the form (a_i,n_i), where a_i is the age of the ith user and n_i is the number of friends, what kind of model would you use to capture the relationship between age and number of friends? If a new user comes in with age α, how would you predict the number of friends they have? (You don't need to provide any numerical answers – just explain the procedure you would use.)

Solution:

The number of friends looks like it depends roughly quadratically on the age of the user:

$n_i = c_0 * a_i^2 + c_1 * a_i + c_2$

To predict the number of a friends a new user would have, we can find the c_0, c_1, and c_2 coefficients via a least squares fit of the data we have available. In other words, we are looking for the least squares solution to:

$$\begin{bmatrix} a_1^2 & a_1 & 1 \\ a_2^2 & a_2 & 1 \\ \vdots & & \\ a_m^2 & a_m & 1 \end{bmatrix} \begin{bmatrix} c_0 \\ c_1 \\ c_2 \end{bmatrix} = \begin{bmatrix} n_1 \\ n_2 \\ \vdots \\ n_m \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_m \end{bmatrix}$$

or

$$A\vec{c} = \vec{n} + \vec{\varepsilon}$$

The solution to this problem is of course:

$$\vec{c} = (A^T A)^{-1} A^T \vec{n}$$

Using these estimated coefficients, we can then plug in any new age α and predict the number of friends using the original quadratic relationship – i.e.,

$n = c_0 * \alpha^2 + c_1 * \alpha + c_2$

(b) You realize that just age is not a perfect predictor of the number of friends – clearly there are other factors that influence this. In fact, you realize people who live in urban areas tend to have more friends than people who live in rural areas. So you develop a metric called "urbanity" (u) that maps every location to a number from 1 to 10 where 10 is most urban and 1 is the most rural setting. You expect to have a linear relationship between the number of friends of a user and the degree of urbanity u_i of the ith user's location. How would you augment your model above to account for this? Now, if you have a new user come in with age α and urbanity u, how would you predict their number of friends?

Solution:

There are two potential interpretations for what the effect of "u" would be given the guidance of a "linear" relationship. Let's first look at a version where u has a multiplicative effect on number of friends; we will then look at a version where u is an additive effect.

<u>Multiplicative:</u>
All we have to do is augment our original quadratic model to include a scale factor depending on the urbanity u:

$n_i = u_i * (c_0 * a_i^2 + c_1 * a_i + c_2)$

We will still use a least squares solution to find the best fit coefficients c_0, c_1, and c_2 by solving the following problem:

$$\begin{bmatrix} u_1 a_1^{\,2} & u_1 a_1 & u_1 \\ u_2 a_2^{\,2} & u_2 a_2 & u_2 \\ \vdots & & \\ u_m a_m^{\,2} & u_m a_m & u_m \end{bmatrix} \begin{bmatrix} c_0 \\ c_1 \\ c_2 \end{bmatrix} = \begin{bmatrix} n_1 \\ n_2 \\ \vdots \\ n_m \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_m \end{bmatrix}$$

or

$A_u \vec{c} = \vec{n} + \vec{\varepsilon}$

and hence:

$\vec{c} = (A_u^{\,T} A_u)^{-1} A_u^{\,T} \vec{n}$

As in part (a), we can then predict the number of friends a new user will have by plugging their α and u in to the augmented model – i.e.:

$n = u*(c_0*\alpha^2 + c_1*\alpha + c_2)$

Additive:

Now all we have to do is augment our original quadratic model to include an additive term depending on the urbanity u:

$n_i = c_0*a_i^2 + c_1*a_i + c_2 + c_3*u_i$

We will once again use a least squares solution to find the best fit coefficients c_0, c_1, c_2, and c_3 by solving the following problem:

$$\begin{bmatrix} a_1^{\,2} & a_1 & 1 & u_1 \\ a_2^{\,2} & a_2 & 1 & u_2 \\ \vdots & & & \\ a_m^{\,2} & a_m & 1 & u_m \end{bmatrix} \begin{bmatrix} c_0 \\ c_1 \\ c_2 \\ c_3 \end{bmatrix} = \begin{bmatrix} n_1 \\ n_2 \\ \vdots \\ n_m \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_m \end{bmatrix}$$

or

$A_u \vec{c} = \vec{n} + \vec{\varepsilon}$

and hence:

$\vec{c} = (A_u^{\,T} A_u)^{-1} A_u^{\,T} \vec{n}$

As in part (a), we can then predict the number of friends a new user will have by plugging their α and u in to the augmented model – i.e.:

$n = c_0*\alpha^2 + c_1*\alpha + c_2 + c_3*u$

5. Medical Imaging

It turns out that solving underdetermined systems of equations can be very useful in medical imaging applications. Specifically, we are often in a situation where we want to image parts of the body in order to find abnormalities in the tissue. One of the techniques to do this is called tomography, and we described the basics behind in lecture. Tomography uses the fact that different materials in the body absorb different amounts of light, and thus readings of the absorption of beams of light from various directions onto the tissue can be used to reconstruct an image of the tissue.

We won't be developing a true tomography system here, but let's consider a simplified model that utilizes the same basic principles. Consider an unknown vector $x = [x_1\ x_2\ \ldots\ x_n]^T$ that represent the "image" of the tissue (i.e., samples of light absorption of different parts of the body) and where n = 10^8. Let's assume that if the tissue is normal and healthy – which should be the case for the large majority of the pixels in the image – the absorption of light is essentially equal to 0. Let's further assume that if there is e.g. a blood clot (or some other abnormality) in the tissue, the absorption value is very high.

Because each absorption measurement may take anywhere from several ms to even several seconds in order to achieve reasonable accuracy, it is typically infeasible to get 10^8 or more measurements in order to estimate the value of every pixel in the image using a technique like least squares. Because of this, we would like to use the fact that number of blood clots if very low, and thus the number of non-zero entries within the vector x should also be very low. This situation can be approximated by thinking about the vector x as having a small norm.

Although we can't measure the entire tissue image directly, let's say that we are able to get 10^3 measurements of the total absorption for a volume of tissue that spans multiple pixels in the original image. In other words, the result of each absorption measurement b_i is equal to the dot product of a "sampling vector" a_i (note that a_i is a column vector) and the image vector x.

(a) Set up a matrix-vector equation using the a_i's, b_i's and x that captures the measurements that were taken.

Solution:

$$\begin{bmatrix} a_1^T \\ a_2^T \\ \vdots \\ a_{1000}^T \end{bmatrix} x = \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_{1000} \end{bmatrix} \rightarrow Ax = b$$

(b) Recalling that a vector with a small number of non-zero entries should have a small norm, how could you "solve" the system of equations you set up in part (a) to find a good estimate for the image vector x?

Solution:

We're looking for the solution that has the smallest norm while satisfying the constraints created by the original measured values. This solution is of course the "least norm" solution – i.e.:

$$x = A_u^T (A_u A_u^T)^{-1} b$$

6. Practice with Underdetermined Systems

Note that you can find the numerical solutions for the problems below using a computer; on the actual exam you will not be asked to manually invert anything larger than a 2x2 matrix. We would however encourage you to compute by hand the intermediate terms (e.g., AA^T) of the minimum norm solution for the problems below.

(a) Find the minimum norm *x* for the system

$$\begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 & 1 \\ 1 & 1 & 1 & 1 & 0 \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \\ x_5 \end{bmatrix} = \begin{bmatrix} 10 \\ 8 \\ 8 \end{bmatrix}$$

Solution:

$$\begin{bmatrix} x_1 & x_2 & x_3 & x_4 & x_5 \end{bmatrix}^T = \begin{bmatrix} 2 & 2 & 2 & 2 & 2 \end{bmatrix}^T$$

(b) Find the minimum norm x for the system

$$\begin{bmatrix} 1 & 1 & 1 & 0 & 1 \\ 1 & 1 & 0 & 1 & 1 \\ 1 & 1 & 1 & 1 & 0 \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \\ x_5 \end{bmatrix} = \begin{bmatrix} 10 \\ 8 \\ 8 \end{bmatrix}$$

Solution:

$$\begin{bmatrix} x_1 & x_2 & x_3 & x_4 & x_5 \end{bmatrix}^T = \begin{bmatrix} 2.6 & 2.6 & 2.4 & 0.4 & 2.4 \end{bmatrix}^T$$