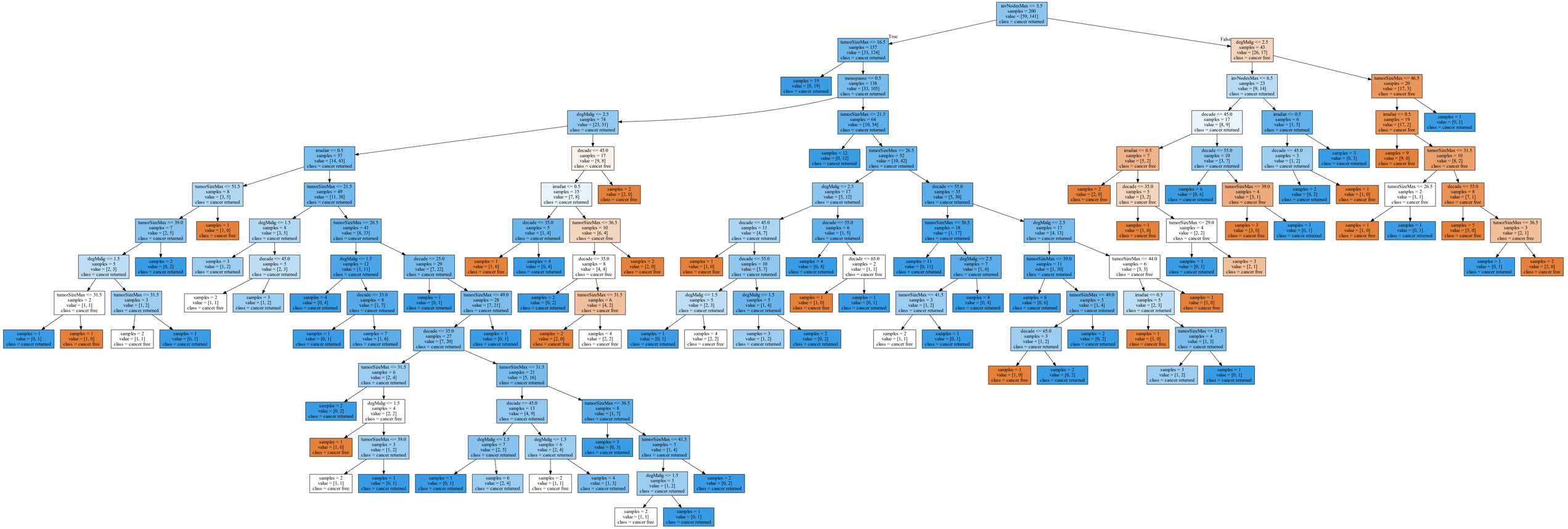
invNodesMax <= 3.5
samples = 200
value = [59, 141]
class = cancer returned
True
False
tumorSizeMax <= 16.5
samples = 157
value = [33, 124]
class = cancer returned
degMalig <= 2.5
samples = 43
value = [26, 17]
class = cancer free
samples = 19
value = [0, 19]
class = cancer returned
menopause <= 0.5
samples = 138
value = [33, 105]
class = cancer returned
invNodesMax <= 6.5
samples = 23
value = [9, 14]
class = cancer returned
tumorSizeMax <= 46.5
samples = 20
value = [17, 3]
class = cancer free
degMalig <= 2.5
samples = 74
value = [23, 51]
class = cancer returned
tumorSizeMax <= 21.5
samples = 64
value = [10, 54]
class = cancer returned
decade <= 45.0
samples = 17
value = [8, 9]
class = cancer returned
irradiat <= 0.5
samples = 19
value = [17, 2]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
irradiat <= 0.5
samples = 57
value = [14, 43]
class = cancer returned
decade <= 45.0
samples = 17
value = [9, 8]
class = cancer free
samples = 12
value = [0, 12]
class = cancer returned
tumorSizeMax <= 26.5
samples = 52
value = [10, 42]
class = cancer returned
irradiat <= 0.5
samples = 7
value = [5, 2]
class = cancer free
decade <= 55.0
samples = 10
value = [3, 7]
class = cancer returned
decade <= 45.0
samples = 3
value = [1, 2]
class = cancer returned
samples = 3
value = [0, 3]
class = cancer returned
samples = 9
value = [9, 0]
class = cancer free
tumorSizeMax <= 31.5
samples = 10
value = [8, 2]
class = cancer free
tumorSizeMax <= 51.5
samples = 8
value = [3, 5]
class = cancer returned
tumorSizeMax <= 21.5
samples = 49
value = [11, 38]
class = cancer returned
irradiat <= 0.5
samples = 15
value = [7, 8]
class = cancer returned
samples = 2
value = [2, 0]
class = cancer free
degMalig <= 2.5
samples = 17
value = [5, 12]
class = cancer returned
decade <= 55.0
samples = 35
value = [5, 30]
class = cancer returned
samples = 2
value = [2, 0]
class = cancer free
samples = 6
value = [0, 6]
class = cancer returned
tumorSizeMax <= 39.0
samples = 4
value = [3, 1]
class = cancer returned
samples = 1
value = [0, 1]
class = cancer returned
tumorSizeMax <= 26.5
samples = 26
value = [6, 20]
class = cancer returned
tumorSizeMax <= 39.0
samples = 7
value = [2, 5]
class = cancer returned
degMalig <= 1.5
samples = 8
value = [3, 5]
class = cancer returned
tumorSizeMax <= 26.5
samples = 41
value = [8, 33]
class = cancer returned
decade <= 35.0
samples = 5
value = [1, 4]
class = cancer returned
tumorSizeMax <= 36.5
samples = 10
value = [6, 4]
class = cancer free
decade <= 45.0
samples = 1
value = [4, 7]
class = cancer returned
decade <= 55.0
samples = 6
value = [1, 5]
class = cancer returned
tumorSizeMax <= 36.5
samples = 18
value = [1, 17]
class = cancer returned
degMalig <= 2.5
samples = 17
value = [4, 13]
class = cancer returned
tumorSizeMax <= 26.5
samples = 2
value = [1, 1]
class = cancer free
decade <= 55.0
samples = 8
value = [7, 1]
class = cancer free
degMalig <= 1.5
samples = 7
value = [2, 3]
class = cancer returned
samples = 2
value = [2, 0]
class = cancer free
samples = 3
value = [1, 2]
class = cancer returned
decade <= 45.0
samples = 5
value = [2, 3]
class = cancer returned
degMalig <= 1.5
samples = 12
value = [1, 11]
class = cancer returned
decade <= 25.0
samples = 29
value = [7, 22]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer returned
samples = 4
value = [0, 4]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer returned
samples = 4
value = [0, 4]
class = cancer returned
decade <= 35.0
samples = 8
value = [4, 4]
class = cancer free
samples = 2
value = [2, 0]
class = cancer free
samples = 4
value = [0, 4]
class = cancer returned
decade <= 65.0
samples = 2
value = [1, 1]
class = cancer free
samples = 11
value = [0, 11]
class = cancer returned
degMalig <= 2.5
samples = 7
value = [1, 6]
class = cancer returned
tumorSizeMax <= 39.0
samples = 11
value = [1, 10]
class = cancer returned
tumorSizeMax <= 44.0
samples = 6
value = [3, 3]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
samples = 3
value = [2, 1]
class = cancer free
samples = 1
value = [1, 0]
class = cancer free
samples = 1
value = [1, 0]
class = cancer free
samples = 1
value = [1, 0]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
samples = 5
value = [5, 0]
class = cancer free
tumorSizeMax <= 36.5
samples = 3
value = [2, 1]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
samples = 2
value = [2, 0]
class = cancer free
tumorSizeMax <= 39.0
samples = 3
value = [1, 2]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer free
samples = 2
value = [0, 2]
class = cancer returned
tumorSizeMax <= 41.5
samples = 3
value = [1, 2]
class = cancer returned
samples = 4
value = [0, 4]
class = cancer returned
tumorSizeMax <= 49.0
samples = 5
value = [1, 4]
class = cancer returned
irradiat <= 0.5
samples = 5
value = [2, 3]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer free
decade <= 65.0
samples = 3
value = [1, 2]
class = cancer returned
samples = 2
value = [0, 2]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer free
tumorSizeMax <= 31.5
samples = 4
value = [1, 3]
class = cancer returned
samples = 3
value = [1, 2]
class = cancer returned
samples = 1
value = [0, 1]
class = cancer returned
tumorSizeMax <= 31.5
samples = 2
value = [1, 1]
class = cancer returned
tumorSizeMax <= 31.5
samples = 3
value = [1, 2]
class = cancer returned
samples = 2
value = [1, 1]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
degMalig <= 1.5
samples = 5
value = [2, 3]
class = cancer returned
degMalig <= 1.5
samples = 5
value = [7, 21]
class = cancer returned
tumorSizeMax <= 49.0
samples = 28
value = [7, 21]
class = cancer returned
samples = 2
value = [0, 2]
class = cancer returned
tumorSizeMax <= 31.5
samples = 6
value = [4, 2]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
samples = 4
value = [2, 2]
class = cancer free
samples = 3
value = [1, 2]
class = cancer returned
samples = 2
value = [0, 2]
class = cancer returned
samples = 2
value = [0, 2]
class = cancer free
samples = 4
value = [2, 2]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
samples = 0
value = [0, 1]
class = cancer returned
samples = 7
value = [1, 6]
class = cancer returned
decade <= 35.0
samples = 27
value = [7, 20]
class = cancer returned
samples = 1
value = [0, 1]
class = cancer returned
tumorSizeMax <= 31.5
samples = 6
value = [2, 4]
class = cancer returned
tumorSizeMax <= 31.5
samples = 21
value = [5, 16]
class = cancer returned
samples = 2
value = [0, 2]
class = cancer returned
degMalig <= 1.5
samples = 4
value = [2, 2]
class = cancer free
decade <= 45.0
samples = 13
value = [4, 9]
class = cancer returned
tumorSizeMax <= 36.5
samples = 8
value = [1, 7]
class = cancer returned
samples = 1
value = [1, 0]
class = cancer returned
tumorSizeMax <= 39.0
samples = 3
value = [1, 2]
class = cancer returned
degMalig <= 1.5
samples = 7
value = [2, 5]
class = cancer returned
degMalig <= 1.5
samples = 6
value = [2, 4]
class = cancer returned
samples = 3
value = [0, 3]
class = cancer returned
tumorSizeMax <= 41.5
samples = 5
value = [1, 4]
class = cancer returned
samples = 2
value = [1, 1]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned
samples = 6
value = [2, 4]
class = cancer returned
samples = 2
value = [1, 1]
class = cancer free
samples = 4
value = [1, 3]
class = cancer returned
degMalig <= 1.5
samples = 3
value = [1, 2]
class = cancer returned
samples = 2
value = [0, 2]
class = cancer returned
samples = 2
value = [1, 1]
class = cancer free
samples = 1
value = [0, 1]
class = cancer returned