COMP 204

Review and final exam preparation

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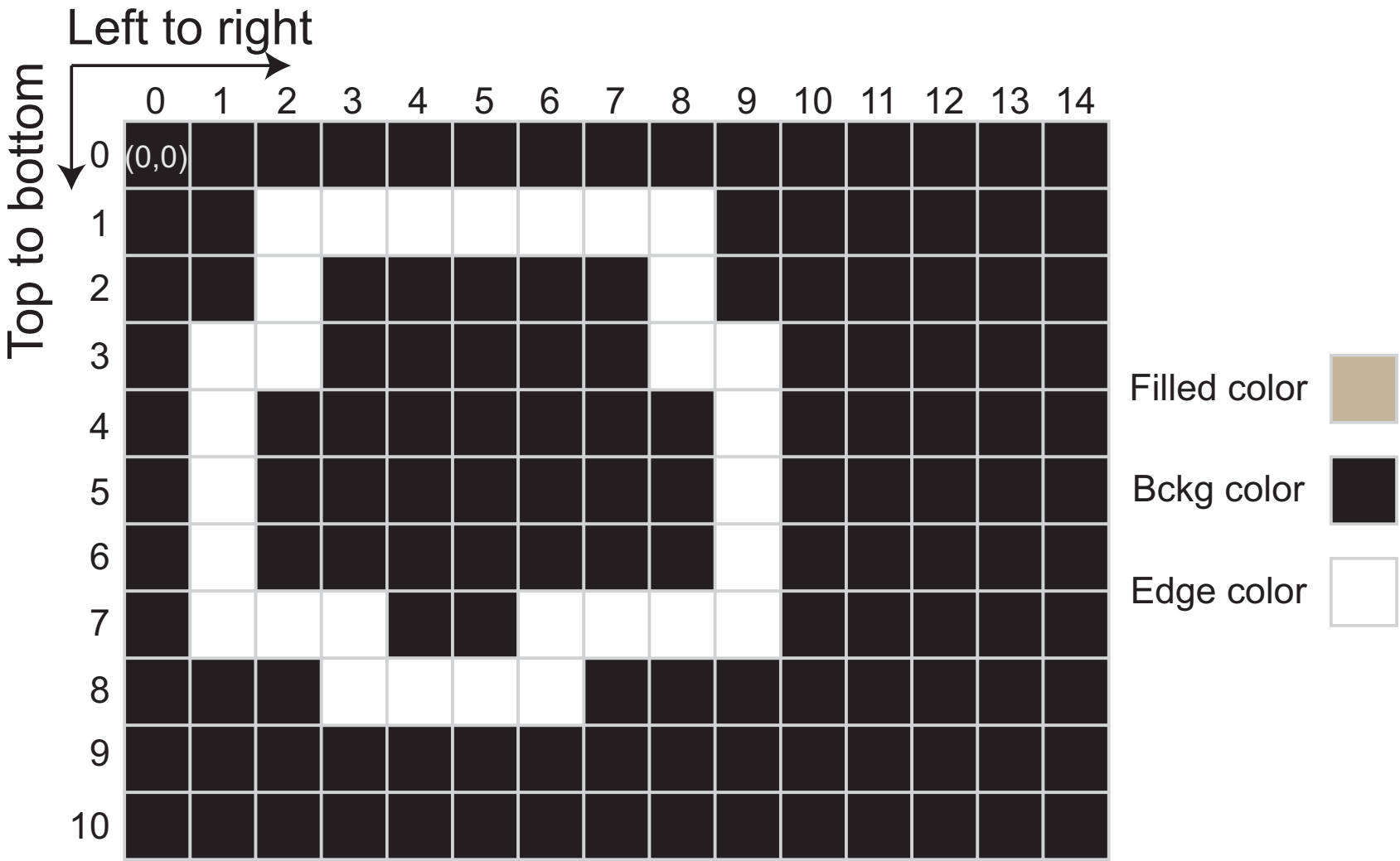
Outline

Seed filling algorithm (revisit)

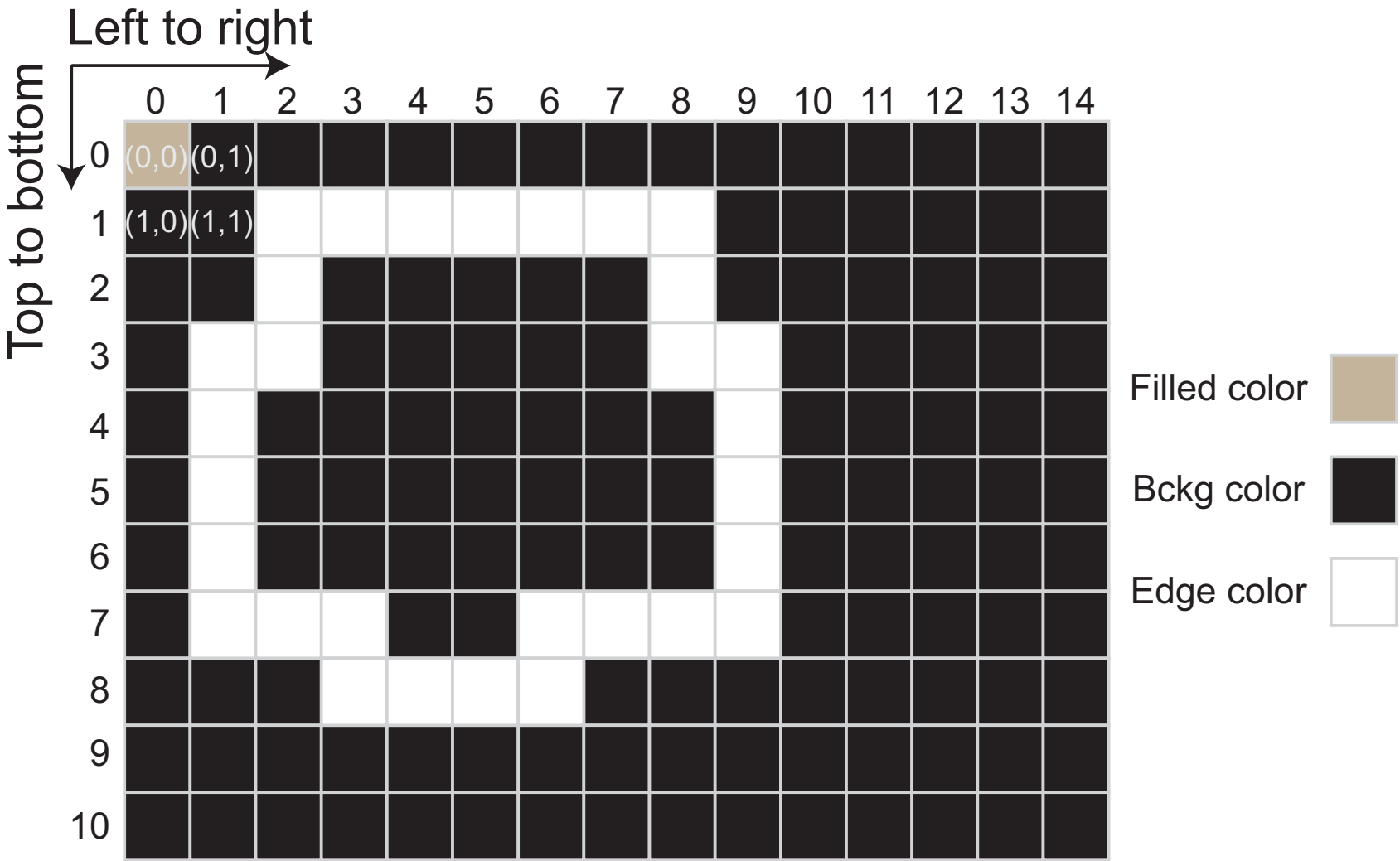
Final exam (April 30 6:30 PM)

In-class practice questions

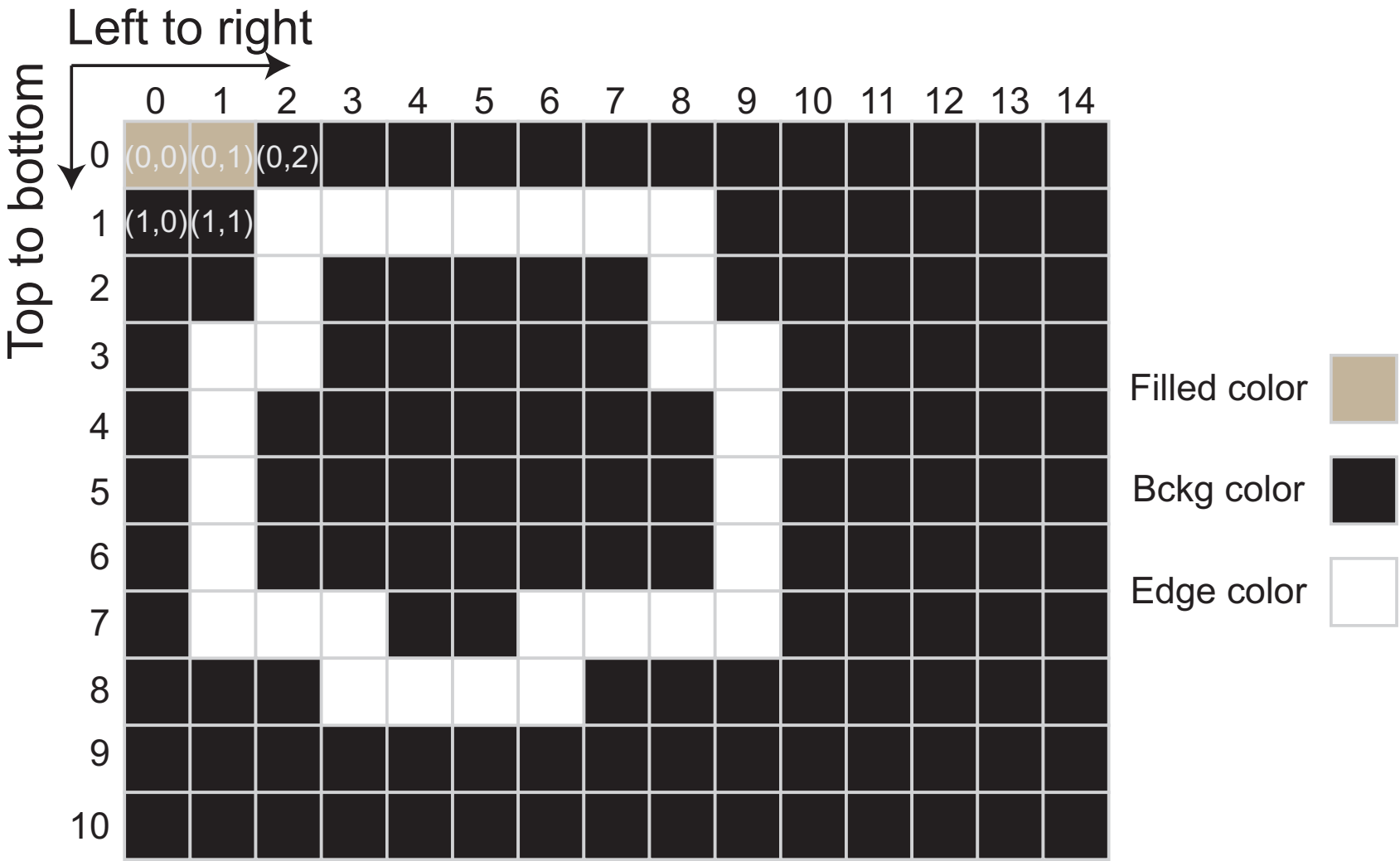
```
front: [(0,0)]
```


Left to right
Top to bottom
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
0 1 2 3 4 5 6 7 8 9 10
(0,0)
Filled color
Bckg color
Edge color

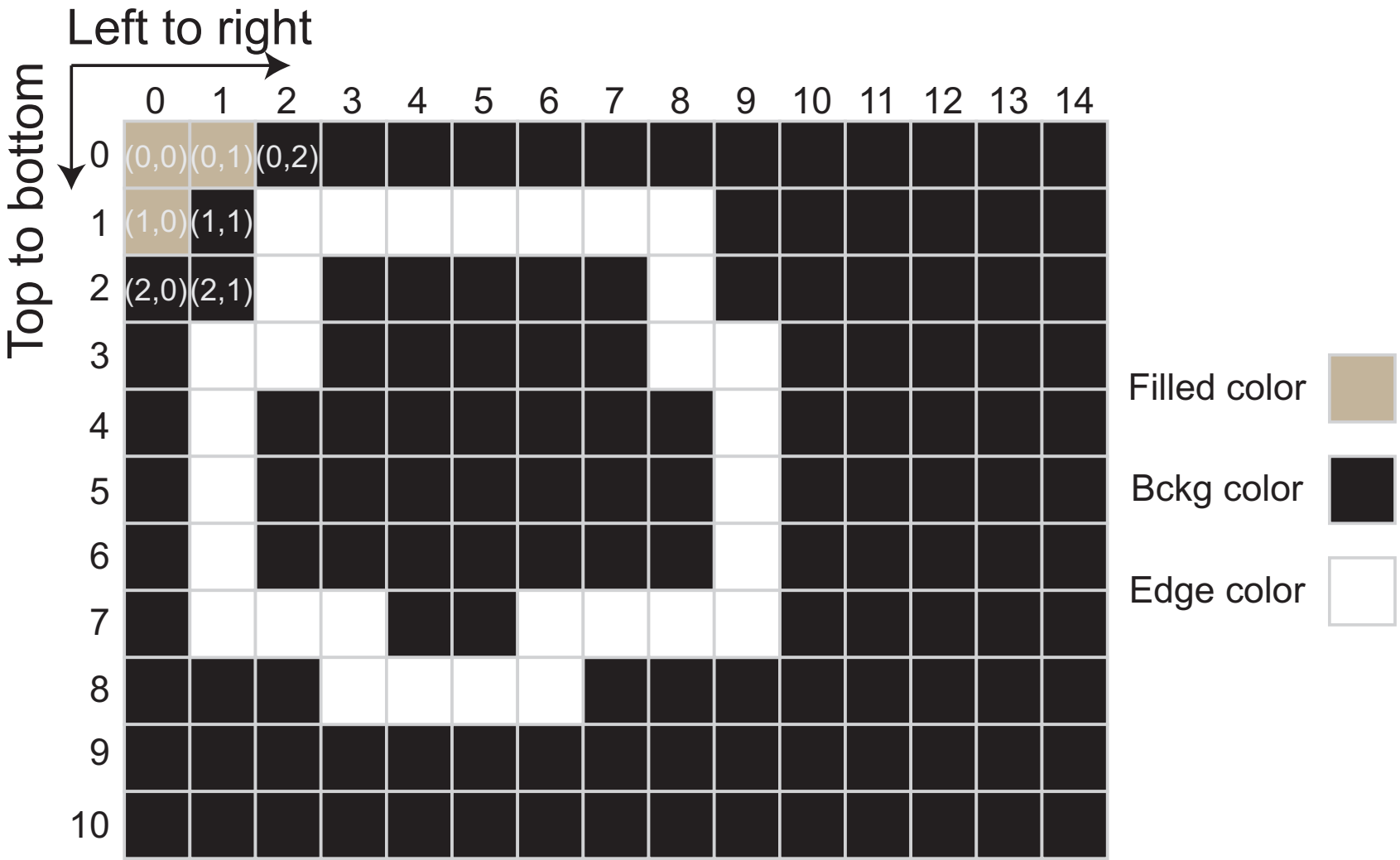
```
front: [(0,1),(1,0),(1,1)]
```



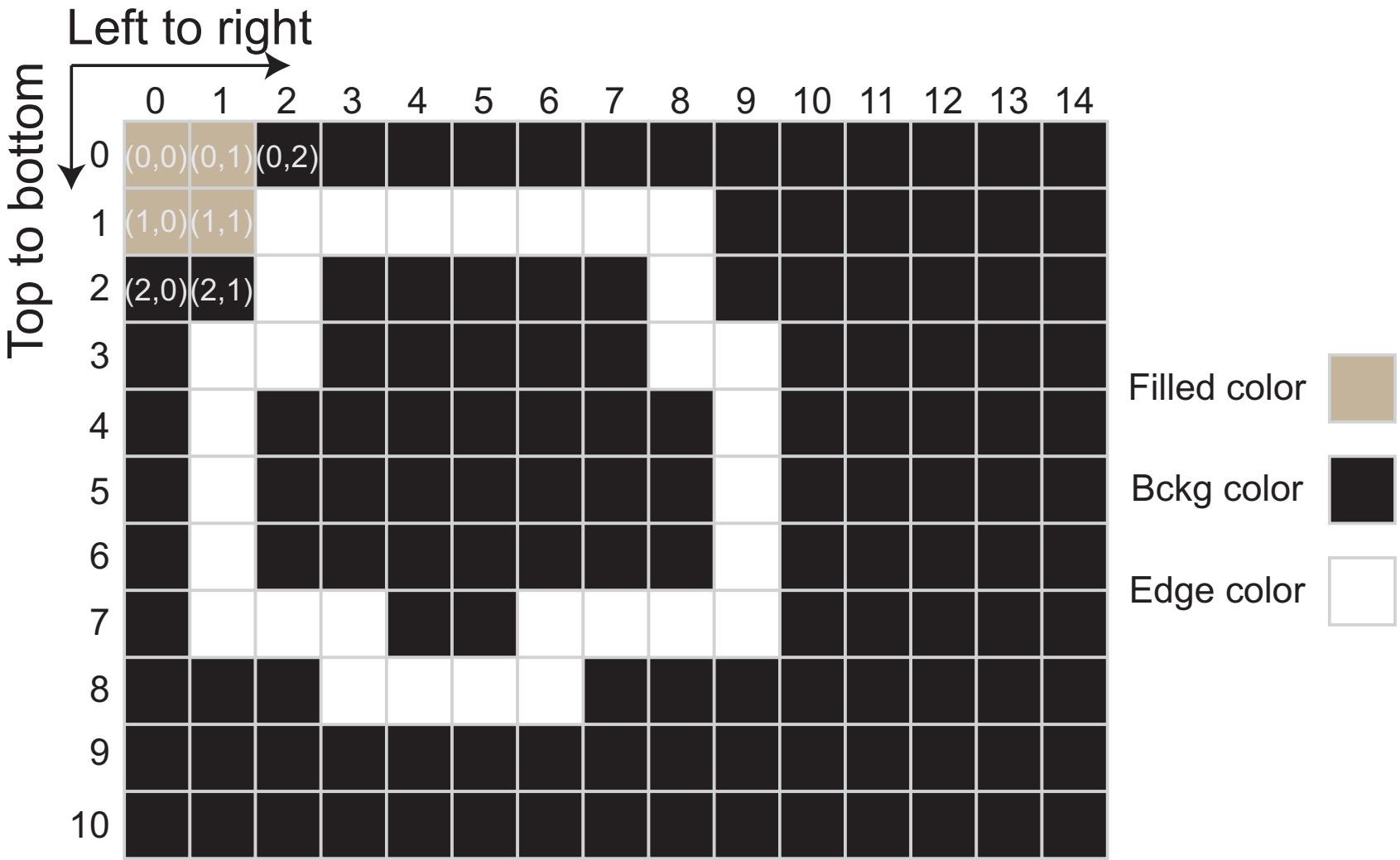
```
front: [(1,0),(1,1),(0,2)]
```



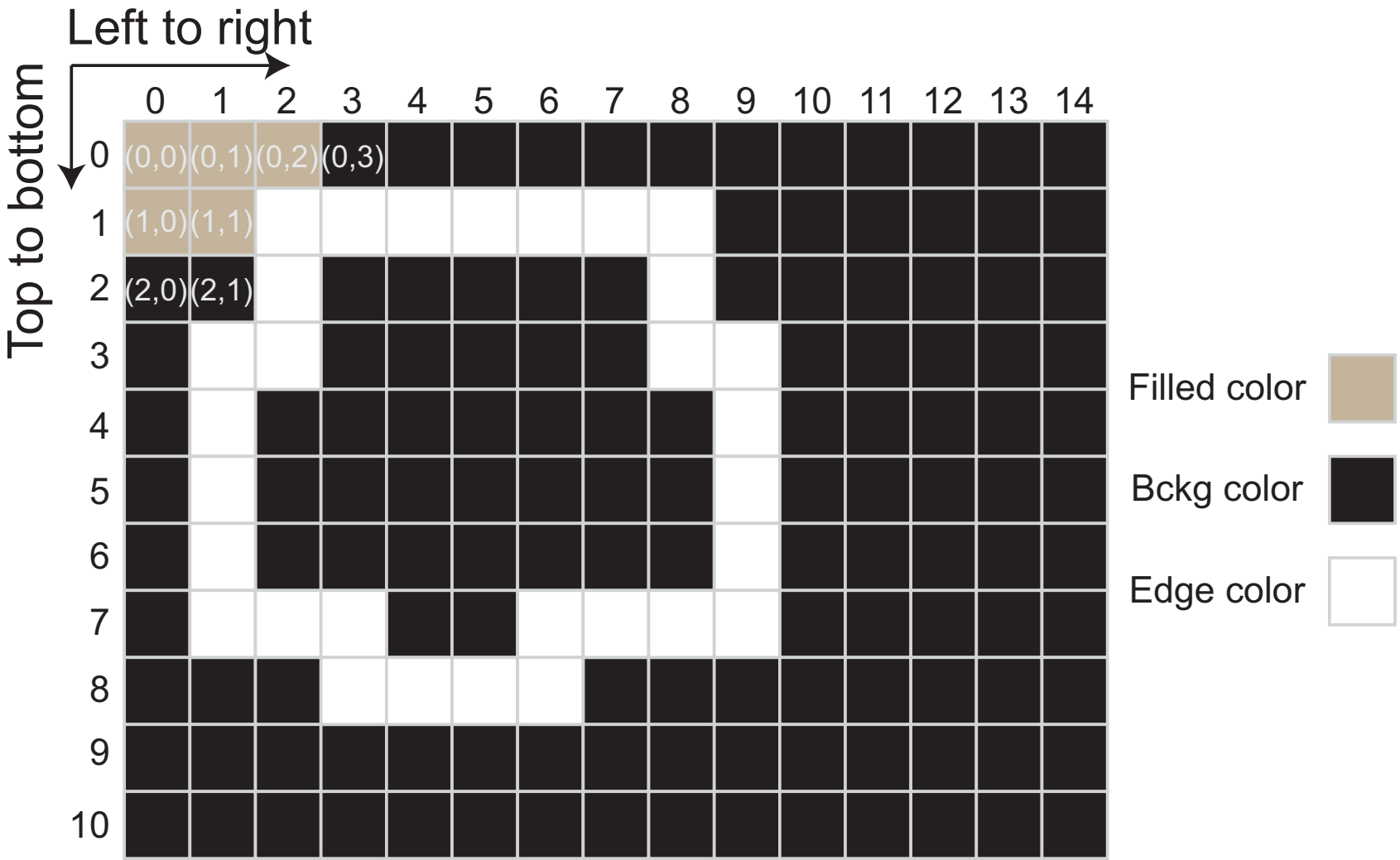
```
front: [(1,1),(0,2),(2,0),(2,1)]
```



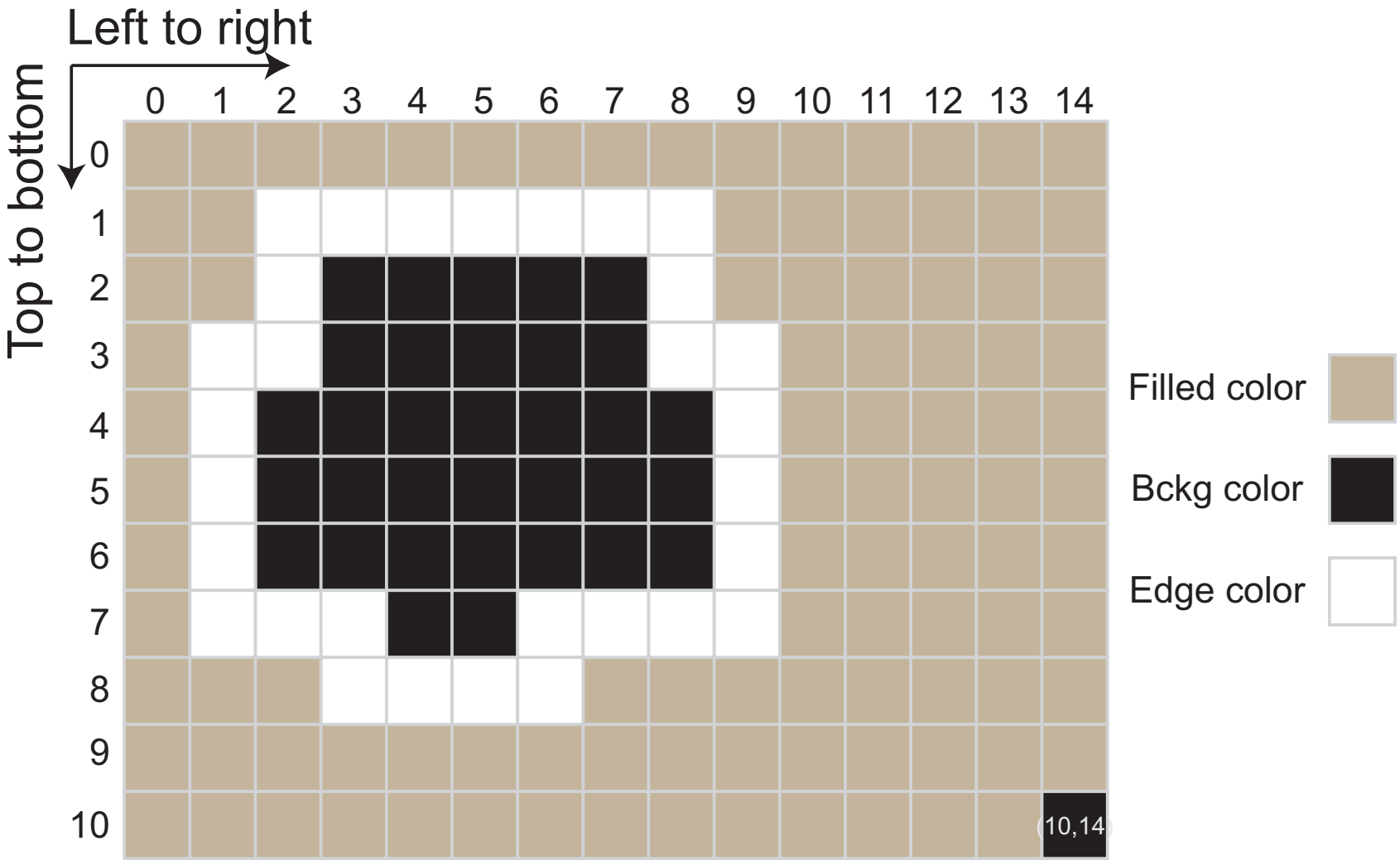
```
front: [(0,2),(2,0),(2,1)]
```



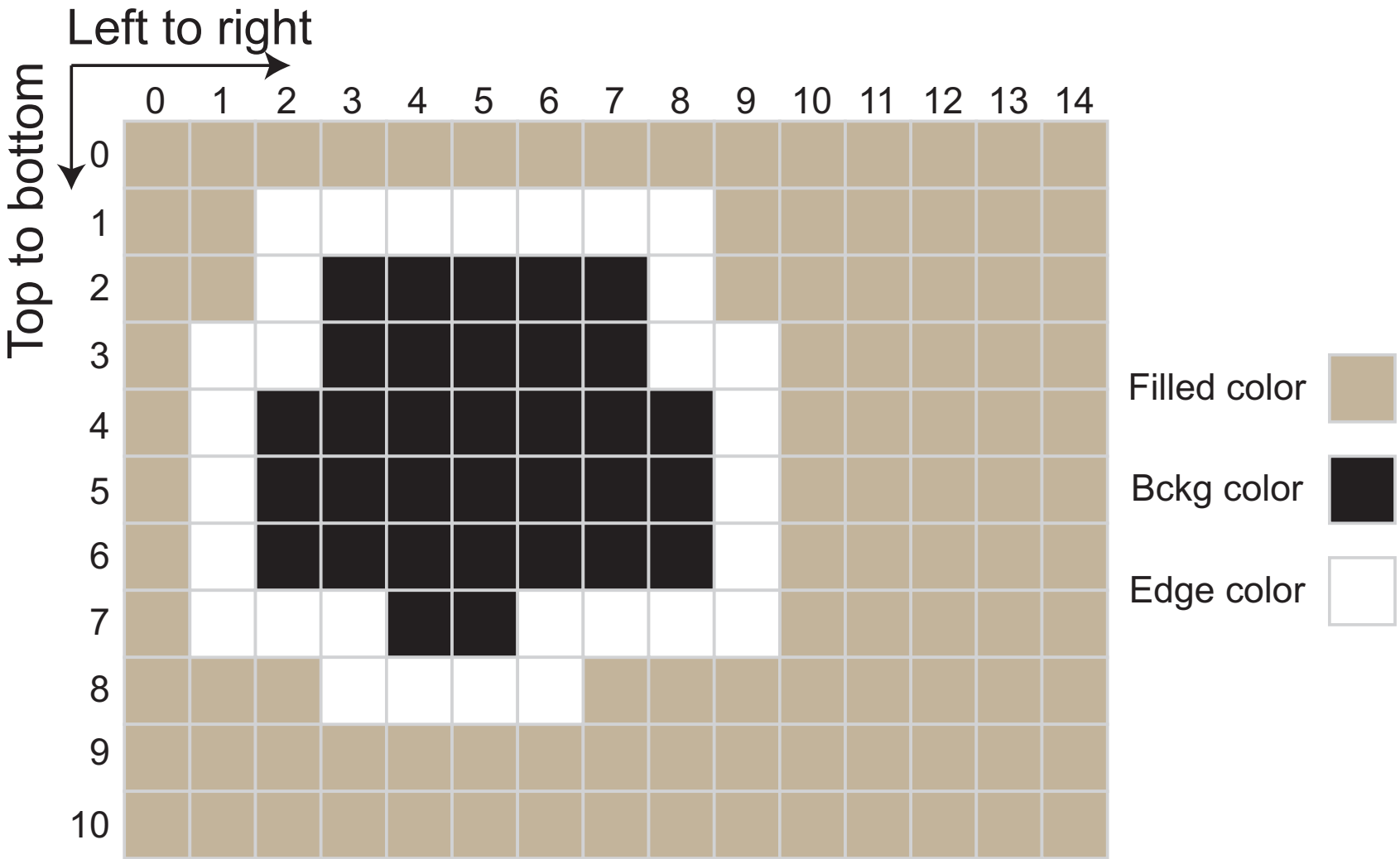
```
front: [(2,0),(2,1),(0,3)]
```



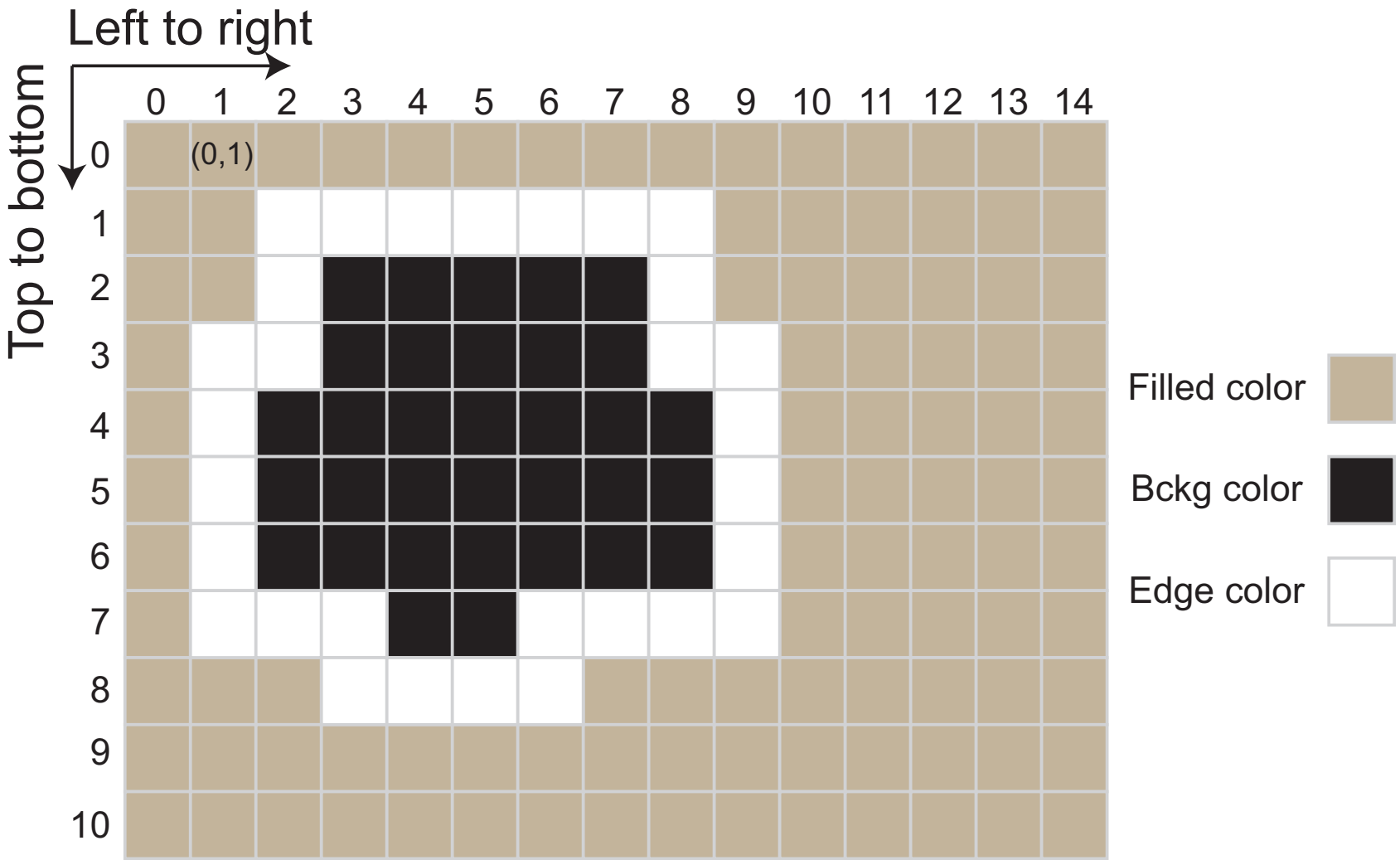
```
front: [(10,14)]
```


Left to right
Top to bottom
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
0 1 2 3 4 5 6 7 8 9 10
(10,14)
Filled color
Bckg color
Edge color

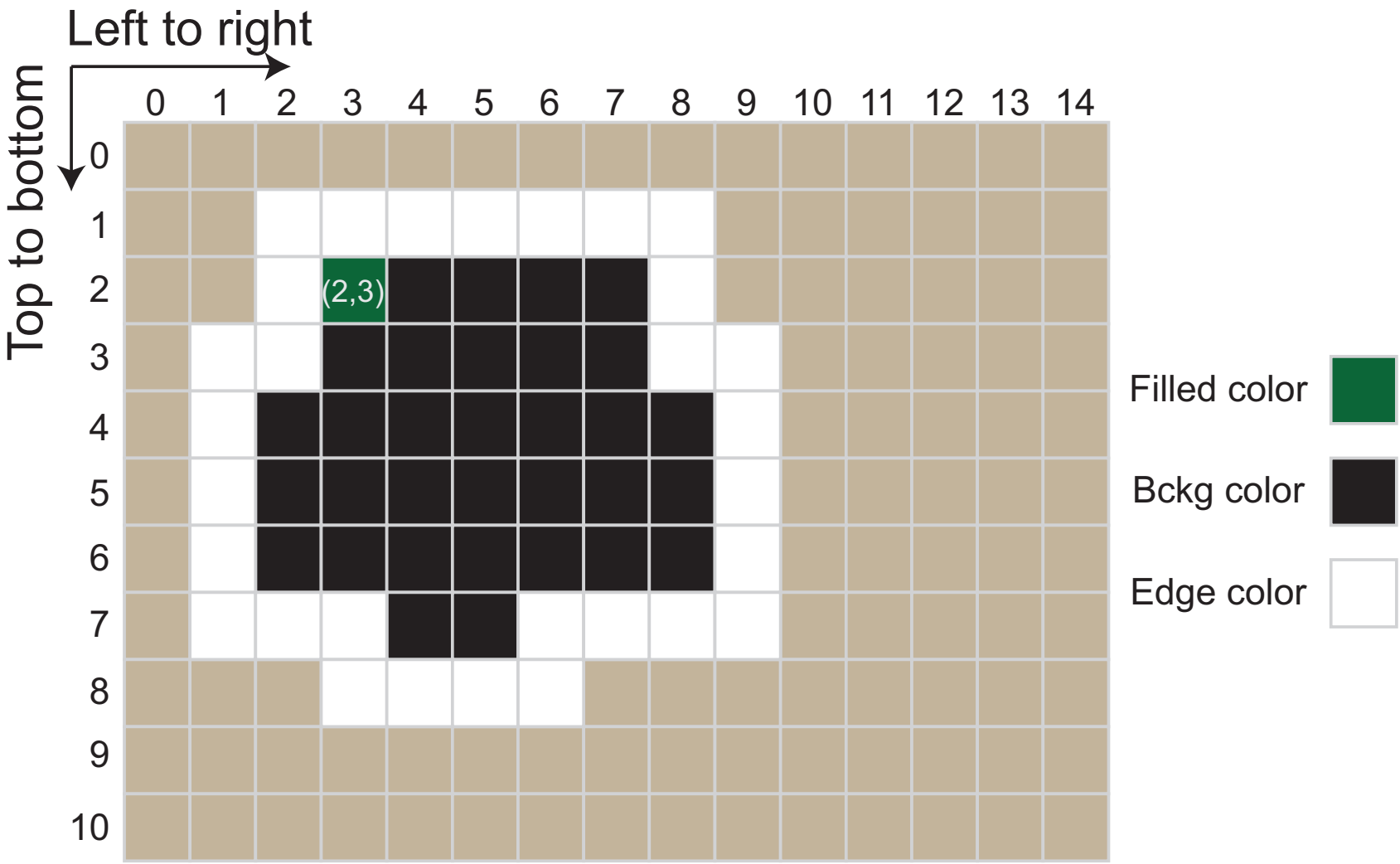
```
front: []
```


Left to right
Top to bottom
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
0 1 2 3 4 5 6 7 8 9 10
Filled color
Bckg color
Edge color

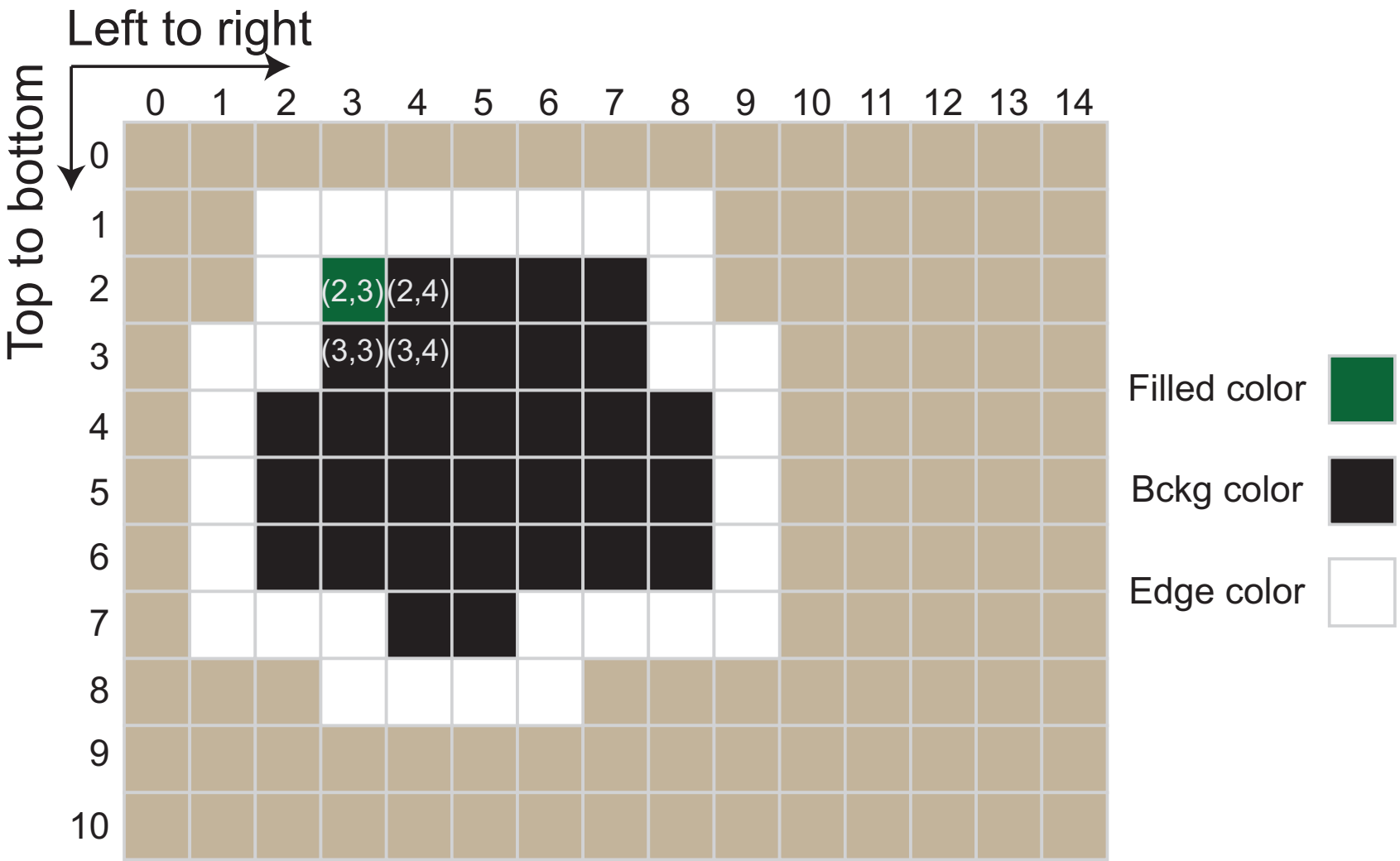
- We just came back from the `seedfill` function!
- The “cell” size is the number of the pixels outside of the cell (too big as a “cell”)
- The next pixel to go: i = 0, j = 1
- But pixel (0, 1) is already filled with color (i.e., no longer background)
- We keep going until we see another background pixel: (2,3)



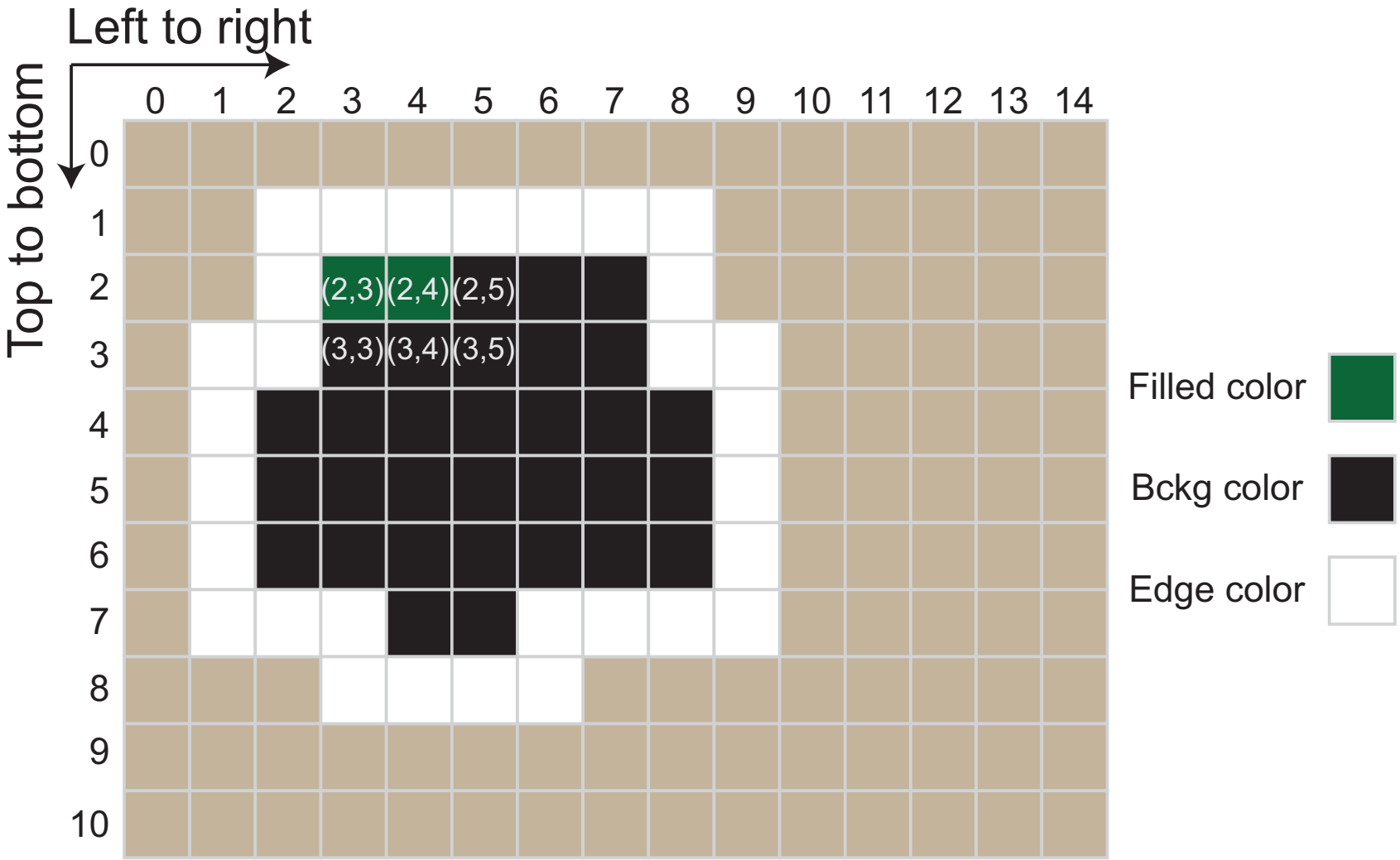
```
front: [(2,3)]
```


Left to right
Top to bottom
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
0 1 2 3 4 5 6 7 8 9 10
(2,3)
Filled color
Bckg color
Edge color

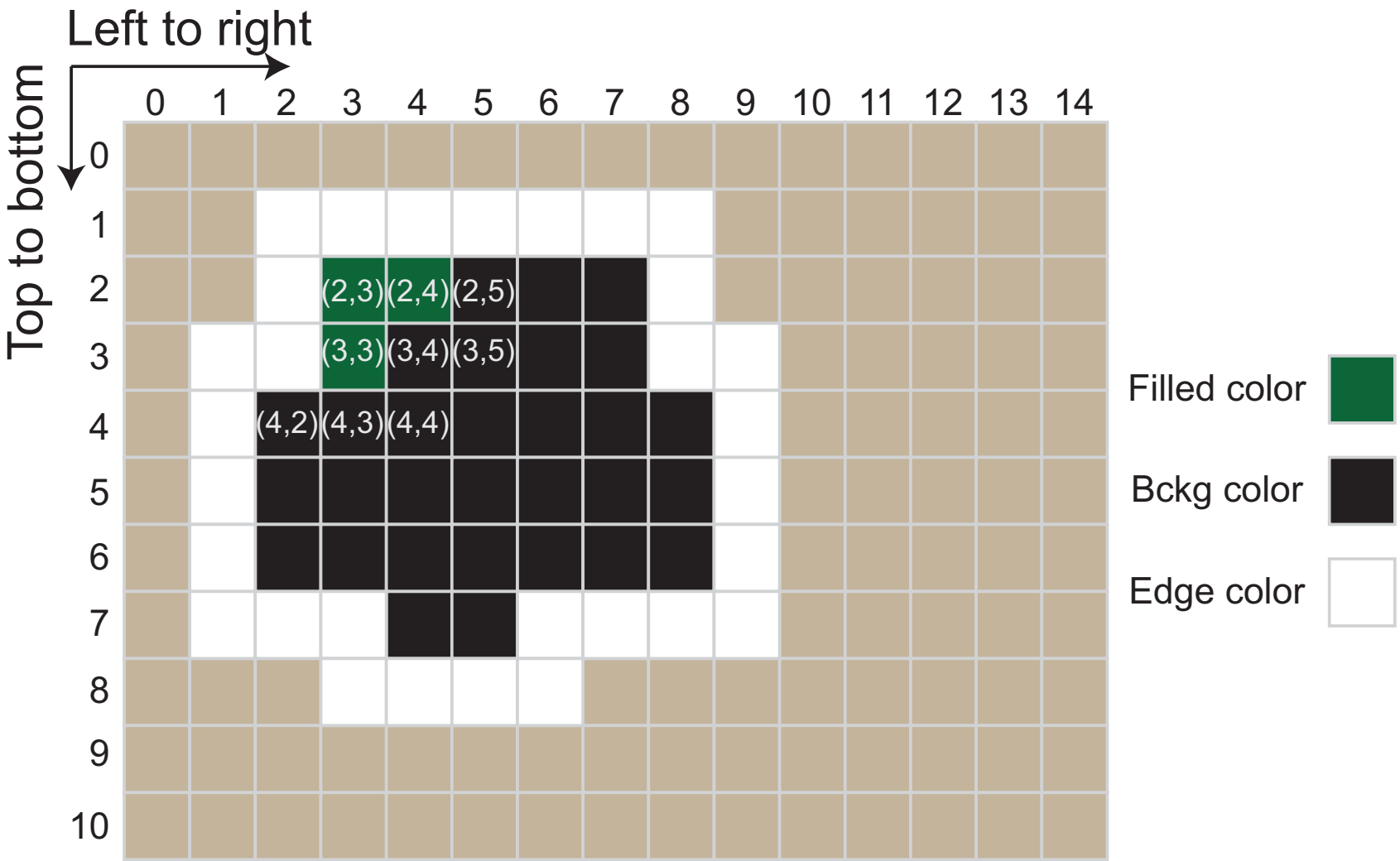
```
front: [(2,4),(3,3),(3,4)]
```



```
front: [(3,3),(3,4),(2,5),(3,5)]
```



```
front: [(3,4),(2,5),(3,5),(4,2),(4,3),(4,4)]
```



Seed filling implementation

```
23  def seedfill(im, seed_row, seed_col, fill_color,bckg):
24      """
25      im: The image on which to perform the seedfill
    ↪   algorithm
26      seed_row and seed_col: position of the seed pixel
27      fill_color: Color for the fill
28      bckg: Color of the background, to be filled
29      Returns: Nothing
30      Behavior: Modifies image by performing seedfill
31      """
32      size=0  # keep track of patch size
33      n_row, n_col, foo = im.shape
34      front=[(seed_row,seed_col)]  # initial front
35
36      while len(front)>0:
37          r, c = front.pop(0)  # remove 1st element of front
38          if np.array_equal(im[r, c,:],bckg):
39              im[r, c]=fill_color  # color pixel
40              size+=1
41              # look at all neighbors
42              for i in range(max(0,r-1), min(n_row,r+2)):
43                  for j in range(max(0,c-1),min(n_col,c+2)):
44                      # if background, add to front
45                      if np.array_equal(im[i,j,:], bckg)
                        ↪  and\
46                         (i,j) not in front:
47                          front.append((i,j))
48      return size
```

Seeding from all possible starting pixel...

```
137 min_cell_size=100  # based on prior knowledge
138 max_cell_size=300  # based on prior knowledge
139 n_cells=0
140 # look for a black pixel to seed the filling
141 for i in range(image.shape[0]):
142     for j in range(image.shape[1]):
143         if np.array_equal(edge[i,j,:],(0,0,0)):
144             rand_color = (random.randrange(255),
145                           random.randrange(255),
146                           random.randrange(255))
147             size=seedfill_with_animation(edge, i ,j,
                ↪  rand_color, (0,0,0) )
148             if size>= min_cell_size and
                ↪  size<max_cell_size:
149                 n_cells+=1
150 print("Number of cells:",n_cells)
151
```

Outline

Seed filling algorithm (revisit)

Final exam (April 30 6:30 PM)

In-class practice questions

Final exam info

- Date: April 30, 6:30-9:30 PM; Location: TBD
- Weight: 35% of your final grade (or 55% if better than midterm grade for students who opted the second non-programming midterm assignment option)
- Closed book but 8.5 x 11 double-sided crib sheet allowed.
- Questions:
  - 9 multiple choice questions (total 27%). Answer on Scantron (**not on exam**). Follow instructions for each questions: For some questions you need to indicate the only ONE correct answer. For other questions you need to indicate ALL correct answers.
  - Answer the rest of the questions directly on exam
  - 8 short answer questions (7 questions each worth 4 points and 1 question worth 5 points) (total: 33%).
  - 1 bonus short answer question worth 5 point.
  - 4 long answer questions (10 point per question; total: 40%).

Final exam content

Main materials that are covered in the final exam include:

- Basics: functions, loops, variables, data types (string, list, tuple, dictionary, sets), difference between pass by copy and pass by memory addresses
- Algorithms: Searching (linear and binary search) and sorting (insertion and selection sort)
- Pattern searching by string indexing and regular expression (simple ones)
- Object oriented programming: class, attributes, class inheritance, class methods
- BioPython sequence handling covered in class (I will remind you what the methods are in the exam)
- Machine learning: know what supervised, unsupervised, reinforcement learning are, problems they can solve, TPR, FPR, overfitting, cross-validation, ROC, decision trees
- Image processing: basic understanding of going from a pixel in the image to numpy ndarray
- What to memorize? Nothing. Use cribsheet to note the

Preparing for the final exam

How best to prepare for the exam:

- Practice, practice, practice.
- Review all lecture notes, assignment solutions, midterm solutions
- Practice on the problems we've posted on MyCourses-Content
- Attend CSUS review session
- Come to my office hours:
  - Wednesday: 11:30-12:30

Outline

Seed filling algorithm (revisit)

Final exam (April 30 6:30 PM)

In-class practice questions

Functions

What prints out?

```
1  def myfun(x, y):
2      x = x + 1
3      y = y + 1
4      return x + y
5
6  x = 0
7  y = 1
8  z = myfun( myfun(x,y), x)
9  print(z)
```

Functions (pass by memory address)

What prints out?

```
1  def myfun(x, y):
2      x[0] = x[0] + 1
3      y[0] = y[0] + 1
4      return [x[0] + y[0]]
5
6  x = [0]
7  y = [1]
8  z = myfun( myfun(x,y), x)
9  print(z)
```

Linear and binary search

How to search number 9 in this list by linear search and binary search? [2,5,7,9,10]

Insertion and selection sort

How to sort the following list by insertion sort and selection sort?
[2,10,5,9,7]

Sequence alignment (A2)

Given match score $+3$, mismatch score -2, gap score -1. What's the similarity score between sequence GGC with sequence GTC?

List comprehension

Convert the following for loop into list comprehension with one line of code:

```
1 x = []
2 for i in range(5):
3     x.append(-2*i)
```

Object oriented programming: attributes

What are attributes in `Myclass`

```
1  class MyBus:
2      def __init__(self, stationID, passengers):
3          self.s = stationID
4          self.p = passengers
5          terminal = 0
```

Object oriented programming: methods

What prints out?

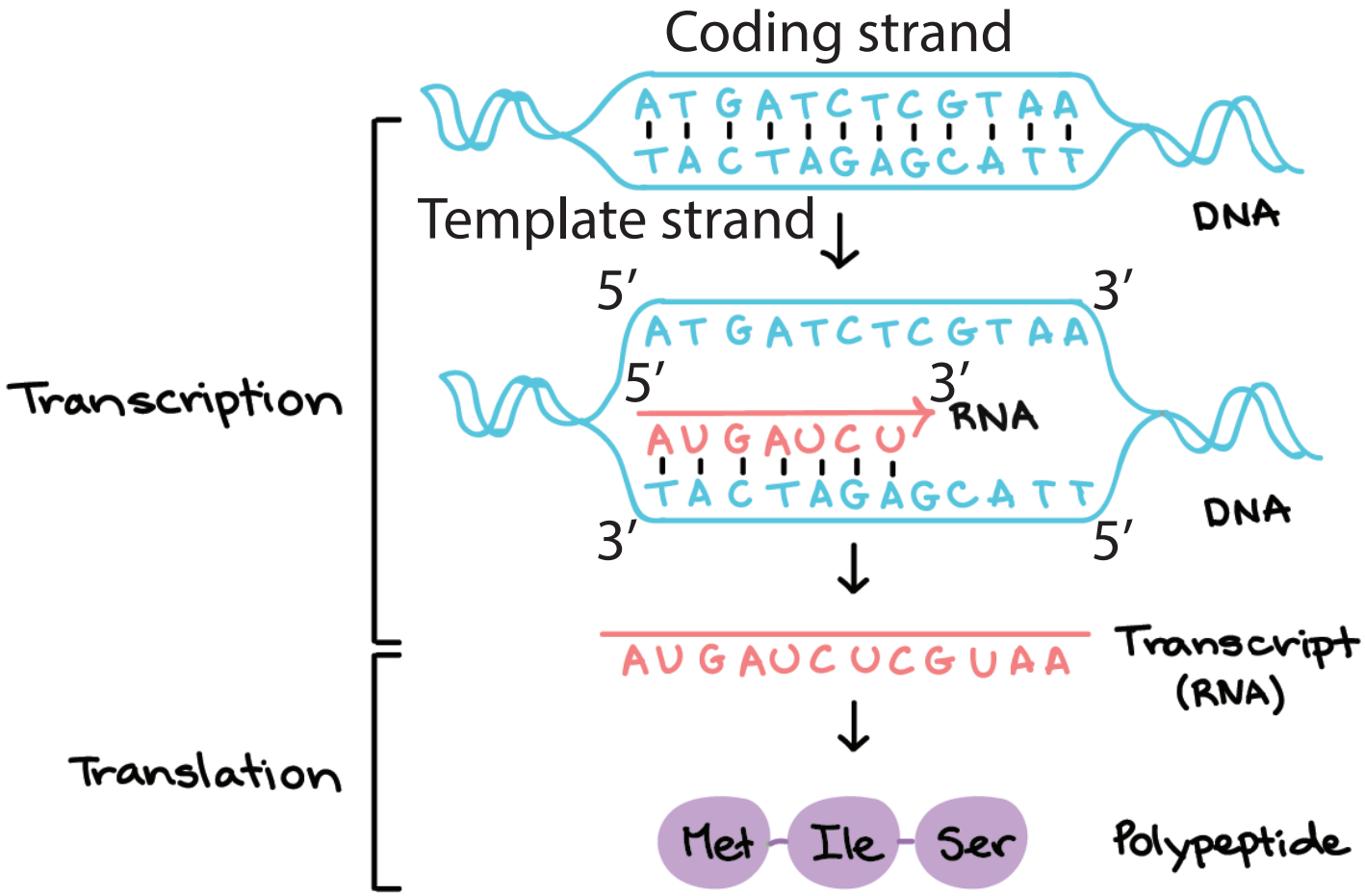
```
1  class Animal:
2      def __init__(self, age):
3          self.age = 0
4          self.claws=0
5      def grow(self):
6          self.age += 1
7          claws = self.claws + 1
8  animal = Animal()
9  animal.grow()
10 print(animal.age)
11 print(animal.claws)
```

Object oriented programming: class inheritance

What prints out?

```
1  class Animal():
2      def __init__(self, age):
3          self.age = 0
4          self.claws=0
5      def grow(self):
6          self.age += 1
7          claws = self.claws + 1
8  class Predator(Animal):
9      def __init__(self):
10         Animal.__init__(self, 0)
11         self.horns = 0
12         self.eyes = 0
13     def grow(self):
14         Animal.grow(self)
15         self.horns += 1
16         eyes = self.eyes + 1
17
18 pred = Predator()
19 pred.grow()
20 print(pred.claws, pred.age, pred.horns, pred.eyes)
```

Central dogma



Every three DNA letters (i.e., codon) code for an amino acid

Transcription

Given a DNA string as the template strand say 5'-AGATCAT-3', write a function called `transcribe(dna)` that returns the transcribed RNA sequence (i.e., AUGAUCU)

```
1  def transribe(dna):
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19 return rna
```

Translation: codon table

1st base	2nd base								3rd base
	T		C		A		G		
T	TTT	(Phe/F) Phenylalanine	TCT	(Ser/S) Serine	TAT	(Tyr/Y) Tyrosine	TGT	(Cys/C) Cysteine	T
	TTC		TCC		TAC		TGC		C
	TTA	(Leu/L) Leucine	TCA		TAA	Stop (*Ochre*)[B]	TGA	Stop (*Opal*)[B]	A
	TTG[A]		TCG		TAG	Stop (*Amber*)[B]	TGG	(Trp/W) Tryptophan	G
C	CTT		CCT	(Pro/P) Proline	CAT	(His/H) Histidine	CGT	(Arg/R) Arginine	T
	CTC		CCC		CAC		CGC		C
	CTA		CCA		CAA	(Gln/Q) Glutamine	CGA		A
	CTG[A]		CCG		CAG		CGG		G
A	ATT	(Ile/I) Isoleucine	ACT	(Thr/T) Threonine	AAT	(Asn/N) Asparagine	AGT	(Ser/S) Serine	T
	ATC		ACC		AAC		AGC		C
	ATA		ACA		AAA	(Lys/K) Lysine	AGA	(Arg/R) Arginine	A
	ATG[A]	(Met/M) Methionine	ACG		AAG		AGG		G
G	GTT	(Val/V) Valine	GCT	(Ala/A) Alanine	GAT	(Asp/D) Aspartic acid	GGT	(Gly/G) Glycine	T
	GTC		GCC		GAC		GGC		C
	GTA		GCA		GAA	(Glu/E) Glutamic acid	GGA		A
	GTG		GCG		GAG		GGG		G

Not all mutation leads to a different animo acid

e.g., GCT and GCC both code for Alanine

Translation

Assume the codon table is provided to you as a dictionary `ct` with key as the 3-letter DNA string and value as the amino acid, write a function that translates an RNA into the amino acid sequence

```
1  def translate(rna, ct):
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19 return aa
```

Sort cells by size

Suppose we obtain a collection of unknown cells from a patient. Each cell is a Cell object. We are provided with a function called `cancer_cell_score(cell)` that give a cancer score to the unknown cell. Write a function that return the highest scoring cell.

```
1  def get_most_similar_cell(cancer_cell, unknown_cells):
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17 return ccc # candidate cancer cell
```