

Simulations for two-dimensional distance sampling with time

David L. Borchers and Martin J. Cox

June 18, 2014

1 Set-up

1.1 Load packages and code and set-up

```
> source("~/dropbox/packages/2D distance sampling with time/R/2D_LT_functions V2a1.r")
>
```

Set-up maximum distances:

```
> ystart=3 #maximum y-dimension distance
> w=1 #truncation distance
```

Set-up survey grid

```
> gridx=seq(w/100,w,length=100)
> gridy=seq(ystart/100,ystart,length=100)
```

1.2 Specifications for true animal density

True variation in animal density with respect to the track line is defined by `pi.x`:

```
> ##Truncated normal
> mu.pi=0#0.5
> sd.pi=0.2
> pi.x=pi.norm; logphi=c(mu.pi,log(sd.pi))
> ##Uniform:
> #pi.x=pi.const; logphi=c(1,NA)
> ##Hazard rate - form 2
> #pi.x=pi.hr2; logphi=log(c(0.75,1))
```

NB hazard rate density is used to test the MLE to ensure the density distribution can be disentangled from the detection function - we can assume perfect detectability and a hazard density distribution, then obtain MLE results. The selected true perpendicular density `pi.x`, with parameters `logphi` is shown in Fig. 1.

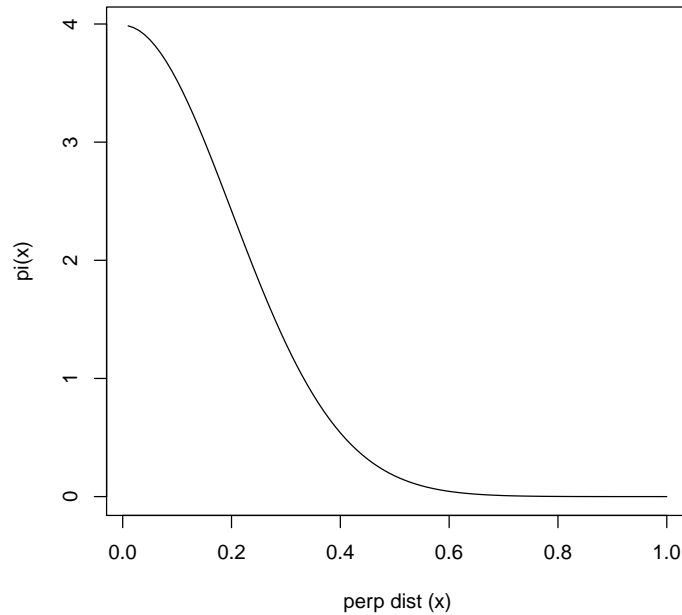


Figure 1: Perpendicular density distribution, $\pi(x)$ as specified in `pi.x` and parameters `logphi`.

```
> adbn=pi.x(gridx,logphi,w)
> plot(gridx,adbn,type="l",ylim=c(0,max(adbn)),
+       xlab="perp dist (x)",ylab="pi(x)")
```

1.3 Hazard rate

The true hazard rate function is specified using:

```
> #hr=h1; b=log(c(0.75,0.2))
> #hr=h1; b=log(c(0.001,1))
> #hr=h.okamura; b=log(c(50,25))
> hr=h2; b=log(c(0.75,1)) # this produces a sensible h-r p(x) shape
> #hr=h.const; b=c(1,NA)
```

The selected true hazard function `hr`, with parameters `b` is shown in Fig. 2.

```
> haz=outer(gridx,gridy,FUN=hr,b=b)
> persp(gridx,gridy,log(haz),theta=45,phi=35)
```

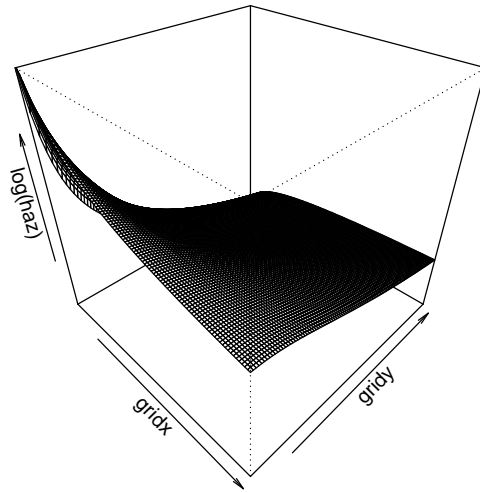


Figure 2: Hazard rate function, $h(y|x)$, displayed on the log scale as specified in `pi.x` with parameters `b`.

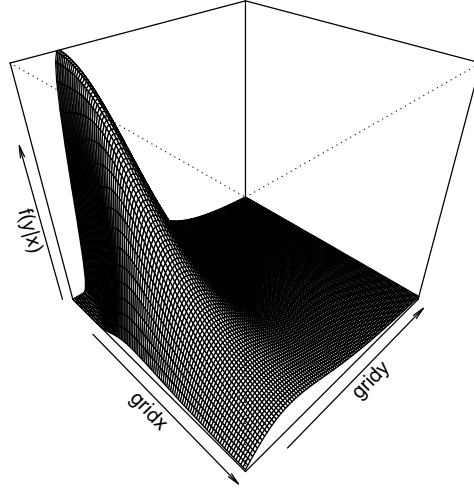


Figure 3: PDF of waiting distance, $f(y|x)$.

A pdf of *waiting distance* - the y -dimension distance when detections occur - $f(y|x)$ across the x, y grid is given in Fig. 3.

```
> f=outer(gridy,gridx,FUN=fyx,b=b,hr=hr,ystart=ystart)
> persp(gridx,gridy,t(f),theta=45,phi=35,zlim=c(0,max(f)),zlab="f(y|x)")
```

and the survival function $p(x)$ is given in Fig. 4.

```
> p.x=px(gridx,b,hr,ystart,nint=100)
> plot(gridx,p.x,type="l",ylim=c(0,max(p.x)),xlab="prep. distance, x",ylab="p(x)")
```

2 Simulating sightings

Now we have specified a survival function and density distribution we can simulate sightings from a known population of N animals:

```
> N=50
> simRes=simXY(N=N,pi.x=pi.x,logphi=logphi,
+             hr=hr,b=b,w=w,ystart=ystart)
> x=simRes$locs$x; y=simRes$locs$y
```

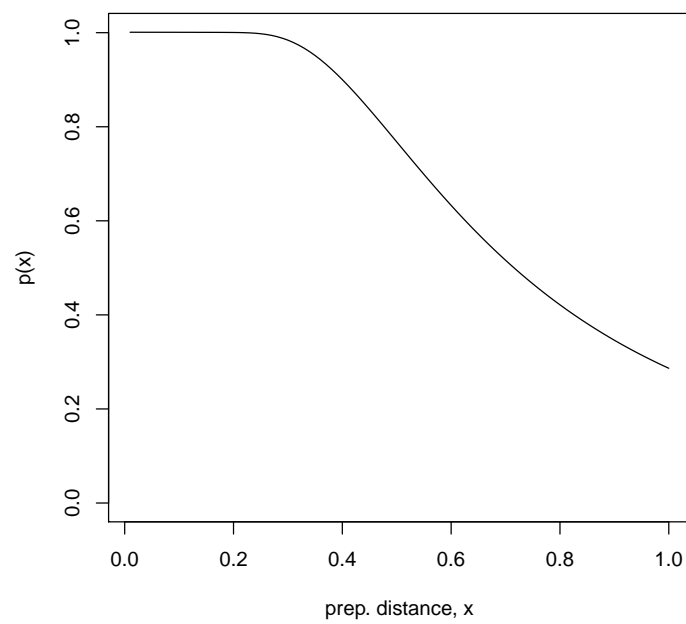


Figure 4: Survival function, $p(x)$.

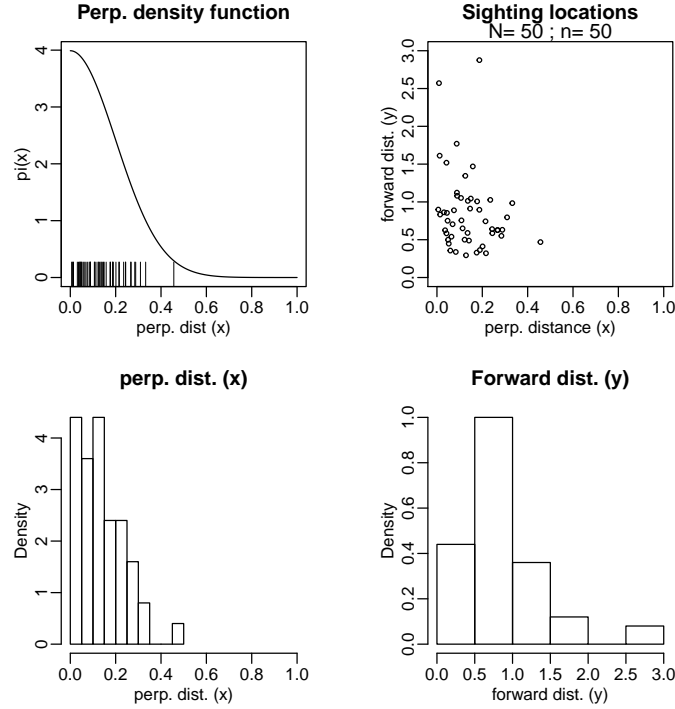


Figure 5: Simulated positions.

and plot the results (Fig. 5).

3 Maximum likelihood estimation

Now we have specified a true hazard function, $h(y|x)$ (R object `hr`) and perpendicular density distribution $\pi(x)$ (R object `pi.x`) and simulated sightings (R objects `x` and `y`), we can use our maximum likelihood to estimate parameters for $h(y|x)$ and $\pi(x)$. In our first example, we use the known forms of $h(y|x)$ and $\pi(x)$ and use their true parameters as starting values:

```
> #(pars=c(b,logphi))
> (pars=c(b,0.3,-1.2))

[1] -0.2876821  0.0000000  0.3000000 -1.2000000

>
```

The negative log-likelihood function that we will maximise is:

```
> (negloglik.yx(y,x,pars,hr,ystart,pi.x,w))
```

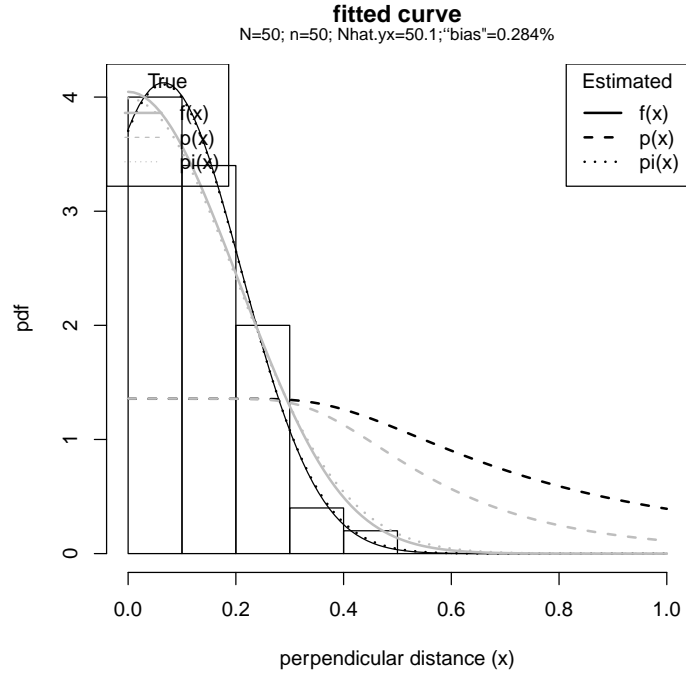


Figure 6: Maximum likelihood fit.

```
[1] 0.4922518
```

```
>
```

and is maximised here:

```
> est.yx=fityx(y,x,b,hr,ystart,pi.x,logphi,w)#,control=list(trace=5))
```

4 Results

The resulting fit is plotted in Fig. 6, and from a population of $N = 50$ animals, of which $n = 50$ were seen, the MLE gave $\hat{N} = 50.1$ and was 0.284% biased.