Problem 1.

a. Prepare a scatter plot for each of the predictor variables vs. Y. Are any noteworthy features revealed by these plots?

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

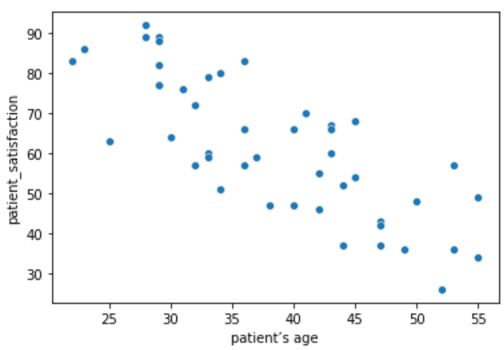
In [2]:
```
df = pd.read_csv('6.15.txt', sep = '\s+', header =None, names=['patient_satisfaction','patient’s age','severity of illness', 'an

x1= df['patient’s age']
x2= df['severity of illness']
x3= df['anxiety level']
y= df['patient_satisfaction']
df.head()
```

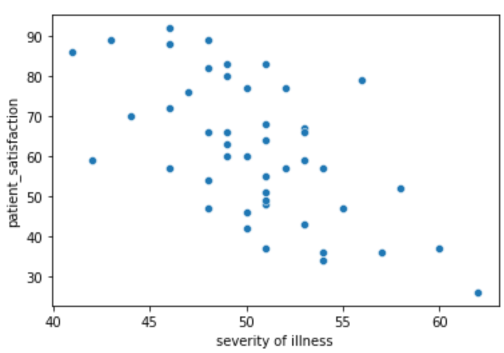
Out[2]:

	patient_satisfaction	patient’s age	severity of illness	anxiety level
0	48	50	51	2.3
1	57	36	46	2.3
2	66	40	48	2.2
3	70	41	44	1.8
4	89	28	43	1.8

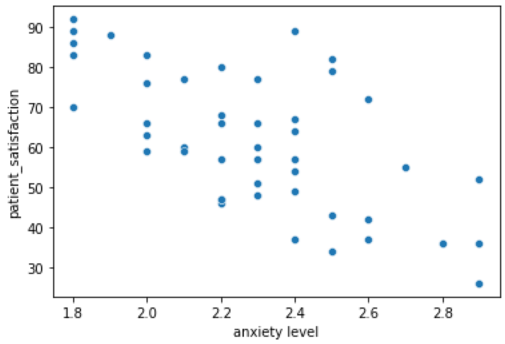
In [3]:
```
# scatter plot for X1 vs Y
sns.scatterplot(x='patient’s age', y='patient_satisfaction', data=df);
```



In [4]:
```
# scatter plot for X2 vs Y
sns.scatterplot(x='severity of illness', y='patient_satisfaction', data=df);
```



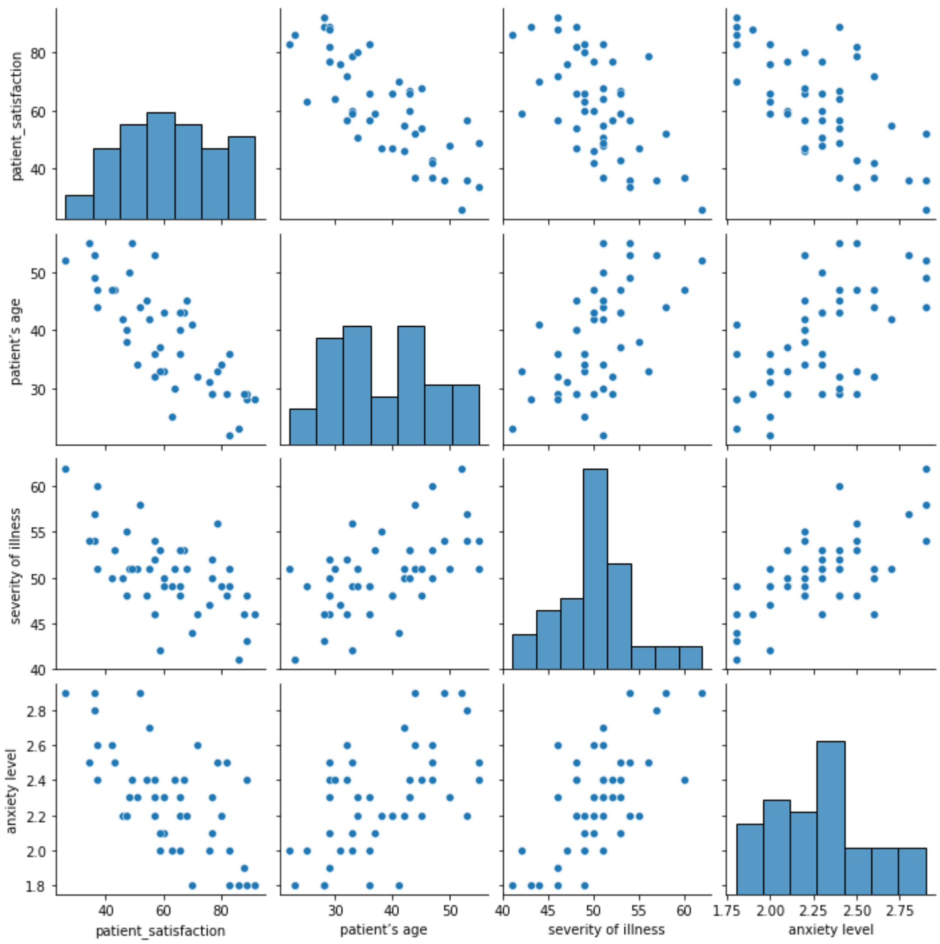
In [5]:
```
# scatter plot for X3 vs Y
sns.scatterplot(x='anxiety level', y='patient_satisfaction', data=df);
```



Conclusion: Compared to X2 and X3, X1 is more negaive to Y

b. Obtain the scatter plot matrix and the correlation matrix. Interpret these and state your principal findings.

In [6]:
```
#the scatter plot matrix
sns.pairplot(data=df);
```



In [7]:
```
# the correlation matrix
matrix = df.corr()
print(matrix)
```

```
                       patient_satisfaction  patient’s age  \
patient_satisfaction               1.000000      -0.786756
patient’s age                     -0.786756       1.000000
severity of illness               -0.602942       0.567950
anxiety level                     -0.644591       0.569677

                       severity of illness  anxiety level
patient_satisfaction             -0.602942      -0.644591
patient’s age                     0.567950       0.569677
severity of illness               1.000000       0.670529
anxiety level                     0.670529       1.000000
```

Information from these diagnostic aids: From the correlation matrix, we can conclude that Y (patient satisfaction) is negatively correlated to X1 (patient’s age), X2 (severity of illness) and X3 (anxiety level). Moreover, The correlation is stronger between Y and X2 (-0.6) than between Y and X1 (-0.78) and between Y and X3 (-0.64)

c. Calculate coefficients in regression model for three predictor variables and state the estimated regression function. How is b_2 interpreted here?

In [8]:
```
import statsmodels.api as sm
import statsmodels.formula.api as smf
model = smf.ols('y ~ x1+x2+x3', data=df)
results = model.fit()
results.summary()
```

Out[8]:

OLS Regression Results

Dep. Variable:	y	**R-squared:**	0.682
Model:	OLS	**Adj. R-squared:**	0.659
Method:	Least Squares	**F-statistic:**	30.05
Date:	Sat, 12 Nov 2022	**Prob (F-statistic):**	1.54e-10
Time:	18:21:27	**Log-Likelihood:**	-169.36
No. Observations:	46	**AIC:**	346.7
Df Residuals:	42	**BIC:**	354.0
Df Model:	3		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
Intercept	158.4913	18.126	8.744	0.000	121.912	195.071

Coefficients

- b0 = 158.4913
- b1 = -1.1416
- b2 = -0.442
- b3 = -13.4702

Regression function: Y_hat = beta[0] + beta[1]*X1 + beta[2]*X2 + beta[3]*X3

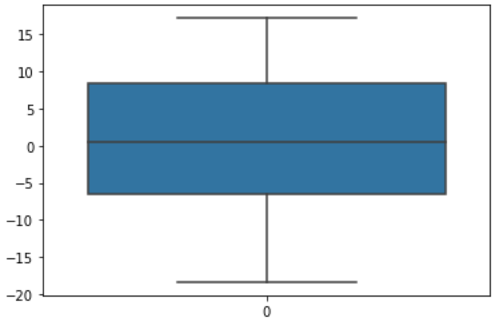
Y_hat = 158.4913 + (-1.1416)X1 + (-0.442)X2 + (-13.4702)X3

b2 = −0.442; for every unit increase in the illness severity index, mean satisfaction is reduced by 0.442 units.

d. Obtain the residuals and prepare a box plot of the residuals. Do there appear to be any outliers?

In [9]:
```
resid = results.resid
```

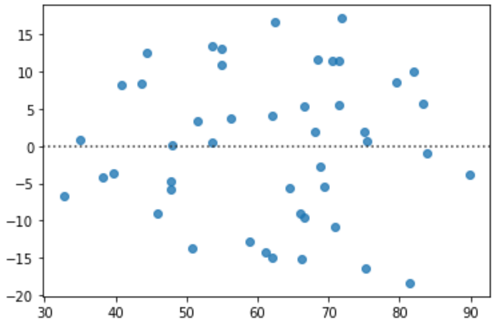
In [10]:
```
sns.boxplot(data=resid);
```



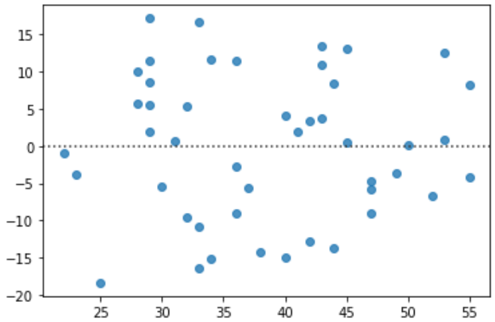
No, because the residuals are evenly distributed and centered around 0 The boxplot shown above shows that there are no outliers in this data and that the number of positive and negative residuals is approaching equality. The residuals are additionally uniformly distributed and centered at 0. As a result, we may say that the regression model accurately predicts the data.

e. Plot the residuals against Yˆ, each of the predictor variables, and each two-factor interaction term on separate graphs. Also prepare a normal probability plot. Interpret your plots and summarize your findings.

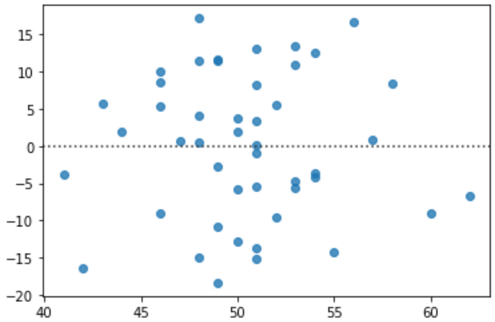
In [11]:
```
#Y_hat
Y_hat = results.predict()
sns.residplot(x=Y_hat, y=resid, data=df);
```



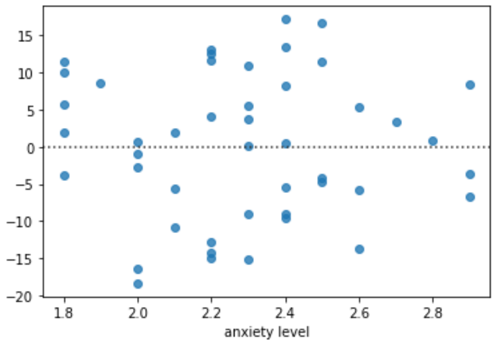
In [12]:
```
# x1
sns.residplot(x=x1, y=resid, data=df);
```



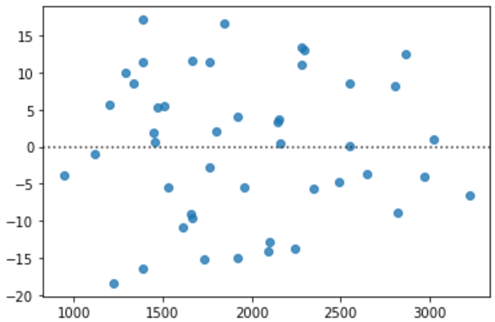
In [13]:
```
# x2
sns.residplot(x=x2, y=resid, data=df);
```



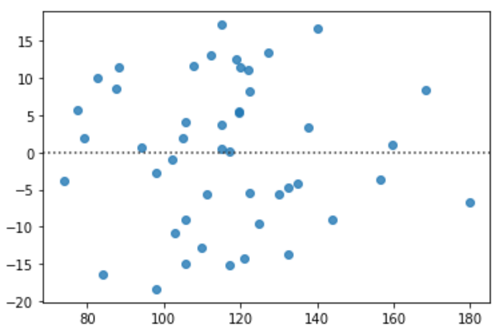
In [14]:
```
# x3
sns.residplot(x=x3, y=resid, data=df);
```



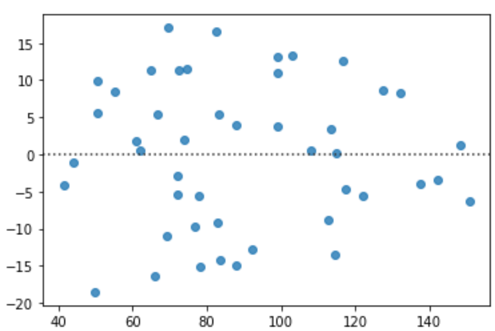
In [15]:
```
# X1X2
X1X2 = x1*x2
sns.residplot(x=X1X2, y=resid, data=df);
```



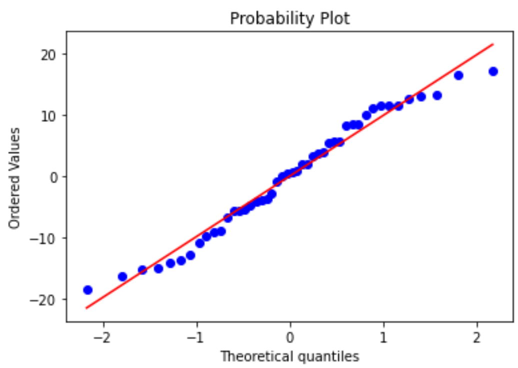
In [16]:
```
#X2X3
X2X3 = x2*x3
sns.residplot(x=X2X3, y=resid, data=df);
```



In [17]:
```
# X1X3
X1X3 = x1*x3
sns.residplot(x=X1X3, y=resid, data=df);
```



In [18]:
```
import scipy.stats as stats
stats.probplot(resid, dist="norm", plot = plt);
plt.show();
```



There is a slight increase in variability for ei vs. Y_hat, but overall it looks okay. The normal probability plot of the residuals looks fine (relatively straight). The plots of the residuals vs. each predictor and each two-way interaction all look appropriately “random.”

f. Test whether there is a regression relation; use α = .10. State the alternatives, decision rule, and conclusion. What does your test imply about β_1,β_2,β_3? What is the P-value of the test?

In [40]:
```
sse = np.sum((results.fittedvalues - df.patient_satisfaction)**2)
print(sse)
ssr = np.sum((results.fittedvalues - df.patient_satisfaction.mean())**2)
print(ssr)
p=4
n = len(y)
MSR = ssr/(p-1)
MSE = sse/(n-p)
print(MSR,MSE)
```

```
4248.840681833575
9120.463665992784
3040.154555330928 101.1628733769899
```

In [38]:
```
Y_Y = np.dot(y.T,y)

J = np.ones((len(x1)))

SSTO = Y_Y - (1/len(x1))*(y.T@J)**2
SSE = np.dot(resid.T,resid)
SSR = SSTO - SSE
```

In [39]:
```
p=4
n = len(y)
MSR = SSR/(p-1)
MSE = SSE/(n-p)
print(MSR,MSE)
```

```
3040.154555330835 101.16287337698991
```

F Test for Regression Relation

Hypothesis:

- H0: β1 = β2 = β3 = 0
- Hα: not all βi = 0 (i=1,2,3)

  test statistic: F* = MSR/MSE

  The decision rule to control the Type I error at α is:
- If F∗ ≤ F(1 − α; p − 1, n − p), conclude H0
- If F∗ > F(1 − α; p − 1, n − p), conclude Ha

In [21]:
```
Fstar = MSR/MSE
print(Fstar)
f = stats.f.ppf(q=1-0.1,dfn=p-1,dfd=n-p)
print(f)
```

```
30.05207793971605
2.2190585583443494
```

Since F*= 30.05 > F = 2.21, we conclude Ha

In [22]:
```
p =1- stats.chi2.cdf(x=(ssr/2) / ((sse/n)**2),df=1)
print(p)
```

```
0.4647138978790545
```

p-value of the test is 0.46

g. Conduct the Breusch-Pagan test for constancy of the error variance, assuming log(σ_i^2)=γ_0+γ_1 X_i1+γ_2 X_i2+γ_3 X_i3; use α = .01. State the alternatives, decision rule, and conclusion.

In [33]:
```
import statsmodels.stats.api as sms
from statsmodels.compat import lzip
fit = smf.ols('y ~ x1+x2+x3', data=df).fit()
names = ['Lagrange multiplier statistic', 'p-value',
         'f-value', 'f p-value']
test_result = sms.het_breuschpagan(fit.resid, fit.model.exog)
lzip(names, test_result)
```

Out[33]:
```
[('Lagrange multiplier statistic', 2.558325446496668),
 ('p-value', 0.4648425187864703),
 ('f-value', 0.824474576983472),
 ('f p-value', 0.48779314523870854)]
```

The Breusch-Pagan test gives p = 0.46, no evidence of non-constant variance.