# Numerical Integration with an application to Sample size re-estimation 

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## Outline

- Give a brief introduction to quadrature
- Describe the Stata command and MATA function
- how to use these for simple integrals
- Numerical difficulties
- Apply it to a harder problem of sample size re-estimation


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## Quadrature

Quadrature is another name for numerical integration, which is essentially transforming integration into a summation

$$
\int_{a}^{b} W(x) f(x) \mathrm{d} x \approx \sum_{j=0}^{N-1} w_{j} f\left(x_{j}\right)
$$

where $w_{j}$ are weights and $x_{j}$ are the abscissas.

- Functions $W(x)$ are chosen for the appropriate interval $[a, b]$
- the corresponding $w_{j}$ and $x_{j}$ values are found using o polynomials (defined by recurrence functions)


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## Common forms of the weight function

Only considered three $W(x)$ functions over three ranges

1. $[-1,1]$ - Gauss-Legendre quadrature, $W(x)=1$
2. $[0, \infty]-$ Gauss-Lageurre quadrature, $W(x)=\exp (-x)$
3. $[-\infty, \infty]$ - Gauss-Hermite Quadrature, $W(x)=\exp \left(-x^{2}\right)$

All of these methods have been implemented in a Stata command
integrate available on SSC.
Most of the calculation are written in MATA and uses the trick
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## How to find the weights/abscissas

The roots of the Legendre polynomial defined by

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\begin{aligned}
P_{0}(x) & =1 \\
P_{1}(x) & =x \\
(n+1) P_{n+1}(x) & =(2 n+1) x P_{n}(x)-n P_{n-1}(x)
\end{aligned}
$$

are the abscissas.

- Finding the roots say using polyroots() has limited precision of the machine.
- Golub and Welch solution was to construct a similarity matrix


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## Similarity Matrix corresponding to Legendre polynomial

$$
\left(\begin{array}{ccccc}
0 & \frac{1}{\sqrt{41^{2}-1}} & & & \\
\frac{1}{\sqrt{4 * 1^{2}-1}} & 0 & \frac{2}{\sqrt{4 * 2^{2}-1}} & & \\
& \frac{2}{\sqrt{4 * 2^{2}-1}} & \ddots & \ddots & \\
& & \ddots & & \\
& & & 0 & \frac{n-1}{\sqrt{4 *(n-1)^{2}-1}} \\
& & & \frac{n-1}{\sqrt{4 *(n-1)^{2}-1}} & 0
\end{array}\right)
$$

The eigenvalues are the abscissas and the eigenvectors are used to find the weights.

Hermite polynomial with $n>60$ gives the wrong answers using eigensystem() function.

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## Basic syntax

To calculate the following expression

$$
\int_{a}^{b} f(x) d x
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In Stata
integrate, function( $f(x)$ ) lower(a) upper(b)
In Mata if the function $f()$ already exists then the function
address is passed to integrate
integrate( (\&工(), a, b)

- $-\infty$ is specified by setting $a=$
- similarly if $b=$ then the unner limit is $\infty$


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- similarly, if $b=$. then the upper limit is $\infty$


## Simple example - Stata

$$
\begin{equation*}
\int_{0}^{3} x^{2} d x \tag{1}
\end{equation*}
$$

## Using the Stata command

```
integrate, f(x:^2) l(0) u(3)
    Note: The function to be integrated will be compiled using Mata and stored in your personal
    directory ~/ado/personal/ (make sure this is writeable)
The integral = 9
```

Could have done
integrate, $f\left(x^{*} 2\right)$ l(0) u(3) vectorise

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## Could have done

integrate, $f\left(x^{\wedge} 2\right)$ l(0) $u(3)$ vectorise

## Simple example - Mata

First define the integrand as a new function, the function must return a row vector and the variable of integration must be a rowvector.

```
real rowvector f(real rowvector x)
{
    return(x:^2)
}
```

Then to integrate this function type with Mata
: integrate(\&f(), 0, 3) 9

All the examples from now on will be based only on the Mata function. Which is available via SSC, integrate.mata contains a do file to compile the mata code

## Mata syntax

The syntax of the Mata function
real scalar integrate(\&function(), real scalar lower, real scalar upper $\mid$, real scalar quadpts, real rowvector xarg)
has optional arguments for number of quadrature points and a rowvector of additional arguments that are passed to the function()

- Note that integrate returns a real scalar


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## Double Integration

$$
\int_{0}^{1} \int_{0}^{1} x+y d x d y
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Want to just write integrate ( integrate (\&f(), 0,1 ) , 0,1 )

- However integrate() does not return a rowvector so this syntax would fail


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## Solution

First define

```
real rowvector fxy(real rowvector x, real rowvector y)
{
    return(x:+y)
}
```

real rowvector f_inner (real rowvector y)
for (i=1; i<=cols(y);i++) \{
if (i==1) f=integrate(\&fxy(), 0, 1, 40, y[i])
else $f=f, i n t e g r a t e(\& f x y(), 0,1,40, y[i])$
return (f)
\}
: integrate(\&f_inner(), 0, 1)
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}
```

: integrate(\&f_inner(), 0, 1) 1

## Further Double Integration

$$
\int_{0}^{2} \int_{0}^{y^{2}} 6 x y d x d y
$$

This is also a simple extension to the previous code

## Solution

```
real rowvector fxy2(real rowvector x, real rowvector y)
{
    return(6:*x:*y)
}
```

real rowvector f_inner2(real rowvector y)
for (i=1; i<=cols(y);i++)
if (i==1) f=integrate(\&fxy2(), 0, y[i] $2,40, y[i])$
else $f=f$, integrate(\&fxy2(), 0, y[i] $2,40, y[i])$
\}
return(f)
: integrate(\&f_inner2(), 0, 2)
32

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```
real rowvector fxy2(real rowvector x, real rowvector y)
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    return(6:*x:*y)
}
real rowvector f_inner2(real rowvector y)
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    for(i=1; i<=cols(y);i++) {
        if (i==1) f=integrate(&fxy2(), 0, y[i]^2, 40, y[i])
        else f = f, integrate(&fxy2(), 0, y[i]^2, 40, y[i])
    }
    return(f)
}
```

: integrate(\&f_inner2(), 0, 2)
32

## Sample size re-estimation

Usually when designing a clinical trial we pre-specify the value of a treatment effect (and all the nuisance parameters) to find the sample size.

- We plan to do a single interim analysis to re-evaluate this sample size
- Going to apply the methods to a real trial example


## Trial details

- Currently limited treatment options for Osteoarthritis (OA) of the knee. Not suitable or ineffective for many people. Surgery often only remaining option
- Methotrexate used effectively for Rheumatoid arthritis but not OA
- Promising results from pilot study $(\mathrm{n}=30)$ showed significant pain reduction for methotrexate in OA
- Study team proposed to test the drug's performance in addition to standard care in a double blind, randomized, placebo controlled trial


## The problem

- Initial grant application received positive feedback from funder
- Unfortunately it was rejected due to lack of evidence about the effect size likely to be seen in the RCT


## Potential solution

Wanted to use a method that:

1. can be fully specified in advance of the trial;
2. can be implemented by an independent non-expert data monitoring committee;
3. is not motivated via a complex conditional error function; and
4. is motivated by clear decision framework linking interim effect size with future sample size via a simple and familiar formula

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## Notation

- Assume observations in experimental treatment group $X$ and standard therapy group Y are normally distributed with means $\mu_{x}$ and $\mu_{y}$ and have a common known variance of $\sigma^{2}$
- Parameter of interest is $\delta=\frac{\mu_{x}-\mu_{y}}{\sigma} . H_{0}: \delta \leq 0$
- Fixed design: n patients per arm
- Choose $n=\frac{2}{\delta^{2}}\left(Z_{\alpha}+Z_{\beta}\right)^{2}$, where $Z_{u}=\Phi^{-1}(1-u)$
- e.g. if $\delta=0.35, \alpha=0.025$ and $\beta=0.2$ then $n=128$ patients per arm

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## Estimation and inference for $\delta$

- $\bar{x} \sim N\left(\mu_{x}, \sigma^{2} / n\right), \bar{y} \sim N\left(\mu_{y}, \sigma^{2} / n\right)$ and $\hat{\delta}=\frac{\bar{x}-\bar{y}}{\sigma}$
- $z=\frac{\hat{\delta}}{\sqrt{2 / n}} \sim N\left(\frac{\delta}{\sqrt{2 / n}}, 1\right)$

- if $\delta \ll 0.35$ then substantially more than 128 people needed
- if $\delta \gg 0.35$ then trial is a waste of resources

A general two stage strategy

- Suppose instead $n_{1}(\ll n)$ patients initially recruited giving: $\hat{\delta}_{1}=\frac{\bar{x}-\bar{y}}{\sigma}$ and $z_{1}=\frac{\hat{\delta}_{1}}{\sqrt{2 / n_{1}}} \sim N\left(\frac{\hat{\delta}}{\sqrt{2 / n_{1}}}, 1\right)$ at the interim analysis. Then if:
$\left\{\begin{array}{cl}z_{1}>k & : \text { Stop the trial for efficacy } \\ z_{1}<h & : \text { Stop the trial for futility } \\ h \leq z_{1} \leq k & : \text { Recruit further } n_{2} \text { patients }\left(z_{1} \uparrow \Rightarrow n_{2} \downarrow\right)\end{array}\right.$

Base inference at stage 2 on combined data via test statistic:


How to choose design parameters $h, k, C$ and function $n_{2}\left(z_{1}\right)$ ?

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\end{array}\right.
$$

Base inference at stage 2 on combined data via test statistic:

$$
z=\frac{\sqrt{n_{1}} z_{1}+\sqrt{n_{2}\left(z_{1}\right)} z_{2}}{\sqrt{n_{1}+n_{2}\left(z_{1}\right)}} \text { Reject } H_{0} \text { if } z \geq C
$$

How to choose design parameters $h, k, C$ and function $n_{2}\left(z_{1}\right)$ ?

## Chosing h,k,C via the Li et al. method

- Choose an overall type I error $\alpha$ and conditional power $1-\beta_{1}$
- Choose $h$ and $k$ almost freely (e.g based on p-value for $z_{1}$ )
- There are restrictions based on the error probabilities
- Find $C$ such that:

1. $P\left(z_{1}>k \mid \delta=0\right)+P\left(z>C \mid \delta=0 ; h<z_{1}<k\right)=\alpha$
2. $P\left(z>C \mid \delta=\hat{\delta}_{1}, h<z_{1}<k\right) \geq 1-\beta_{1}$

Given $n_{2}\left(z_{1}\right)=\left(\frac{\left(C+z_{\beta_{1}}\right)^{2}}{z_{1}^{2}}-1\right) n_{1}$, for $z_{1} \in(h, k)$

- A very simple method
- No complex conditional error function (Proschan and Hunsberger, 1995)
- Critical value $C$ independent of $z_{1}$
- Whole design and analysis can be specified in advance


## Finding C

From Li et al. (2002) they state that one can use numerical integration to solve

$$
1-\Phi(h)-\alpha=\int_{h}^{k} \Phi\left[\frac{C\left(C+Z_{\beta_{1}}\right)-z_{1}^{2}}{\sqrt{\left(C+Z_{\beta_{1}}\right)^{2}-z_{1}^{2}}}\right] \phi\left(z_{1}\right) \mathrm{d} z_{1}
$$

this is solved for $c$ (the other design parameters are selected previously)

Need to use optimize() and integrate() together!!

## Programming up finding $C$

```
real rowvector findC(real rowvector x, real rowvector arg)
{
    c=arg[1]
    zb = arg[2]
    return( normal((c:*(c:+Zb):-x:^2):/sqrt((c:+Zb):^2:-x:^2)):*normalden(x) )
}
void evalC(todo, c, h, k, alpha, Zb, y, g, H)
{
    y=(integrate(&findC(),h,k,60,(c, Zb))-(1-normal(h)-alpha))^2
}
```

void calculateC(h, k, alpha, power)
Zb-invormar (power)
C = optimize_init()
optimize_init_which(C, "min")
optimize_init_evaluator (C, \&evalC ())
optimize_init_tracelevel(c, "none")
optimize_init_params(C, 1)
optimize_init_argument (C, 1, h)
optimize_init_argument ( $\mathrm{C}, 2, \mathrm{k}$ )
optimize_init_argument ( $\mathrm{C}, 3$, alpha)
optimize_init_argument ( $\mathrm{C}, 4, \mathrm{Zb}$ )
$\mathrm{c}=$ optimize (C)

## Programming up finding $C$

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    y=(integrate(&findC(),h,k,60,(c, Zb))-(1-normal(h)-alpha))^2
}
void calculateC(h, k, alpha, power)
{
    Zb=invnormal(power)
    C = optimize_init()
    optimize_init_which(C, "min")
    optimize_init_evaluator(C, &evalC())
    optimize_init_tracelevel(C, "none")
    optimize_init_params(C, 1)
    optimize_init_argument(C,1,h)
    optimize_init_argument(C,2,k)
    optimize_init_argument (C,3, alpha)
    optimize_init_argument(C,4,Zb)
    c = optimize(C)
}
```


## Stata code for Sample size re-estimation

```
. ssr
Sample Size Re-estimation
The following are set in the first stage
    The sample size per arm is 50
    The futility bound is 1
    The efficacy bound is 2.76
    The conditional power is . }
    The unconditional power is . }
The Li et al. critical value is 1.923
+----------------------------------------------------
| NOTE
| A fixed sample size requires }129\mathrm{ people
| for a treatment effect of .35,
| unconditional power . }8\mathrm{ and
| one-sided significance of .025
+--------------------------------------------------
```


## ssr,graph



129 is the fixed design sample size

## Conclusions

- integrate is a flexible function
- Still need to get a better Gauss-Hermite solution
- ssr, the Stata command, is available to design sample size re-estimation
- there are several methods that are available in a future publication Bowden and Mander

