Methods for estimating Healthy Life Expectancy

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Introductions

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Actuarial Consultant

Andrew is a qualified actuary with experience in analysing health inequalities, modelling future health outcomes and quantifying risk and uncertainty.

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Analyst

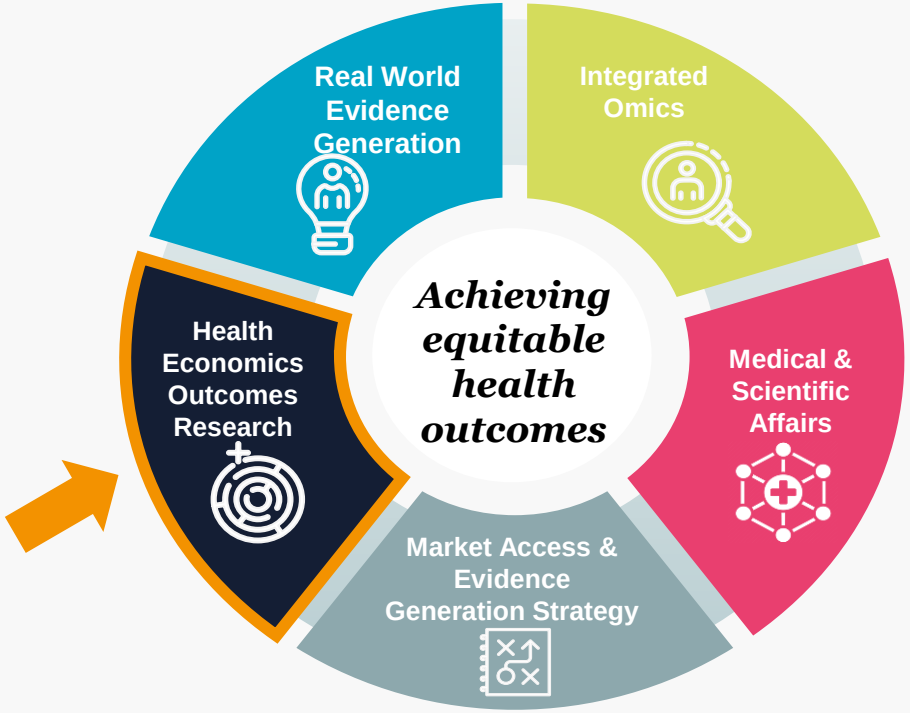
Jamie is an analyst in the HEOR team with experience in data analysis, mathematical modelling across a range of health applications and performing cost analyses for intervention comparisons.

Who are LCP Health Analytics?

LCP is a consultancy and technology firm with >1,000 people working across financial services and health and energy analytics.

Our health analytics team contains clinicians, epidemiologists, data scientists, health economists and actuaries. We leverage real world datasets and applied analytics to analyse the health and economic value of medicines and other healthcare sector interventions.

LCP Health Analytics website



Introduction to HLE

- What is Healthy Life Expectancy (HLE)?
- What are its applications?
- How is it calculated?
- Which method to use?
- Why R?

Recent article on HLE in
ISPOR Value & Outcomes Spotlight

HLE formed a key part of the UK government's 2022 *Levelling Up* mission

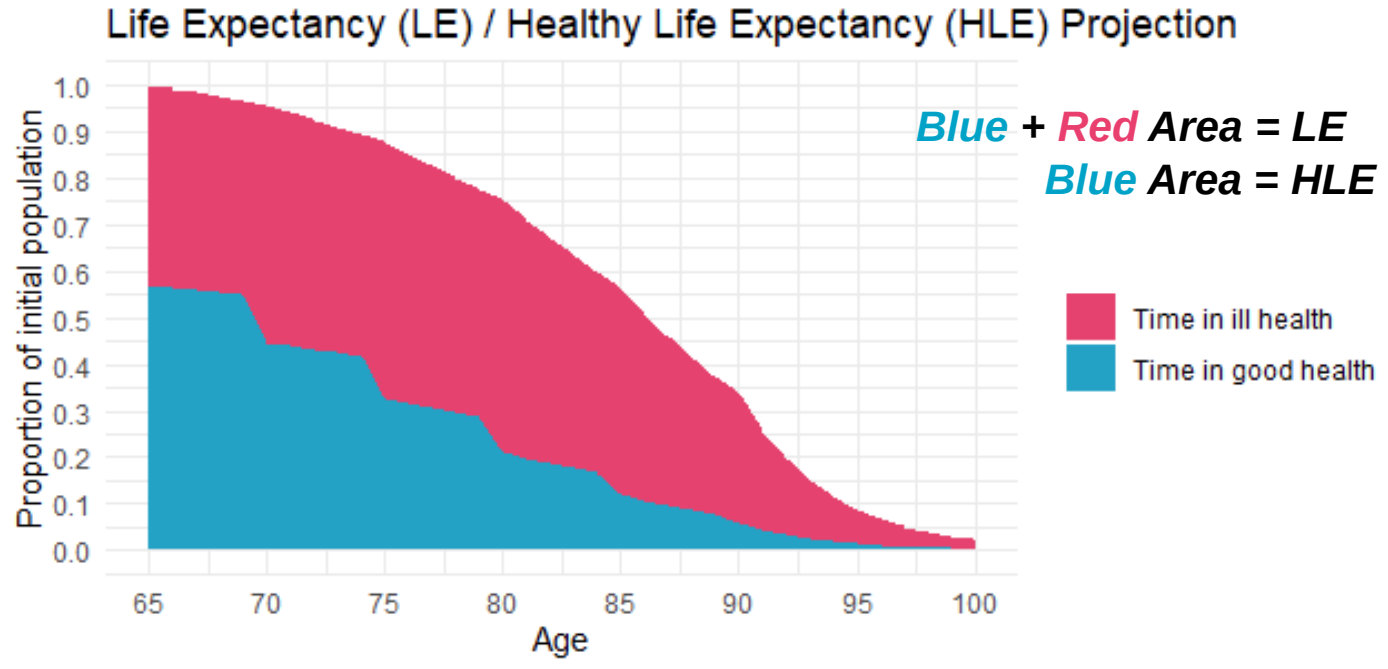
Health	By 2030, the gap in Healthy Life Expectancy (HLE) between local areas where it is highest and lowest will have narrowed, and by 2035 HLE will rise by five years.

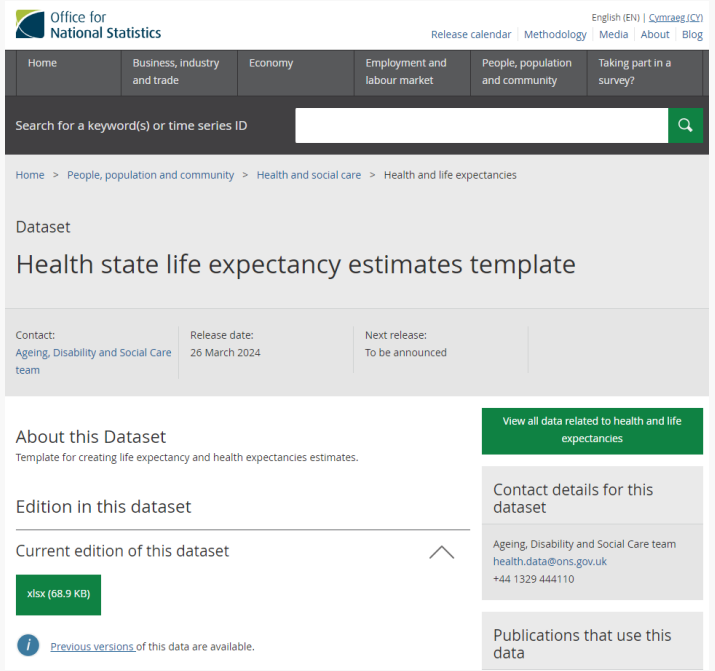
Source: Levelling Up the United Kingdom: Executive Summary (publishing.service.gov.uk)

Sullivan method

Sullivan Method: Summary

- Simplest and most widely used method for estimating HLE
- Requires mortality and health prevalence rates by age
- Can be implemented in Excel (ONS template available[1])
- R useful for repeated calculations – example code on subsequent slides





1. Health state life expectancy estimates template - Office for National Statistics (ons.gov.uk)

Sullivan Method: Life tables

Choose sensible "limiting age", e.g. 100, 110 or 120

Mortality rates

Proportion in good health

Age bands = single years of age

```r
sullivan <- function(Ages,qx,health_prev){

  n <- length(qx) # number of age bands
  px <- 1 - qx # survival rates

  lx <- qx
  lx[1] <- 10^5 # radix
  for (x in 2:n){
    lx[x] <- lx[x-1]*px[x-1]
  }

  tx <- c(cumsum(lx[n:2])[(n-1):1],0) # total future life years in each age band
  ex <- tx/lx # curtate life expectancy
```

Life table notation

- q_x = 1-year mortality rate = probability of death by age *x+1* for an individual currently aged *x*
- p_x = 1-year survival rate = 1 – q_x
- l_x = number of "lives" in the model cohort at age *x*
- t_x = total number of complete (integer) life-years lived by the model cohort from age *x*
- e_x = total number of complete life-years lived by an individual from age *x*

Sullivan Method: HLE calculation

Sullivan calculation
Multiply number of lives by proportion of healthy lives

Divide by **number of lives** (not healthy lives) at age x

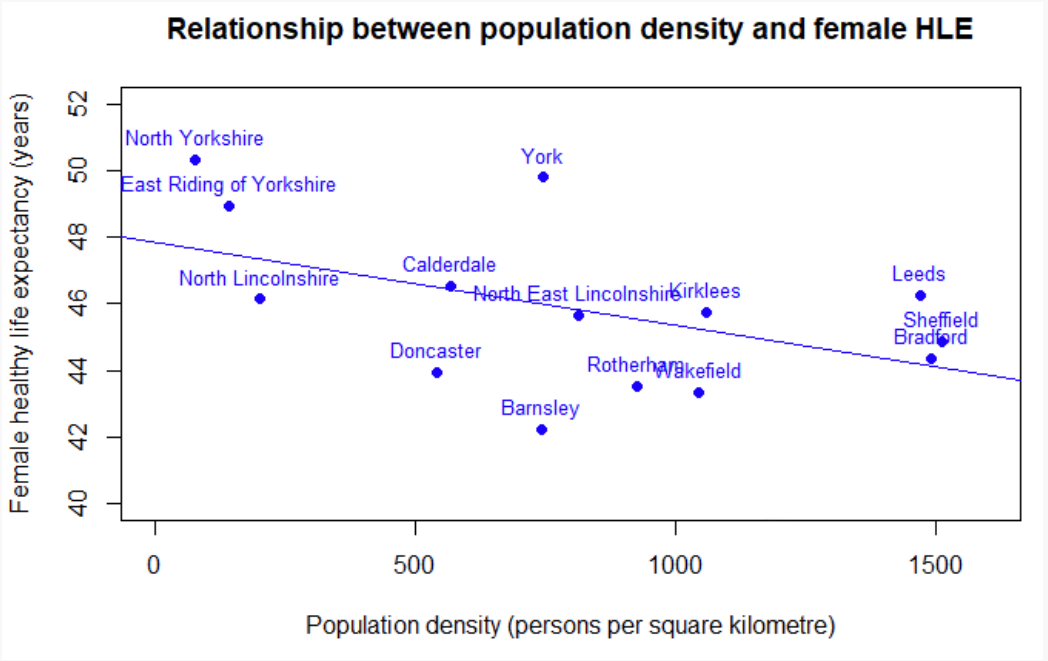
```
tx <- c(cumsum(lx[n:2])[(n-1):1],0) # total future life years in each age band
ex <- tx/lx # curtate life expectancy

lx_healthy <- lx*health_prev # number of healthy lives in each age band
tx_healthy <- c(cumsum(lx_healthy[n:2])[(n-1):1],0) # total future healthy life years in each age band
ex_healthy <- tx_healthy/lx # curtate healthy life expectancy

# Convert curtate life expectancies into whole life expectancies using an approximate half-year adjustment
LE <- round(ex + 0.5,2)
HLE <- round(ex_healthy + 0.5*health_prev,2)

output <- cbind(LE,HLE)
row.names(output) <- paste("Age",Ages)
output <- replace_na(output,0)
return(output) # return an array of LEs and HLEs at each age band
}
```

Example calculation

Age	Number of lives	Health prevalence	Number of healthy lives	Future years of good health (population)	Healthy life expectancy
…	…	…	…		…
49	**97,429**	0.80	97,429*0.80 = **77,515**	77,515/2 + 72,095 + 71,910 + … = **1,760,898**	**1,760,898 / 97,429 = 18.1 years**
50	**97,275**	0.74	97,275*0.74 = **72,095**	72,095/2 + 71,910 + … = **1,686,093**	**1,686,093 / 97,275 = 17.3 years**
51	**97,026**	0.74	97,026*0.74 = **71,910**	71,910/2 + … = **1,614,090**	**1,614,090 / 97,026 = 16.6 years**
…	…	…	…	…	…

Sullivan Method: HLE by local authority

- Function enables us to efficiently loop through HLE calculations for multiple populations and return output across multiple ages.
- We have applied the Sullivan function to ONS mortality and health prevalence data to estimate HLE for a range of local authorities.
- Could model the effect of interventions by editing the underlying mortality or health prevalence rates.

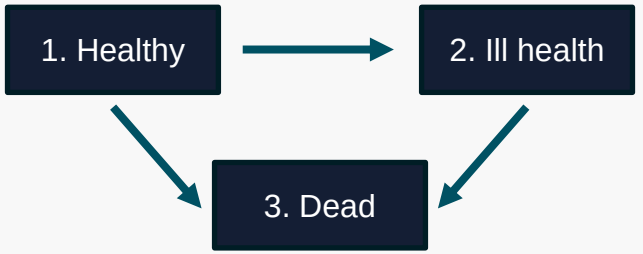


Multi-state models

Multi-state models: theory

Multi-state models

- Used to model systems characterised by a discrete set of states.
- Simplest example is H-I-D model, but can be extended by adding additional health states
- Recoveries (transitions from I to H) may be included or ignored
- Transition rates can be estimated from longitudinal data (regression-based) or set based on expert opinion (non-regression-based)
- Model in R using *msm* package[1].



Assumptions for msm

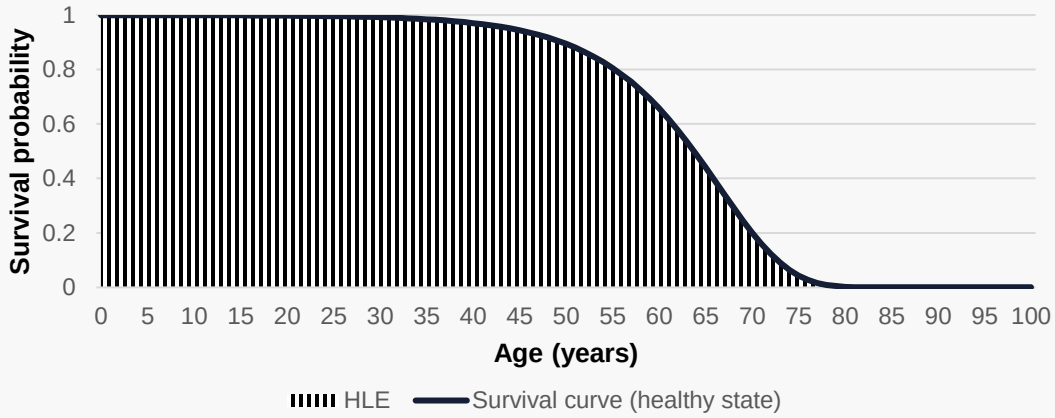
- Markov property: the probability of future transitions is only dependent on the current state and not on history
- Baseline hazards have a parametric form
- Continuous time

1. Jackson C (2011). Multi-state models for panel data: The msm package for R. *Journal of Statistical Software.* https://doi.org/10.18637/jss.v038.i08

Multi-state models: theory

Calculating healthy life expectancy

- Healthy life expectancy is calculated as time spent in the "Healthy" state
- If assuming no recoveries, this is the area under the survival curve for the "Healthy" state
- Calculate in R using *elect* package[1] on *msm* output



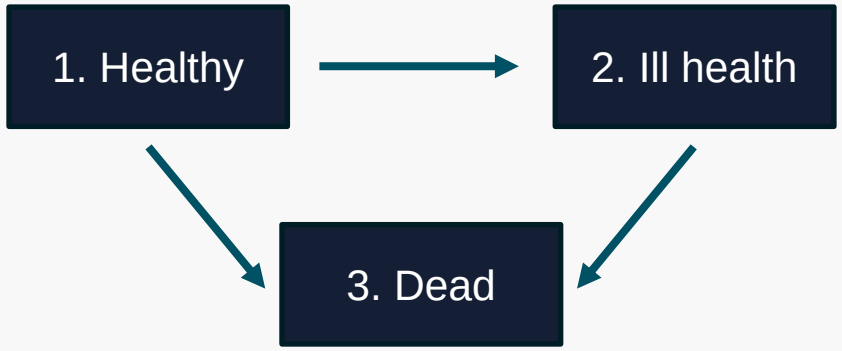
Assumptions for elect

- Baseline hazards defining each transition increase exponentially with age (Gompertz).
- Baseline state distribution

1. van den Hout. A and Sum Chan M (2019). elect: Estimation of Life Expectancies Using Multi-State Models. CRAN: Package elect (r-project.org)

Multi-state models – Code (msm)

- Here we illustrate an example using the simple 3 state H-I-D model.



Data input

- Requires a longitudinal dataset containing a single row for each observation of an individual.

id	age	state	baseline
1	44.4	1	1
1	59.3	2	0
1	76.2	2	0
2	35.2	1	1

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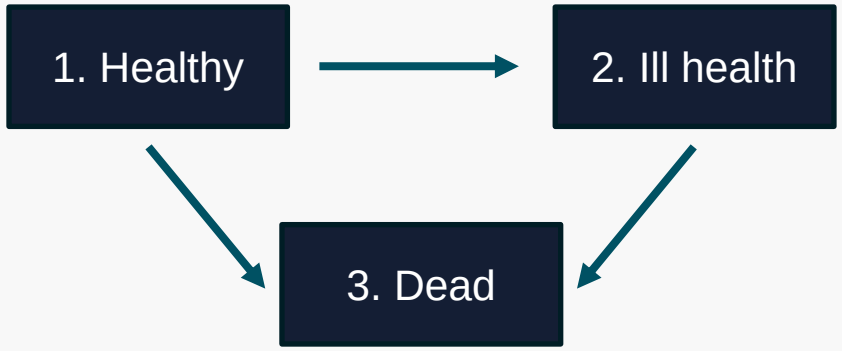

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Simplified code

```
> Q <- rbind(c(NA,0.1,0.1),
           c(NA,NA,0.1),
           c(NA,NA,NA))

> msm.output <- msm(state~age+covars, subject=id,
                    data=dta, qmatrix=Q)
```

The Q-matrix defines the allowable transitions, in this case:

$$\begin{pmatrix} NA & 1 \to 2 & 1 \to 3 \\ NA & NA & 2 \to 3 \\ NA & NA & NA \end{pmatrix}$$

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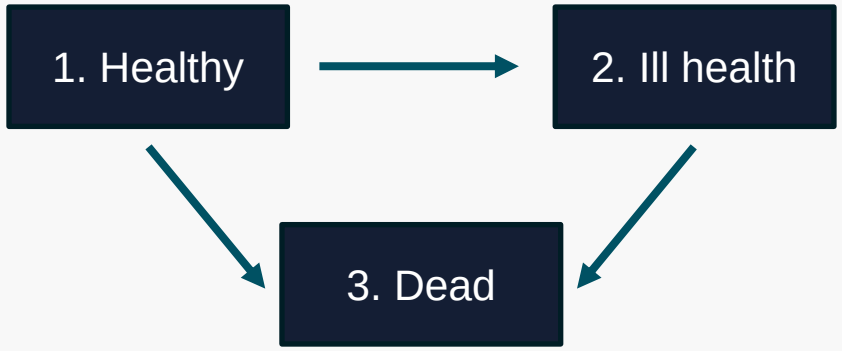

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Other useful arguments

- `obstype` used to specify whether transition times are exactly known, and in more complex models, whether the state immediately before transition is known.
- `deathexact` used to specify whether the entry time to absorbing (death) state is exactly known.

Multi-state models - Code (elect)

- The *elect* package uses the fitted model in *msm* to calculate state-specific life expectancies.

Simplified code

Define baseline state distribution

The first covariate should be age

```
> sddata <- dta[dta$baseline==1,]

> output <- elect(x=msm.output, b.covariates=list(age=0, covars=…),
                  statedistdata=sddata, h=0.1, setseed=1234,
                  age.max=120, S=100, time.scale.msm = “years”)
```

age.max defines the maximum allowed age

S defines the number of iterations if interested in uncertainty

h specifies the grid size to be used to calculate the integrals

time.scale.msm defines the time units used in the multi-state model.

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Output

```
Point estimates, and mean, SEs, and quantiles from simulation:
       pnt     mn    se 0.025q   0.5q 0.975q
e11 62.771 62.771 0.056 62.675 62.775 62.864
e12 16.873 16.876 0.097 16.653 16.880 17.059
e21  0.000  0.000 0.000  0.000  0.000  0.000
e22 42.208 42.216 0.105 42.023 42.217 42.426
e.1 62.771 62.771 0.056 62.675 62.775 62.864
e.2 16.873 16.876 0.097 16.653 16.880 17.059
e   79.645 79.647 0.089 79.475 79.646 79.794
```

e11 provides an estimate of Healthy Life Expectancy

e provides an estimate of Life Expectancy

Conclusions

Recap

Sullivan method

- The Sullivan method incorporates health prevalence rates into standard life table calculations.
- Calculation-light method relying on cross-sectional data.
- Calculations can be carried out in Excel, but R allows for greater efficiency and replicability.

Multi-state models

- Multi-state models can project patient health trajectories and allow for multiple health states.
- However, for regression-based multi-state models the data requirements are more complex.
- Specific R packages can be used to fit multi-state models and produce HLE estimates.

Scope for HLE in HTAs?

Alternative or supplement to QALY calculations

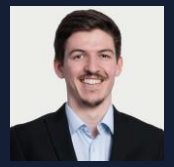
- NICE primarily uses Quality-Adjusted Life Years (QALYs) to measure the benefits of healthcare technologies.
- HLE is an analogous composite measure of longevity and health which can be applied in specific disease areas.
- In certain situations, binary health state data may be easier to collect than the granular QoL data typically required for estimating QALYs.
- HLE can be mapped to QALYs by assigning QoL scores to each health state.

Broader value of measuring HLE

- Analysing the impact of interventions on HLE at a local and national level could provide an intuitive understanding of their benefits, including their contribution towards government HLE targets.

Any questions?

Contact us



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Our strategic mission:
We aim to lead the transition of health systems from importers of illness to exporters of health through realigning value between patients, manufacturers of medicines and payers.

Our mission is to help transition health systems from importers of illness to exporters of health

Addressing the two driving challenges for health systems:

- Increasingly complex multimorbid unmet patient needs
- A misalignment of how HTA bodies and governments value medicines and the value – healthcare and wider societal – of health to patients, populations and economies.

Underpinned by our approach to support clients to improve the population's health and reduce inequalities

Expertise in data science, medicine, research, health economics, epidemiology & statistics

State of the art expertise, methods and technology

Why LCP Health Analytics?

Visionary approach to our clients' challenges

- Leading the market in identifying solutions for tomorrow's challenges for patients, health systems and our clients
- Clear mission-based team and approach

Unique leadership team & sector experience

- Unique combination of leadership experience across science, medicine, pharmaceutical, consultancy and policy sectors
- Demonstrative partnerships and network with key decision makers across the sector

Delivering greater value to clients

- Thought partners who deliver value beyond core issues and leverage early access to emerging datasets and collaborations
- Continuity of team from pitch to delivery, with hands on project leadership by senior experts across service areas

We leverage real world datasets and applied analytics to enable clear articulation of health and economic value of medicines in an increasingly complex healthcare environment.