In [1]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
```

Step-1: Read the data set

1. Sample code number: id number
2. Clump Thickness: 1 - 10
3. Uniformity of Cell Size: 1 - 10
4. Uniformity of Cell Shape: 1 - 10
5. Marginal Adhesion: 1 - 10
6. Single Epithelial Cell Size: 1 - 10
7. Bare Nuclei: 1 - 10
8. Bland Chromatin: 1 - 10
9. Normal Nucleoli: 1 - 10
10. Mitoses: 1 - 10
11. Class: (2 for benign, 4 for malignant)

In [2]:
```
columns = ['idnumber','clumpthick','unicellsize','unicellshape','adhesion','epith
           'barenuclei','chromatin','normnucle','mitoses','type']
```

In [3]:
```
data = pd.read_csv('breast-cancer-wisconsin.data')
data.columns = columns
data.head()
```

Out[3]:

	idnumber	clumpthick	unicellsize	unicellshape	adhesion	epithelcellsize	barenuclei	chromatin
0	1002945	5	4	4	5	7	10	3
1	1015425	3	1	1	1	2	2	3
2	1016277	6	8	8	1	3	4	3
3	1017023	4	1	1	3	2	1	3
4	1017122	8	10	10	8	7	10	9

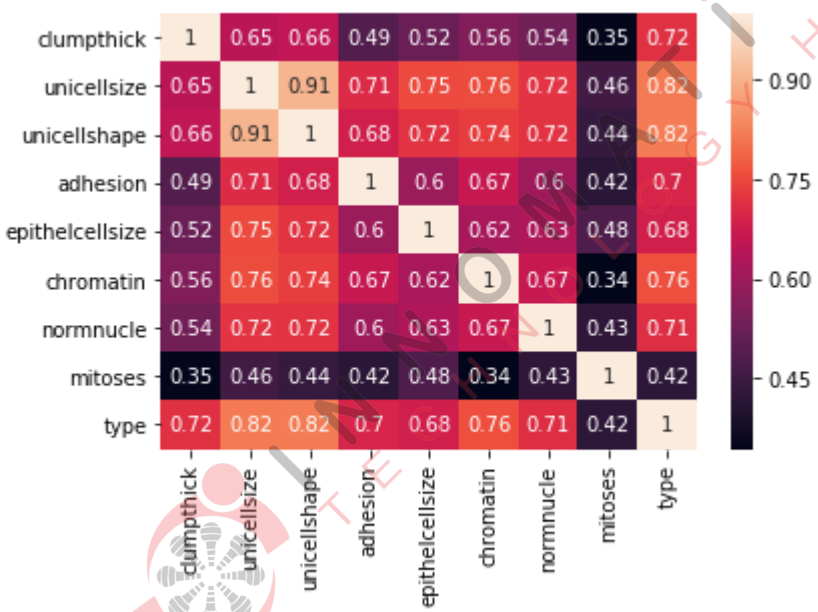
In [4]:
```
data.drop('idnumber',axis=1,inplace=True)
data.head()
```

Out[4]:

	clumpthick	unicellsize	unicellshape	adhesion	epithelcellsize	barenuclei	chromatin	normnucle
0	5	4	4	5	7	10	3	2
1	3	1	1	1	2	2	3	1
2	6	8	8	1	3	4	3	7
3	4	1	1	3	2	1	3	1
4	8	10	10	8	7	10	9	7

In [5]:
```
corr = data.corr()
sns.heatmap(corr,annot=True)
```

Out[5]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x25435cba58>
```



In [6]:
```
data.keys()
```

Out[6]:
```
Index(['clumpthick', 'unicellsize', 'unicellshape', 'adhesion',
       'epithelcellsize', 'barenuclei', 'chromatin', 'normnucle', 'mitoses',
       'type'],
      dtype='object')
```

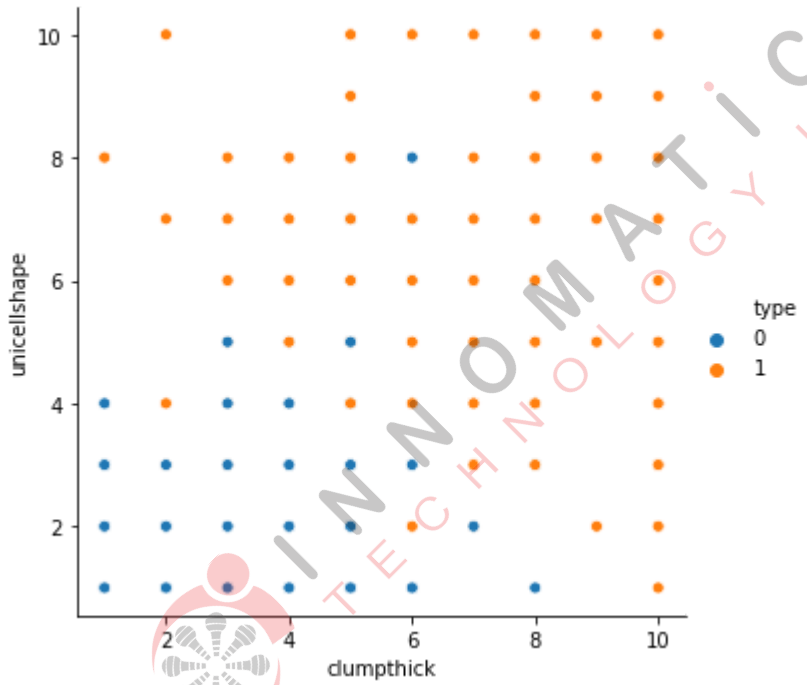
In [7]:
```
# Clump Thickness,  Uniformity of Cell Size
df = data[['clumpthick','unicellshape','type']]
df['type'].replace(to_replace=[2,4],value=[0,1],inplace=True)
```

```
C:\Users\srikanth\Anaconda\lib\site-packages\pandas\core\generic.py:5890: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html#indexing-view-versus-copy (http://pandas.pydata.org/pandas-docs/stable/indexing.html#indexing-view-versus-copy)
  self._update_inplace(new_data)
```

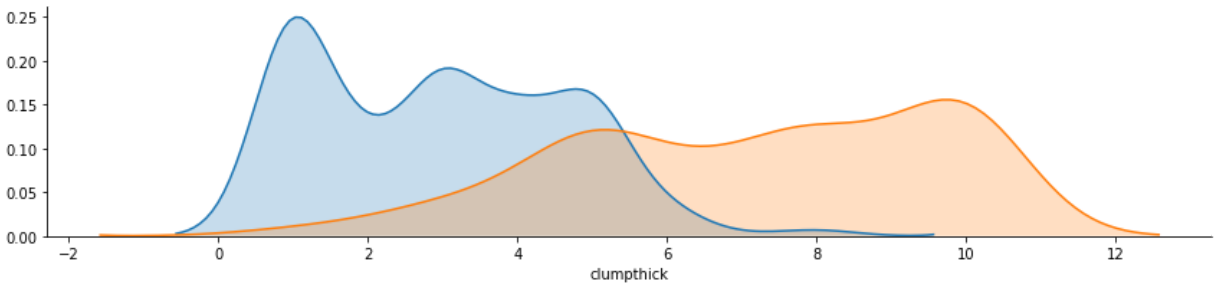
In [8]:
```
sns.relplot(x='clumpthick',y='unicellshape',data=df,hue='type')
```

Out[8]:
```
<seaborn.axisgrid.FacetGrid at 0x2544185c18>
```



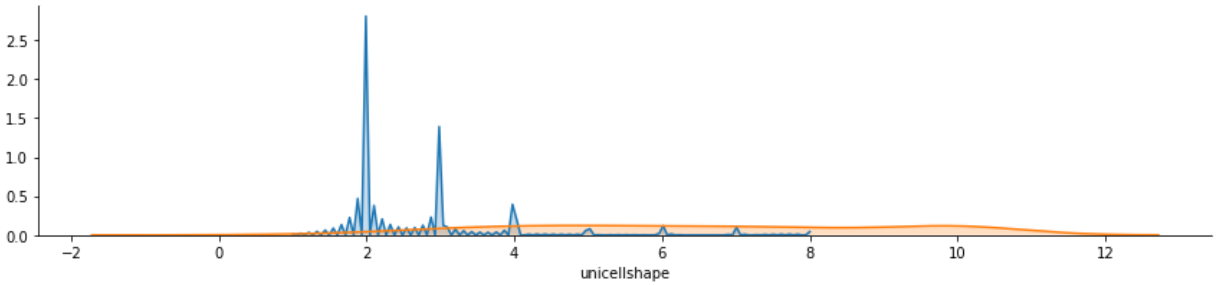
In [9]:
```
fig = sns.FacetGrid(data =df, hue='type',aspect=4)
fig.map(sns.kdeplot,'clumpthick',shade=True)
```

Out[9]:
```
<seaborn.axisgrid.FacetGrid at 0x25441ab6a0>
```



In [10]:
```
fig = sns.FacetGrid(data =df, hue='type',aspect=4)
fig.map(sns.kdeplot,'unicellshape',shade=True)
```

Out[10]: <seaborn.axisgrid.FacetGrid at 0x2544347da0>



In [11]:
```
df.head(2)
```

Out[11]:

	clumpthick	unicellshape	type
0	5	4	0
1	3	1	0

In [12]:
```
# Building Logistics Regression
import statsmodels.formula.api as smf
import statsmodels.api as sm
```

In [13]:
```
model = smf.glm(formula='type~clumpthick+unicellshape',data=df).fit()
print(model.summary())
```

```
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:                   type   No. Observations:                  698
Model:                            GLM   Df Residuals:                      695
Model Family:                Gaussian   Df Model:                            2
Link Function:               identity   Scale:                         0.061922
Method:                          IRLS   Log-Likelihood:                -18.038
Date:                Fri, 22 Mar 2019   Deviance:                       43.036
Time:                        22:44:56   Pearson chi2:                     43.0
No. Iterations:                     3   Covariance Type:             nonrobust
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.97
5]
------------------------------------------------------------------------------
-
Intercept      -0.2046      0.018    -11.668      0.000      -0.239      -0.17
0
clumpthick      0.0533      0.004     12.035      0.000       0.045       0.06
2
unicellshape    0.0980      0.004     23.345      0.000       0.090       0.10
6
==============================================================================
=
```

In [14]:
```
model.null_deviance
```

Out[14]:
```
157.7893982808023
```

Logistic Regression

$$0 = -0.2046 + 0.0533 * clumpthick + 0.0980 * unicellshape$$

In [15]:
```
model.params
```

Out[15]:
```
Intercept      -0.204589
clumpthick      0.053282
unicellshape    0.097963
dtype: float64
```

In [16]:
```
df.head(2)
```

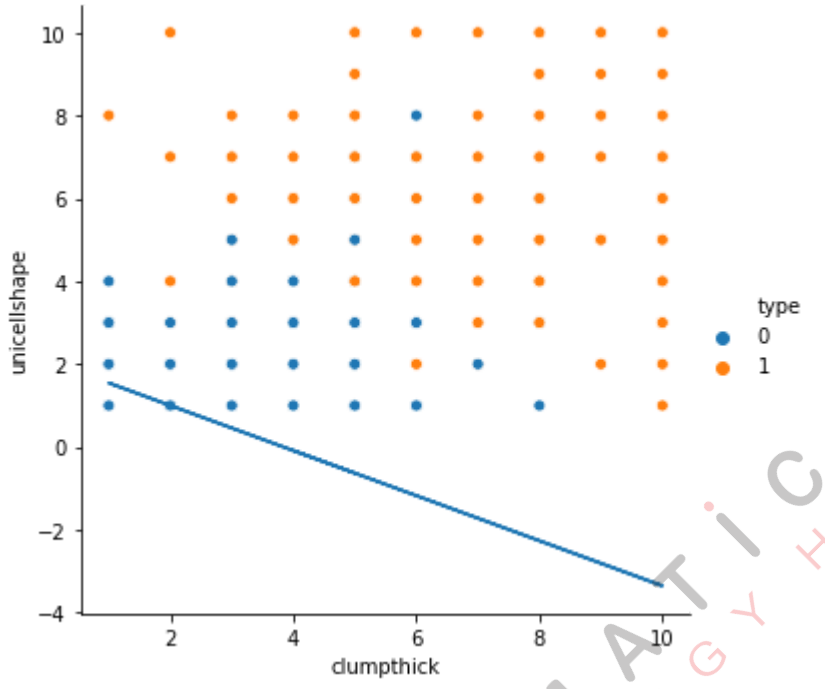
Out[16]:

	clumpthick	unicellshape	type
0	5	4	0
1	3	1	0

In [17]:
```
clumpthick = df['clumpthick'] # get data
unicellshape = df['unicellshape'] # get data
# 0.5 percetage probability
unicellshape = (-model.params['Intercept'] - model.params['clumpthick'] * clumpth
```

In [18]:
```
sns.relplot(x='clumpthick',y='unicellshape',data=df,hue='type')
plt.plot(clumpthick,unicellshape)
```

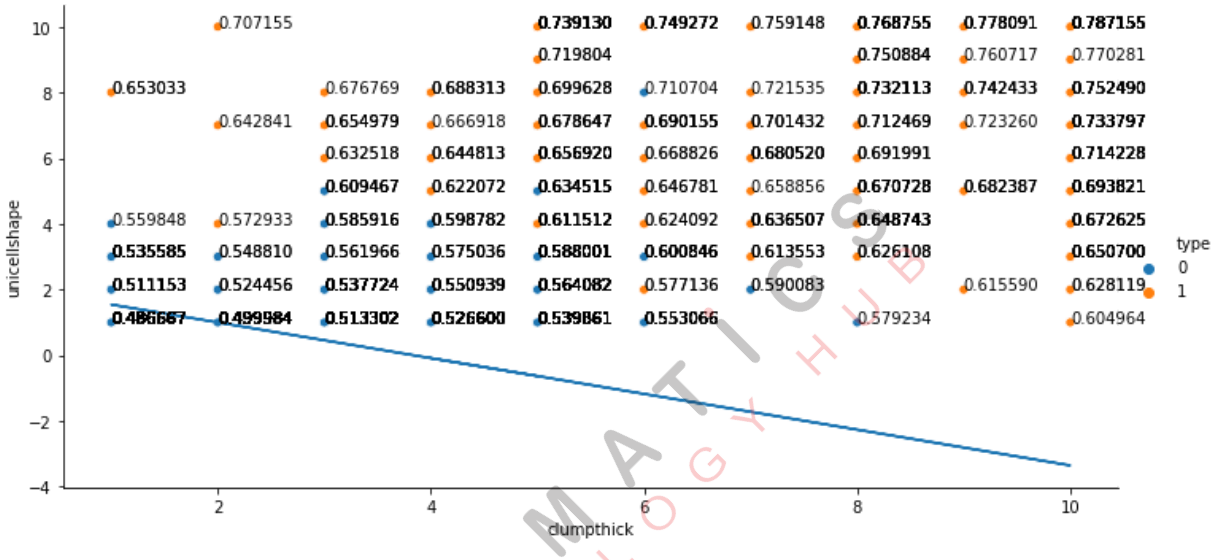
Out[18]:
```
[<matplotlib.lines.Line2D at 0x2544fe44e0>]
```



In [19]:
```
def prediction(x1,x2):
    clumpthick = x1
    unicellshape = x2
    lnor = model.params['Intercept'] + model.params['clumpthick'] * clumpthick +
    # convert into array
    oddsratio = np.exp(lnor)
    p = oddsratio/(oddsratio+1)
    return p
```

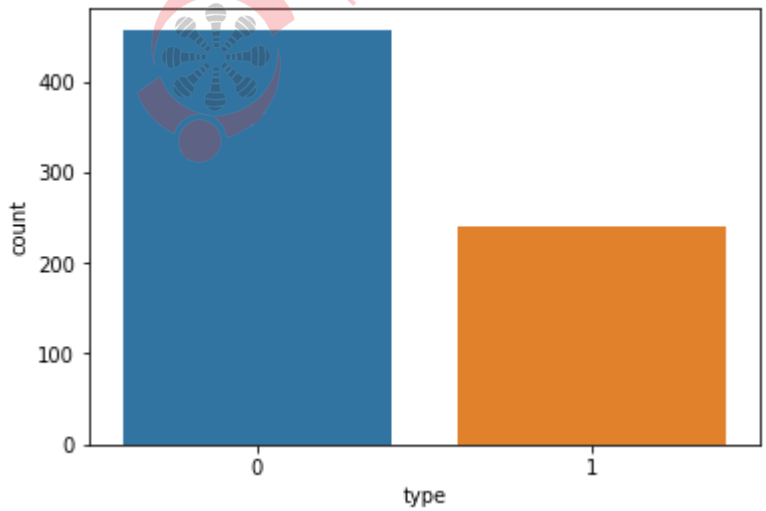
In [20]:
```
plt.figure(figsize=(10,10))
sns.relplot(x='clumpthick',y='unicellshape',data=df,hue='type',aspect=2)
plt.plot(clumpthick,unicellshape)
for i in range(len(df)):
    #print(i)
    plt.text(df['clumpthick'][i],df['unicellshape'][i],"%0.6f"%(prediction(df['cl
```

```
<Figure size 720x720 with 0 Axes>
```



In [21]:
```
sns.countplot(x='type',data =df)
df['type'].value_counts()
```

Out[21]:
```
0    457
1    241
Name: type, dtype: int64
```



In [38]:
```
def predict(prob,thresh=0.5):
    if prob > thresh:
        return 1
    else:
        return 0
```

In [39]:
```
y_pre_prob = prediction(df['clumpthick'],df['unicellshape'])
```

In [40]:
```
y_pred = y_pre_prob.apply(predict)
```

In [41]:
```
y_true = df['type']
```

Confusion Matrix

In [42]:
```
from pandas_ml import ConfusionMatrix
```

In [43]:
```
# data
cm = ConfusionMatrix(y_true,y_pred)
cm
```

Out[43]:
```
Predicted  False  True  __all__
Actual
False        163   294      457
True           0   241      241
__all__      163   535      698
```

In [44]:
```
cm.stats()
```

```
C:\Users\srikanth\Anaconda\lib\site-packages\pandas_ml\confusion_matrix\bcm.py:
346: RuntimeWarning: divide by zero encountered in double_scalars
  return(np.float64(self.LRP) / self.LRN)
```

Out[44]:
```
OrderedDict([('population', 698),
             ('P', 241),
             ('N', 457),
             ('PositiveTest', 535),
             ('NegativeTest', 163),
             ('TP', 241),
             ('TN', 163),
             ('FP', 294),
             ('FN', 0),
             ('TPR', 1.0),
             ('TNR', 0.35667396061269147),
             ('PPV', 0.4504672897196262),
             ('NPV', 1.0),
             ('FPR', 0.6433260393873085),
             ('FDR', 0.5495327102803739),
             ('FNR', 0.0),
             ('ACC', 0.5787965616045845),
             ('F1_score', 0.6211340206185567),
             ('MCC', 0.4008365656358759),
             ('informedness', 0.3566739606126914),
             ('markedness', 0.4504672897196624),
             ('prevalence', 0.3452722063037249),
             ('LRP', 1.554421768707483),
             ('LRN', 0.0),
             ('DOR', inf),
             ('FOR', 0.0)])
```

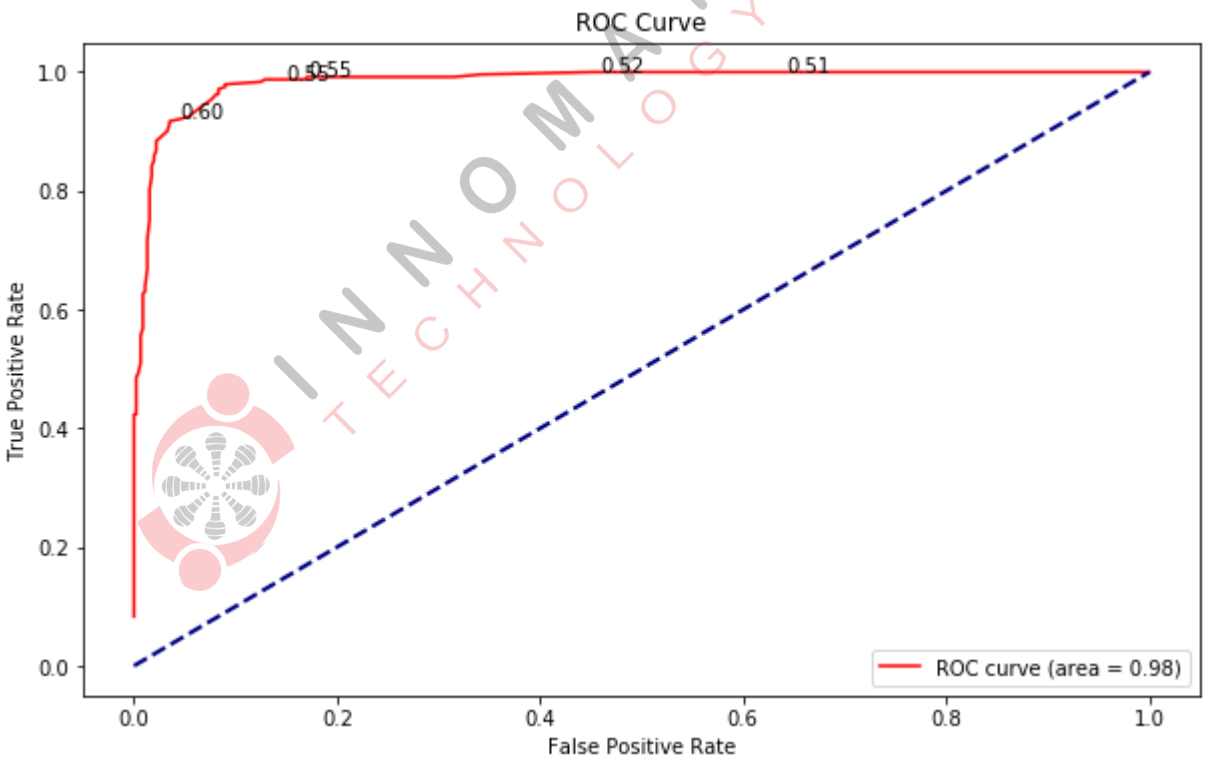
ROC

In [29]:
```
from sklearn.metrics import roc_curve,auc
fpr,tpr,threshold = roc_curve(y_true,y_pre_prob)


plt.figure(figsize=(10,6))
plt.plot(fpr,tpr,color='red',lw=1.5)
plt.plot([0, 1], [0, 1], color='navy',lw = 2, linestyle='--')

for i,value in enumerate(fpr*10):
    try:
        if (round(fpr[i+1]*10) - round(fpr[i]*10)) == 1:
            plt.text(fpr[i],tpr[i],'%0.2f'%(threshold[i]))
    except IndexError:
        print(' ')

plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(['ROC curve (area = %0.2f)' % auc(fpr,tpr)])
plt.show()
```



From ROC: approximate threshold probabality value = 0.6

Hence new logistic regression equation is

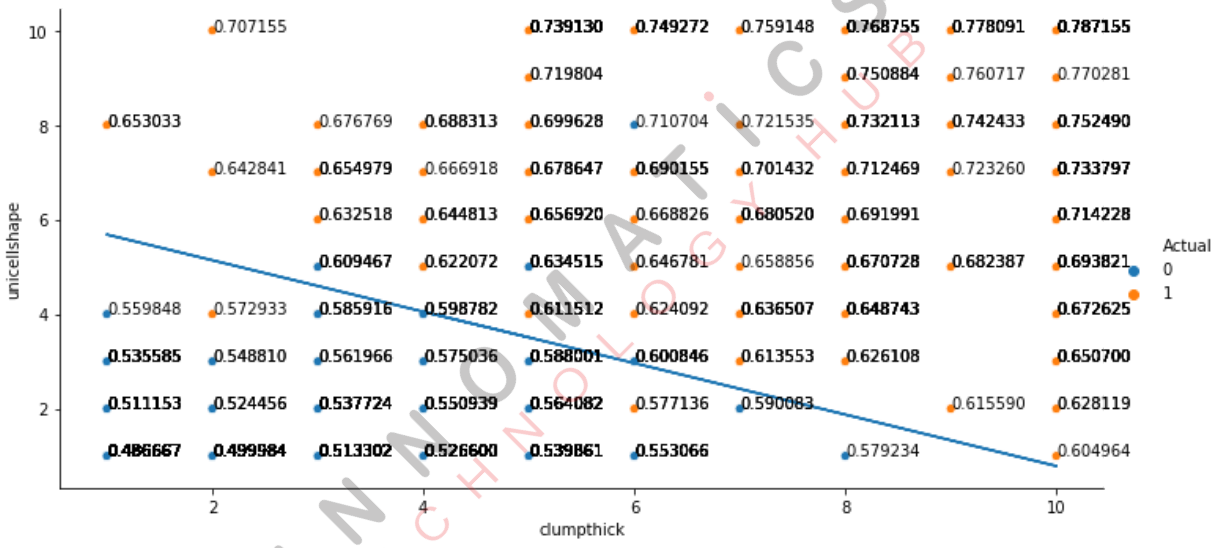
$$ln(\frac{0.6}{0.4}) = -0.2046 + 0.0533 * clumpthick + 0.0980 * unicellshape$$

In [30]:
```
from math import log
```

In [31]:
```
clumpthick = df['clumpthick'] # get data
unicellshape = df['unicellshape'] # get data
# 0.5 percetage probability
unicellshape = (log(0.6/0.4) -model.params['Intercept'] - model.params['clumpthic
```

In [32]:
```
plt.figure(figsize=(10,10))
sns.relplot(x='clumpthick',y='unicellshape',data=df,hue='type',aspect=2)
plt.plot(clumpthick,unicellshape)
for i in range(len(df)):
    #print(i)
    plt.text(df['clumpthick'][i],df['unicellshape'][i],"%0.6f"%(prediction(df['cl
```

```
<Figure size 720x720 with 0 Axes>
```



In [33]:
```
y_pre_prob_new = prediction(df['clumpthick'],df['unicellshape'])

y_pred_new = y_pre_prob_new.apply(predict)
```

In [34]:
```
# data
cm_new = ConfusionMatrix(y_true,y_pred_new)
cm_new
```

Out[34]:
```
Predicted  False  True  __all__
Actual
False        442    15      457
True          24   217      241
__all__      466   232      698
```

In [35]:
```
cm_new.stats()
```

Out[35]:
```
OrderedDict([('population', 698),
             ('P', 241),
             ('N', 457),
             ('PositiveTest', 232),
             ('NegativeTest', 466),
             ('TP', 217),
             ('TN', 442),
             ('FP', 15),
             ('FN', 24),
             ('TPR', 0.9004149377593361),
             ('TNR', 0.9671772428884027),
             ('PPV', 0.9353448275862069),
             ('NPV', 0.9484978540772532),
             ('FPR', 0.03282275711159737),
             ('FDR', 0.06465517241379311),
             ('FNR', 0.0995850622406639),
             ('ACC', 0.9441260744985673),
             ('F1_score', 0.9175475687103594),
             ('MCC', 0.8756797357104631),
             ('informedness', 0.8675921806477387),
             ('markedness', 0.8838426816634599),
             ('prevalence', 0.3452722063037249),
             ('LRP', 27.43264177040111),
             ('LRN', 0.10296464580086741),
             ('DOR', 266.42777777777786),
             ('FOR', 0.05150214592274678)])
```

In [45]:
```
# With 0.5 Threshold
cm.stats_overall
```

```
C:\Users\srikanth\Anaconda\lib\site-packages\pandas_ml\confusion_matrix\stats.p
y:60: FutureWarning: supplying multiple axes to axis is deprecated and will be
removed in a future version.
  num = df[df > 1].dropna(axis=[0, 1], thresh=1).applymap(lambda n: choose(n,
2)).sum().sum() - np.float64(nis2 * njs2) / n2
```

Out[45]:
```
OrderedDict([('Accuracy', 0.5787965616045845),
             ('95% CI', (0.541181988866439, 0.6157422784488367)),
             ('No Information Rate', 'ToDo'),
             ('P-Value [Acc > NIR]', 0.9999999999999999),
             ('Kappa', 0.27685726166228525),
             ("Mcnemar's Test P-Value", 'ToDo')])
```

In [37]:
```
# With 0.6 Threshold
cm_new.stats_overall
```

```
C:\Users\srikanth\Anaconda\lib\site-packages\pandas_ml\confusion_matrix\stats.p
y:60: FutureWarning: supplying multiple axes to axis is deprecated and will be
removed in a future version.
  num = df[df > 1].dropna(axis=[0, 1], thresh=1).applymap(lambda n: choose(n,
2)).sum().sum() - np.float64(nis2 * njs2) / n2
```

Out[37]:
```
OrderedDict([('Accuracy', 0.9441260744985673),
             ('95% CI', (0.9244069670030498, 0.9599701231100523)),
             ('No Information Rate', 'ToDo'),
             ('P-Value [Acc > NIR]', 7.851173105857308e-71),
             ('Kappa', 0.8753171804149682),
             ("Mcnemar's Test P-Value", 'ToDo')])
```

Good Job