**MCS 253**

**HW 5**

[Read this first on what to submit for a homework.](https://drive.google.com/open?id=1vvTZzNrXNrxFCFVuzryEuAX6c8rfGERsEc7t4TS1vAA)

**HW 5.1 (MANDATORY 50 points)**

Implement an AVL tree whose node values are integers. It should be able to support three operations: ***insert***, ***find***, and ***delete***. Implement any replacement operations to use the **predecessor**.

Input:

* a sequence of commands to stdin that ***insert***, ***find***, or ***delete*** an integers.

Output:

* for each command executed, a list of the node-values within the tree that are traversed to find the initial position in the tree to begin to process the command.
  + for ***insert*** it will be the list of values traversed before initially inserting the new value, followed by the value inserted
  + for ***find***, it will be the list of nodes traversed before finding the value we are looking for or before being able to assert the value is not present in the tree. Asserts whether value was found or not.
  + for ***delete***, it will be the list of nodes traversed before finding the node to be deleted or before being able to assert the value is not present in the tree. Asserts whether the node to be deleted was found or not.

Example:

input:

insert 50

insert 25

insert 10

insert 5

insert 7

insert 3

insert 30

insert 20

insert 8

insert 15

find 10

find 12

delete 4

delete 20

find 22

delete 50

find 30

delete 10

find 7

output:

50 (inserted)

50 25 (inserted)

50 25 10 (inserted)

25 10 5 (inserted)

25 10 5 7 (inserted)

25 7 5 3 (inserted)

7 25 50 30 (inserted)

7 25 10 20 (inserted)

7 25 10 8 (inserted)

7 25 10 20 15 (inserted)

10 (found)

10 25 20 15 (not found!)

10 7 5 3 (not found!)

10 25 20 (deleted)

10 25 15 (not found!)

10 25 50 (deleted)

10 25 30 (found)

10 (deleted)

8 5 7 (found)

**HW 5.2 (50 points)**

Given hereditary information about occurrence of dimples (which is a dominant trait) in root ancestors, answer queries about a family member’s chance of having dimples.

Let **D** denote the dominant allele for dimples and **d** denote the recessive allele for not having dimples.

If the genotype and phenotype of a root ancestor is unknown, assume ¼ chance of **DD** (dimples), ½ chance of **Dd** (dimples), and ¼ chance of **dd** (no dimples). If the genotype of a root ancestor is unknown, but it is known they have dimples, assume ⅓ chance **DD** and ⅔ chance **Dd**. If a root ancestor does not have dimples, we know they have the genotype of **dd**.

([some background](https://www.khanacademy.org/science/high-school-biology/hs-classical-genetics/hs-introduction-to-heredity/v/introduction-to-heredity))

Input:

* hereditary information via stdin

Output:

* probability of each member having dimples

Example:

input format: [name] [hereditary information (if root ancestor) or parents if descendant]

hereditary information can be: **DD**, **Dd** (or **dD**), **dd**, **dimples**, **no dimples**, or **unknown**

input:

Bob unknown

Mary DD

Megan dimples

Jane Bob Mary

Brenden Bob Mary

Sam Brenden Megan

output:

Bob: 75.0%

Mary: 100.0%

Megan: 100.0%

Jane: 100.0%

Brenden 100.0%

Sam 91.7%

**Possible LeetCode Substitutions (25 points each)**

**Important Notes:**

* You may only substitute 50pts-worth of LeetCode problems

Possible LeetCode Problems:





