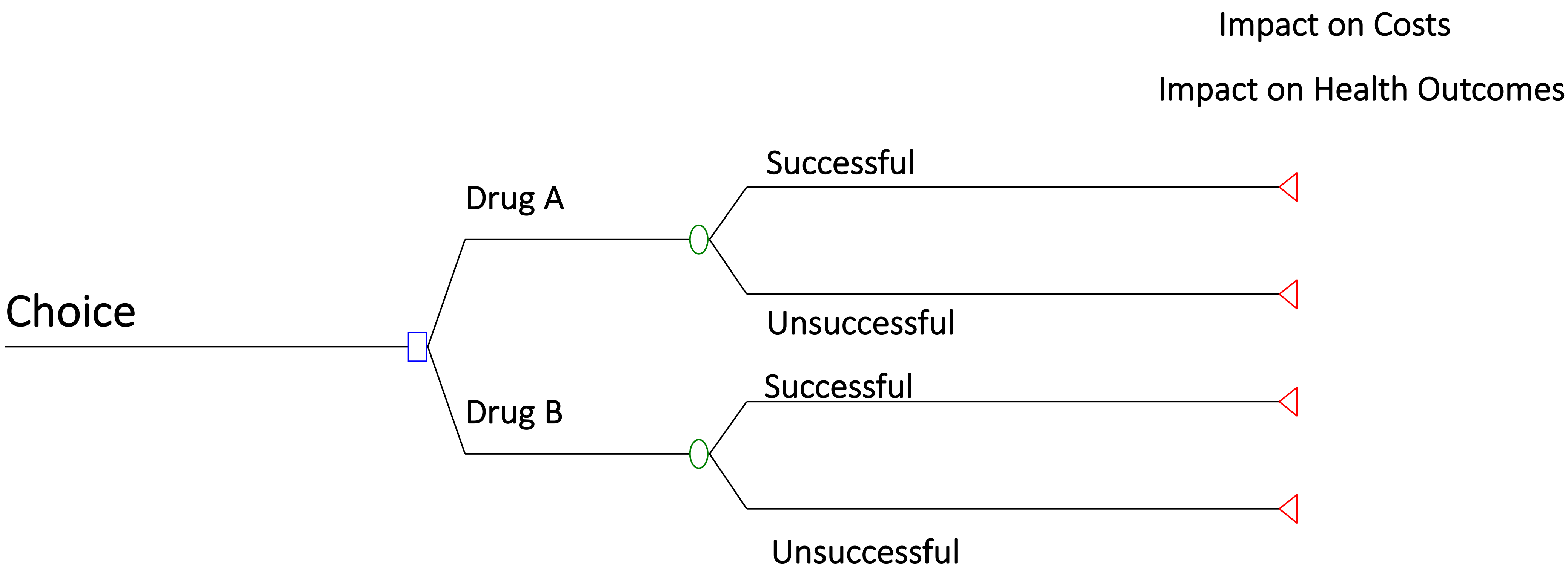
Introduction to Cost-Effectiveness Modelling in R

A Comparative Analysis of Alternative Courses of Action



Quality Adjusted Life Year (QALY)

- The most common measure of consequences in a cost-utility analysis.
- Captures gains from reduced morbidity and reduced mortality of a disease and integrates them into a single measure
- Continuous scale (often from 0 to 1).
- “Measure of a person’s length of life weighted by a valuation of their health-related quality of life” ~ NICE UK

QALY - Example

- Would you rather be in full health for 7 years or alive with a disease for 10 years? Time trade off method
- (Utility A x years spent in health state A) + (utility B x Years spent in health state B) = X QALYs.

Discounting

- 3.5% of both costs and benefits in UK
- Costs and benefits that occur in the future are discounted to reflect society's rate of time preference

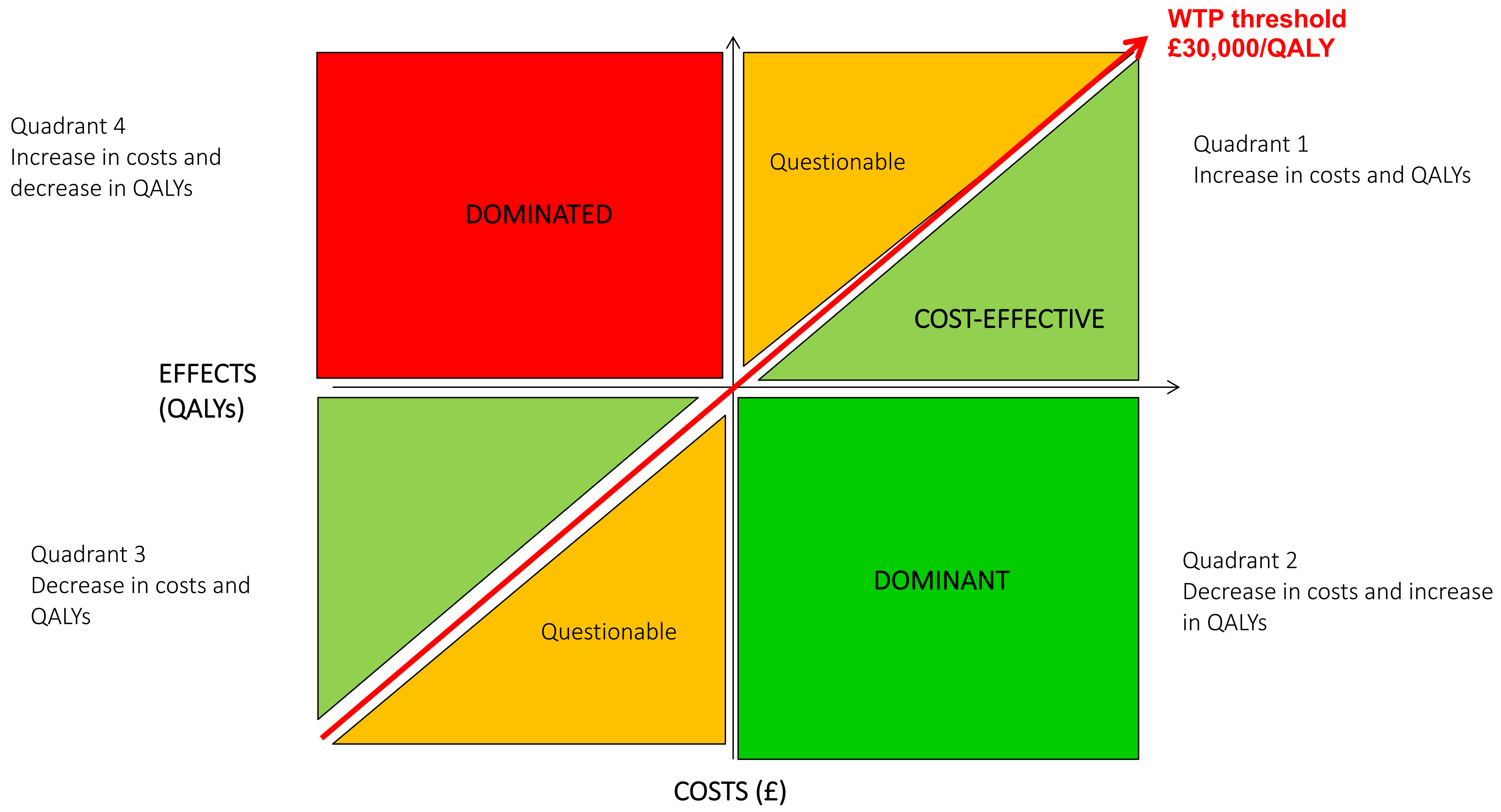
Incremental Cost-Effectiveness Ratio

<u>ICER (or more accurately an ICUR!)</u>

$$\boxed{ICER = \frac{Cost_A - Cost_B}{QALY_A - QALY_B}}$$

The larger the ICER, the more money required to buy each unit of outcome and the less cost-effective the intervention.

Cost-effectiveness plane



The Willingness-to-pay Threshold

- Outcome of the economic analysis is considered in terms of the cost-effectiveness threshold

- UK is £20,000-£30,000/QALY
- Ireland €20,000-€45,000/QALY

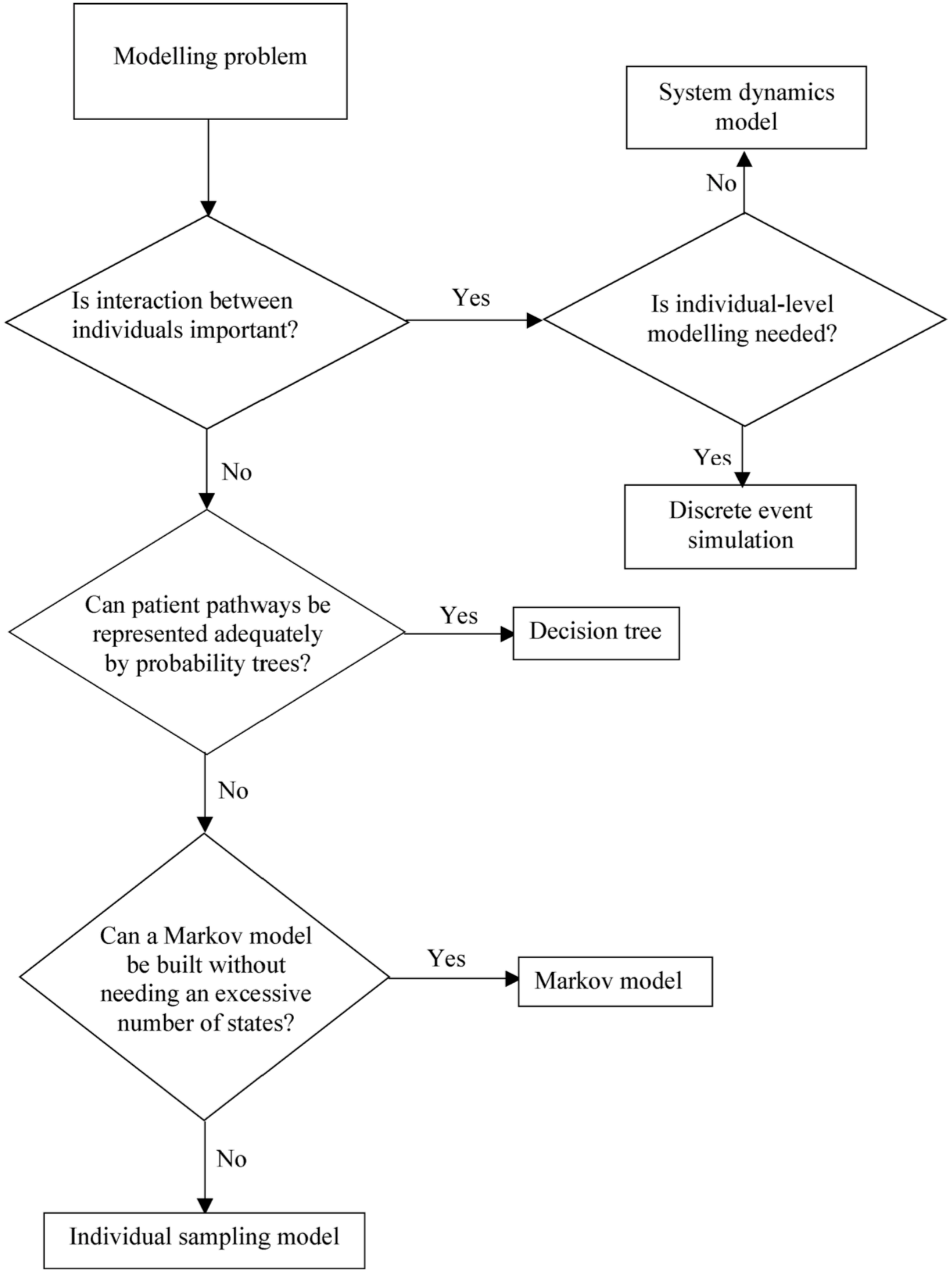
- It is **not the maximum monetary amount** we will pay for a new treatment

Model Types

- Cohort decision tree
  - Simple problem
  - No time-dependent parameters
  - Fixed time horizon
- Cohort Markov model
  - Time-dependent parameters
  - Time to event is important
  - Repeated events
  - Manageable number of health states

Model Types

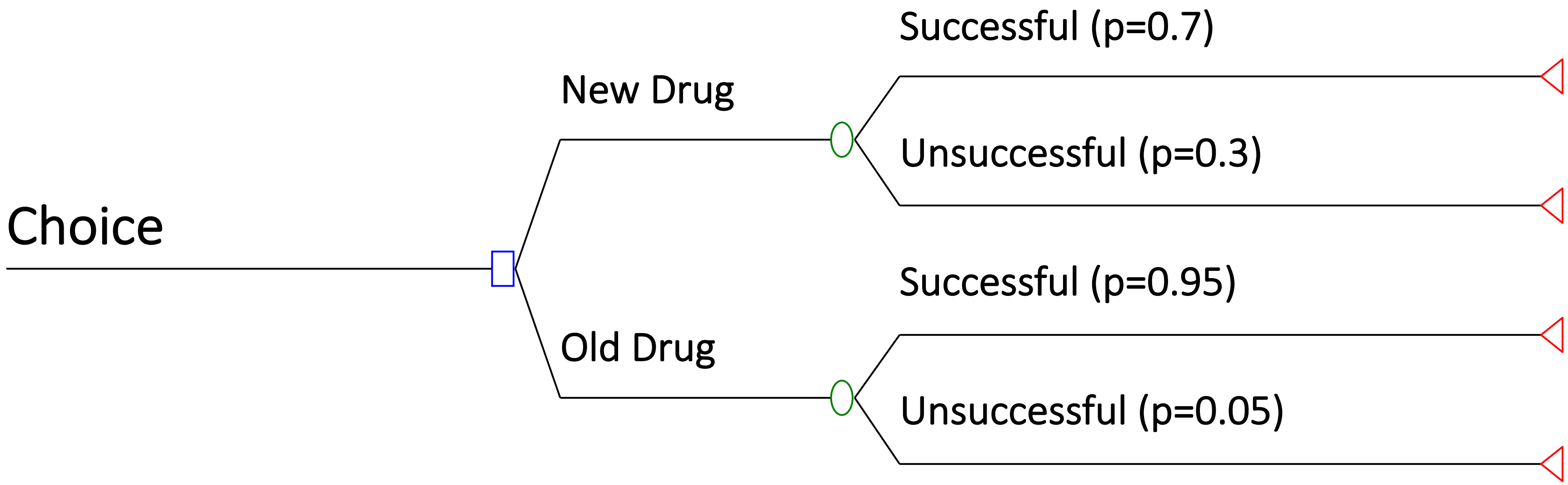
- Individual level state transition models (microsimulation)
  - Level of individual behavioral entity
  - Transition probabilities/outcomes determined by baseline/current patient characteristics, number/time/sequence of events
  - Reporting of distributions (not just means), individual history
- Dynamic transition models
  - Modelling spread of disease over time (transmission rates)
  - Often used for acute infectious diseases
- Discrete event simulation
  - Queueing problems, waiting lines
  - Time to event data
  - Microsimulation


Modelling problem
Is interaction between individuals important?
Yes
Is individual-level modelling needed?
No
System dynamics model
Yes
Discrete event simulation
No
Can patient pathways be represented adequately by probability trees?
Yes
Decision tree
No
Can a Markov model be built without needing an excessive number of states?
Yes
Markov model
No
Individual sampling model

Barton 2004

Decision Tree Exercise

Simple Decision Tree



QALYs

QALYs over patients lifetime if successful

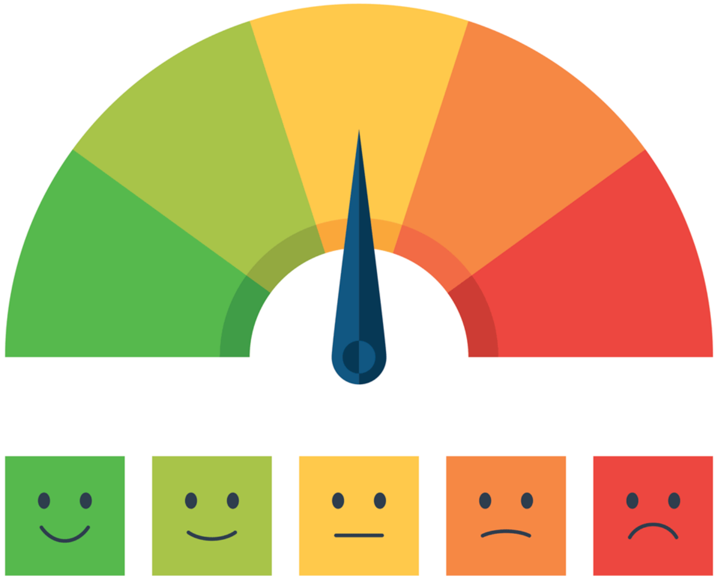
new drug – 30

old drug - 25

QALYs over patients lifetime if unsuccessful

new drug – 15

old drug - 23



Costs

New drug - £2,000
Old Drug - £150

Costs over patients lifetime if successful
- new drug - £10,000
- old drug - £5,000

Costs over patients lifetime if unsuccessful
- new drug - £20,000
- old drug - £10,000

Code

Two treatments, new drug and old drug

```
# Firstly, let's define the number of treatments we are looking at and their names
n.treatments<-2
t.names<-c("New Drug","Old Drug")
```

Code

Some blank space to fill in information

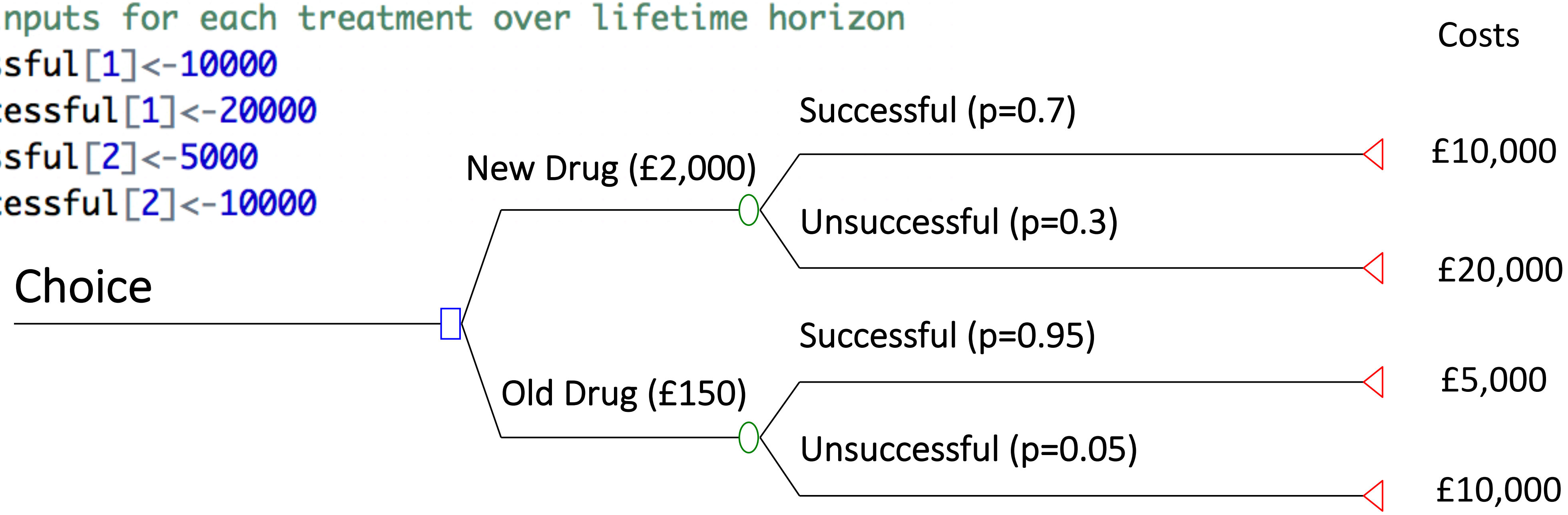
```
# First create some blanks to fill in
c.successful<-c.unsuccessful<-rep(NA,n.treatments)
q.successful<-q.unsuccessful<-rep(NA,n.treatments)
p.successful<-p.unsuccessful<-rep(NA,n.treatments)
```

Match up to the names of the drugs

```
# And we can name the vectors to correspond to the Drug A and Drug B to keep us calculating correctly
names(c.successful)<-names(c.unsuccessful)<-names(q.successful)<-
  names(q.unsuccessful)<-names(p.successful)<-names(p.unsuccessful)<-t.names
```

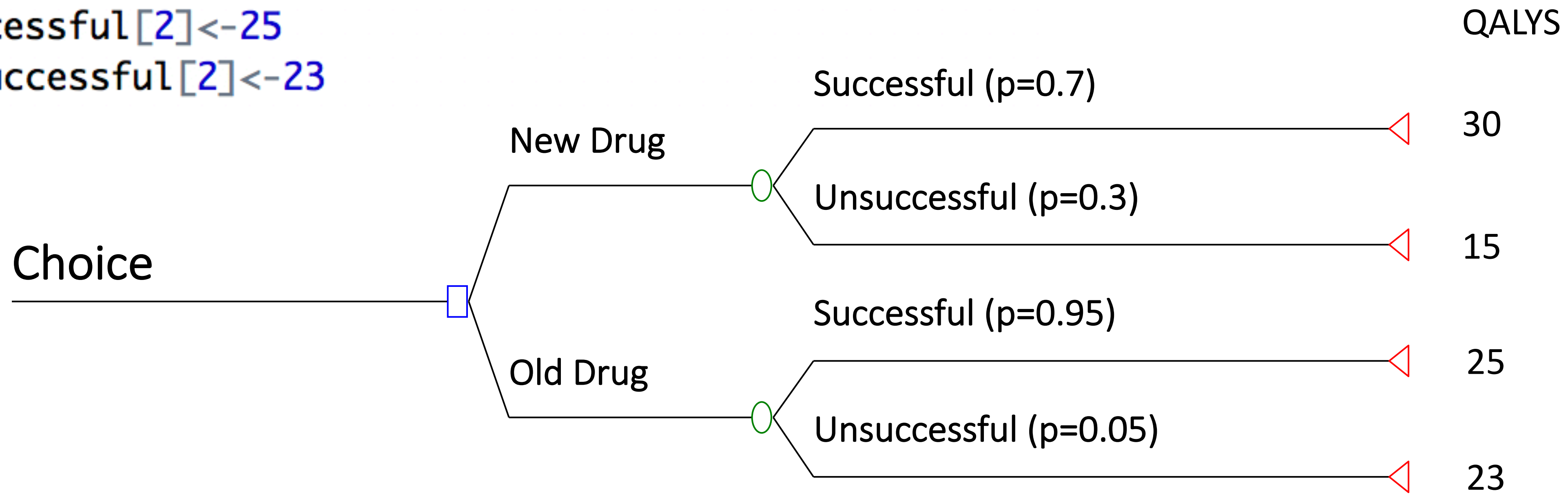
Input costs

```
# Now let's start with adding the cost information

# Cost of treatment
c.treat<-c(2000,150)

# Cost inputs for each treatment over lifetime horizon
c.successful[1]<-10000
c.unsuccessful[1]<-20000
c.successful[2]<-5000
c.unsuccessful[2]<-10000
```



Input QALYs

```
# Let's add in the QALY information

# QALY inputs for each treatment over lifetime horizon
q.successful[1]<-30
q.unsuccessful[1]<-15
q.successful[2]<-25
q.unsuccessful[2]<-23
```



Input probabilities

```
# Let's add in the probabilities

# Probabilities of successful and unsuccessful on new treatment
p.successful[1]<-0.7
p.unsuccessful[1]<-1-(p.successful[1])

# Probabilities of successful and unsuccessful on old treatment
p.successful[2]<-0.95
p.unsuccessful[2]<-1-(p.successful[2])
```

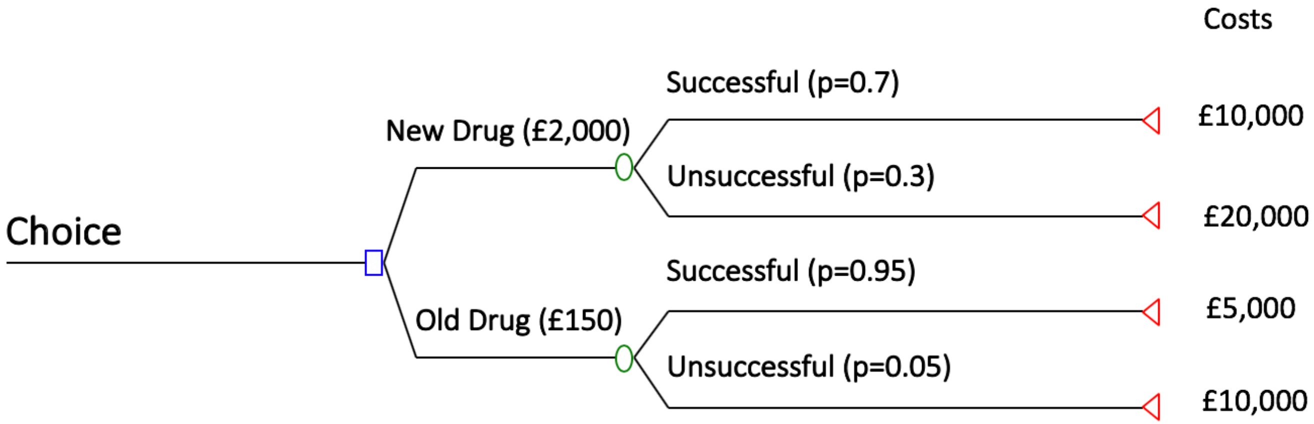
Code

Some blank space to fill in information

```
# Again create some blank cells to fill in for the calculations of costs and QALYs
incremental.costs<-incremental.effects<-costs<-effects<-rep(NA,n.treatments)

# And we can name the vectors so we again have Drug A and Drug B the right way around
incremental.costs<-incremental.effects<-names(c.treat)<-names(costs)<-names(effects)<-t.names
```

Some maths!

```
# Calculate the total costs and effects so we can calculate the ICER
costs<-c.treat+p.successful*c.successful+p.unsuccessful*c.unsuccessful

effects<-p.successful*q.successful+p.unsuccessful*q.unsuccessful
```



Results

```
# Calculate the incremental costs and QALYs
# We use [2] as we are using the old drug as the reference, and want to see the incremental cost per QALY of the new drug
incremental.costs<-costs-costs[2]
incremental.effects<-effects-effects[2]
```

```
# Calculate the incremental cost effectiveness ratio
ICER<-incremental.costs/incremental.effects
```

```
> ICER
New Drug
   16000
```