P-- Question 1

1. 1. For f(x) to hold, f(x) >= 0 for all x and generally, integral from -inf to inf of f(x) dx = 1.  
        
      Given the range, we first show f(x) >= 0 for all x (trivial) and integrate from *1* to inf of f(x) dx, and we can use the range of theta (greater than one) to eventually get (1-θ)/(1-θ) = 1.
   2. *θ =*

Second derivative is negative for all theta

* 1. (since we have unknown variance)  
     Taking for : (since n is large enough for to be approximated by )

There is a 95% chance that the population mean lies between [1.329. 1.671].

Frequentist interpretation: amongst all the possible samples we may observe, and the corresponding intervals , 95% contain the true population mean.

1. **Three different attempts** are presented below. First one is a broken attempt, second one appears to be correct by taking and third one appears to be correct by taking .  
   ---  
   We can model this as a Binomial distribution with X~B(100, p), where p is unknown. As n > 30, we can use the Central Limit Theorem to approximate this to X~N(100p, 100pq), where q=(1-p). So X~N(50, 25).  
     
   Given, "highest number of times that heads is allowed to appear", assume one-tail test, although usually you'd do a two-tail for whether a coin is biased.

For a 99% confidence interval with a one-tailed test, .  
=2.326 and substituting and solving we get, *which doesn't seem right at all*. I guess basd on this we could do and say that 6100-50100p(1-p)1009.2 is the maximum number of heads? But that does seem very much out of range for the 99% confidence interval.  
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For 1% significance level (99% confidence), rejection region is z > 2.326.

For H0 not to be rejected, number of heads *h* needs to satisfy

So *h* < 2.326 \* + 50 = 61.63

--- Slight variant on the solution above, if you find it more intuitive to work directly with the mean number of heads (essentially boils down to the same thing).

Xi ~ Bernoulli(0.5), so by CLT we have X= sum(Xi) ~ N(nμ, nσ) = N(50, 25).

For 1% significance level (99% confidence), rejection region is z > 2.326.t

For H0 not to be rejected, number of heads *h* needs to satisfy

So *h* < 2.326 \* + 50 = 61.63

**(4th Approach)**: Chi-squared Goodness of Fit Test with Binomial(0.5, 100) as the null hypothesis.

Resulted in me getting 62.87 as the value, which was “floored” to 62 (as has to be an integer), which is the same answer above.

Below are the “Observed” and “Expected” values I used, where ‘h’ is the #Heads.

Sample mean is: h/100 (having a realisation of ‘1’ for head and ‘0’ for tail)

Observed Values: h | 100 – h

Expected Values: 50 | 50

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**As a side note in my SGTs, Mario said (not this question but a similar one) that you could get away with doing a Two Sided test or one sided test when it’s unclear so long as you justify why you’re doing it the way you are.**

1. Apply chi-squared distribution! As usual, make sure that the expected value of each row is more than 5 or merge the ranges.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Flavour | Count () |  |  |  |
| Blueberry | 13 | 12.5 | 0.5 | 0.02 |
| Cherry | 15 | 12.5 | 2.5 | 0.5 |
| Green apple | 12 | 12.5 | 0.5 | 0.02 |
| Banana | 19 | 12.5 | 6.5 | 3.38 |
| Grass | 11 | 12.5 | 1.5 | 0.18 |
| Sausage | 8 | 12.5 | 4.5 | 1.62 |
| Black pepper | 16 | 12.5 | 3.5 | 0.98 |
| Toothpaste | 6 | 12.5 | 6.5 | 3.38 |
|  | 100 | 100 | - | 10.08 |

so at the 95% confidence interval for a one tailed test (as chi-squared has to be one-tailed),

Each flavour equally likely

Each flavour not equally likely

As the test statistic 10.08 is not greater than 14.07, there is insufficient evidence to reject the hypothesis. Hence, each flavour is equally likely.

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### Question 2

1. 1. P(defective)   
      = P(site 1 AND defective) + P(site 2 AND defective) + P(site 3 AND defective)  
      = P(defective | site 1)P(site 1) + P(defective | site2)P(site 2) + P(defective | site3)P(site 3)  
      = (0.001)(0.6) + (0.25)(0.003) + (0.15)(0.004)  
      = 0.00195
   2. P(site 1 | defective) = P(site 1 AND defective ) / P(defective) ≈ 0.308  
      P(site 2 | defective) = P(site 2 AND defective ) / P(defective) ≈ 0.385  
      P(site 3 | defective) = P(site 3 AND defective ) / P(defective) ≈ 0.308

* 1. why

*PGF of X is G(z) = E(zx) = = pz + (1-p)z0 = 1 - p + pz*

* 1. how do you even remember proofs

*PGF of Sn is GSn(z) = E(z) = E(zx) = E(zx) = Gx(z)*

* 1. *Could be proven using swum of r. variables Xi ~ Bernoulli(p)?*

By using the previous thingy:

GSn(z) = GXi(z) = (1 - p + pz) = (1 - p + pz)n

E(X) = G'(1) = n(1 - p + p\*1)n - 1p = np

Var(X) = G''(1) + G'(1) - [G'(1)]2 = n\*(n - 1)\*(1 - p + p \* 1)n - 2p2 + np - (np)2=

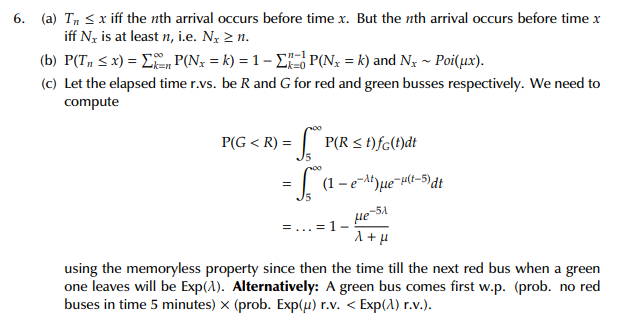
= n\*(n - 1)\*p2+np-(np)2 = np(1 - p)

* 1. We have the sum of 3 binomially distributed random variables.

For independent R.Vs, if X = X1 + X2 + X3, E(X) = E(X1) + E(X2) + E(X3), and similar for variance, Var(X) = Var(X\_1) + Var(X\_2) + Var(X\_3).

E(X) = 83, sd =√( 40 \* 0.4 \* (1-0.4) + 50 \* 0.5 \* (1-0.5) + 60 \* 0.7 \* (1-0.7))

=√34.7 ≈ 5.89  
\*

1. Tutorial 4, Ex6
   1. 

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FUCKING GOOD LUCK NEXT YEAR MAKING THE MARK SCHEME FOR THE 2019 PAPER BITCHES