Exoplanet Population Inference

Josh Speagle (12/10/2016)

This notebook demonstrates how to perform exoplanet populaton inference building on the framework from Foreman-Mackey, Hogg, & Morton (2014) (https://arxiv.org/abs/1406.3020) and well as the "demo" IPython Notebook included in this repository. The goal is to evaluate the frequency of Earth analogs given data from the *Kepler* spacecraft circa 2013 or so.

Let's first initialize the environment to enable easier plotting and use of numerical Python packages and functions.

In [1]:
```
%pylab
%matplotlib inline
from IPython.display import display, Math, Latex
sys.path.insert(0, "./code")

# re-defining plotting defaults
from matplotlib.font_manager import FontProperties
from matplotlib import gridspec
rcParams.update({'xtick.major.pad': '7.0'})
rcParams.update({'xtick.major.size': '7.5'})
rcParams.update({'xtick.major.width': '1.5'})
rcParams.update({'xtick.minor.pad': '7.0'})
rcParams.update({'xtick.minor.size': '3.5'})
rcParams.update({'xtick.minor.width': '1.0'})
rcParams.update({'ytick.major.pad': '7.0'})
rcParams.update({'ytick.major.size': '7.5'})
rcParams.update({'ytick.major.width': '1.5'})
rcParams.update({'ytick.minor.pad': '7.0'})
rcParams.update({'ytick.minor.size': '3.5'})
rcParams.update({'ytick.minor.width': '1.0'})
rcParams.update({'xtick.color': 'k'})
rcParams.update({'ytick.color': 'k'})
rcParams.update({'font.size': 26})
```

```
Using matplotlib backend: Qt5Agg
Populating the interactive namespace from numpy and matplotlib
```

We'll also need a couple system commands, as well as the code Foreman-Mackey has provided for this project.

In [2]:
```
import sys
import load_data
```

Finally, we'll want to import **emcee** (http://dan.iel.fm/emcee/current/), the flexible Markov Chain Monte Carlo (MCMC) sampler developed by Foreman-Mackey et al. (paper (https://arxiv.org/abs/1202.3665)).

```
In [3]: import emcee
```

Introduction

NASA's *Kepler* mission has ushered in a golden age for exoplanet science by enabling the discovery \textit{thousands} of exoplanet candidates. In particular with such large numbers of exoplanet candidates available (most of which are likely real), we are now able to make robust conclusions about the overall population of exoplanets for the first time. In particular, many of these planets orbit "Sun-like" stars, and we now have large enough numbers that it is now possible to infer changes in the population of exoplanets as a function of their physical parameters (mainly period P and radius R). This is interesting not only from the perspective of estimating (crudely) how common our own circumstances are, but also can offer meaningful probabilistic constraints on planet formation theories.

We define the occurence rate of Earth analogs $\Gamma_\oplus$ to be **the expected number of planets per star per natural logarithmic bin in period and radius, evaluated at the period and radius of Earth**:

$$\Gamma_\oplus = \left.\frac{dN}{d\ln P d\ln R}\right|_{R=R_\oplus,\, P=P_\oplus} \quad .$$

As no Earth analogs have been detected, this constraint requires an extrapolation in both period and radius.

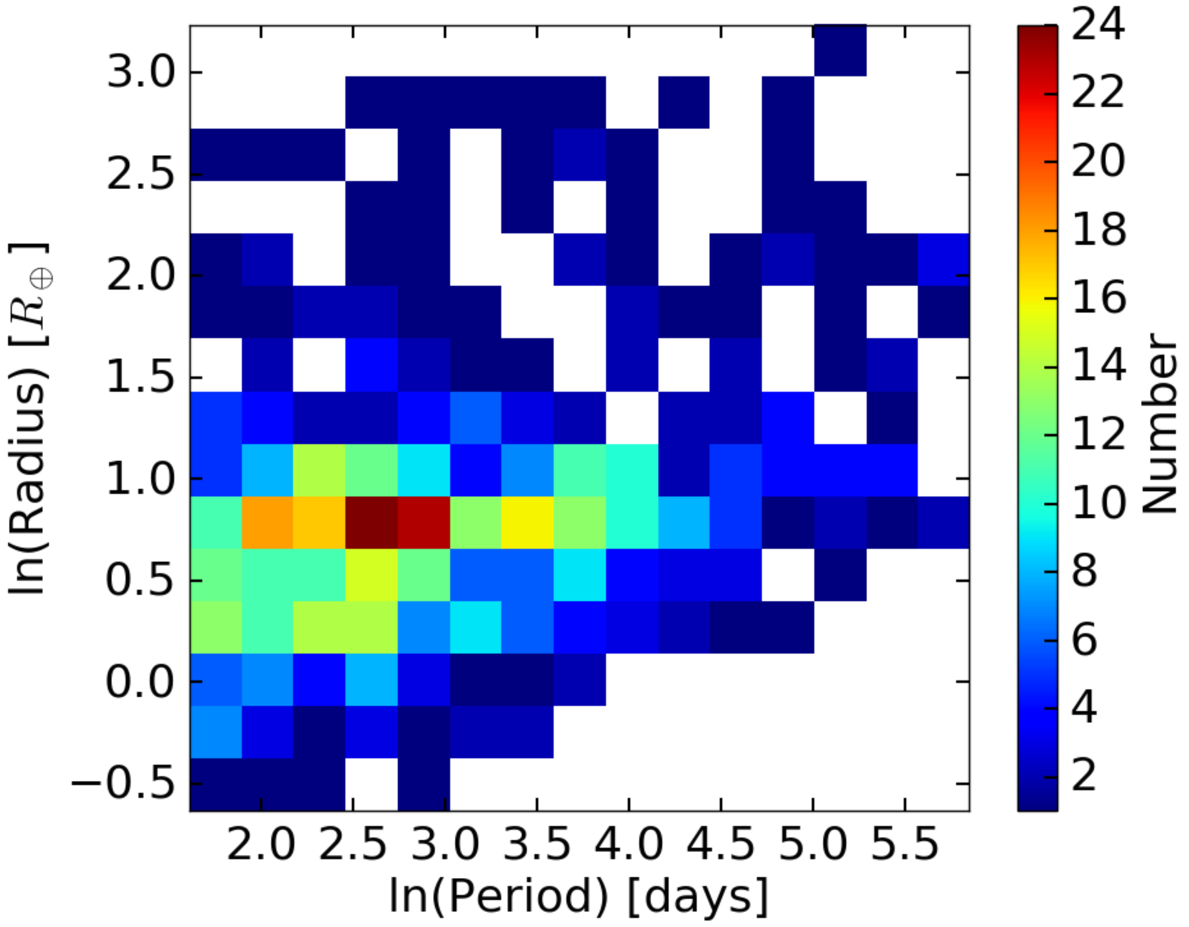
Data

For this analysis, we'll use a sample of $\sim 40,000$ Sun-like stars and an associated set of ~ 600 exoplanet candidates provided by Petigura et al. (2013) (https://arxiv.org/abs/1311.6806). We'll load this in now

```
In [4]: nstar = 42557. # total number of stars in dataset
        _, data, _ = load_data.load_candidates() # load in planet candidate data (peri
        od,radius)
        data = log(data) # convert to log-space
        print 'N:', len(data)

        N: 603
```

This catalog contains 603 exoplanet candidates, whose distributions are shown below.

In [5]:
```
figure(figsize=(10, 8))
h = hist2d(data[:, 0], data[:, 1], bins=15, cmin=1)
xlabel('ln(Period) [days]')
ylabel('ln(Radius) [$R_\oplus$]')
colorbar(label='Number', ticks=arange(0, 50, 2))
tight_layout()
```

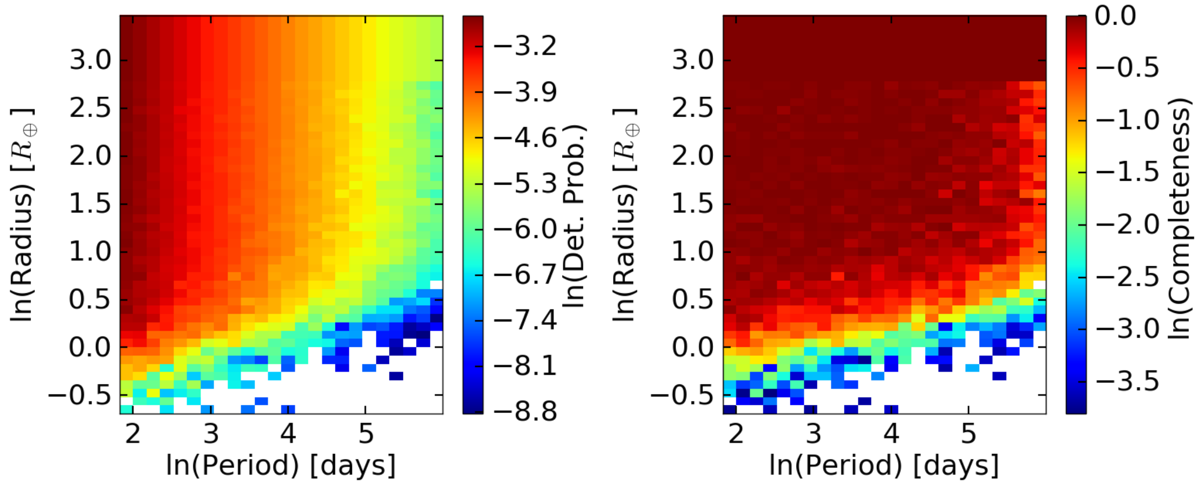


Unfortunately, we can't just try and extrapolate the *underlying* occurrence rate Γ from the *observed* occurrence rate due to strong selection effects. One of the great features of the Petigura et al. catalog is that, in addition to developing their own planet search pipeline, the authors estimated the detection efficiency of their analysis using synthetic planet injections into real *Kepler* light curves to derive detection efficiency and completeness maps.

Let's load these maps now and see what they look like.

In [6]:
```
censor = load_data.load_detection_efficiency()
```

In [7]:
```
xx, yy = meshgrid(censor.bin_centers[0], censor.bin_centers[1]) # Log(P,R) gri
d

figure(figsize=(16, 7))
subplot(1, 2, 1) # detection efficiency
h = hist2d(xx.ravel(), yy.ravel(), bins=censor.bins,
           weights=censor.lnprob[1:-1, 1:-1].swapaxes(0, 1).ravel())
colorbar(label='ln(Det. Prob.)', ticks=arange(-20, 0, 0.7))
xlabel('ln(Period) [days]')
ylabel('ln(Radius) [$R_\oplus$]')
locator_params(axis='x',nbins=8)
tight_layout()
subplot(1, 2, 2)
h = hist2d(xx.ravel(), yy.ravel(), bins=censor.bins,
           weights=censor.lncompleteness[1:-1 ,1:-1].swapaxes(0, 1).ravel())
colorbar(label='ln(Completeness)', ticks=arange(-10, 1, 0.5))
xlabel('ln(Period) [days]')
ylabel('ln(Radius) [$R_\oplus$]')
locator_params(axis='x',nbins=8)
tight_layout()
```



As expected, the detection probability (and completeness) evolve strongly as a function of radius and period. In particular, the detection probability and completeness at the location corresponding to the physical parameters of the Earth $\ln(R_\oplus/R_\oplus) = 0$ and $\ln(P_\oplus/\mathrm{days}) \approx 5.9$ is barely characterized.

Petigura et al. (2013): Our Starting Point

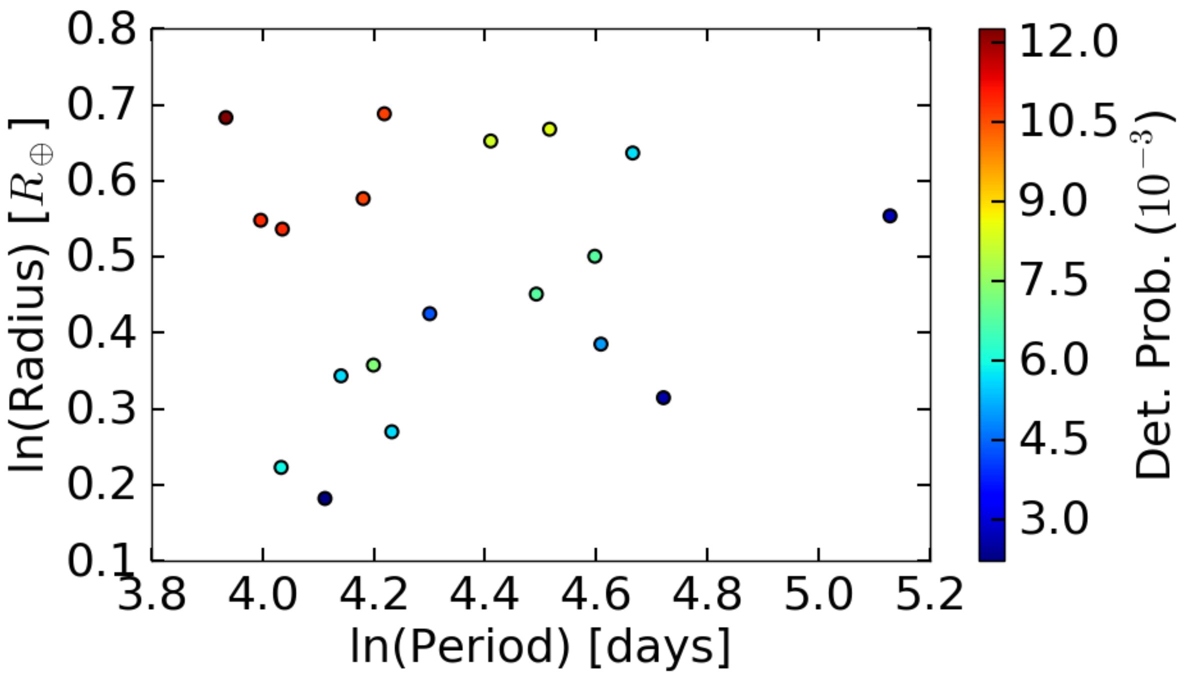
Petigura et al. start by removing the majority of the exoplanet population to limit their analysis to what they consider to be Earth-like analogs. This ends up removing $> 95\%$ of the sample, leaving only 19 planet candidates.

In [8]:
```
lpmn, lpmx = log(50), log(400) # (min,max)=(50,400) bounds for period (days)
lrmn, lrmx = log(1), log(2) # (min,max)=(1,2) bounds for mass (Earth masses)

m = (lpmn < data[:, 0]) & (data[:, 0] < lpmx) & (lrmn < data[:, 1]) & (data[:,
 1] < lrmx) # selection flag
data = data[m] # select planet subset within bounds
print 'N:', len(data)
```

```
N: 19
```

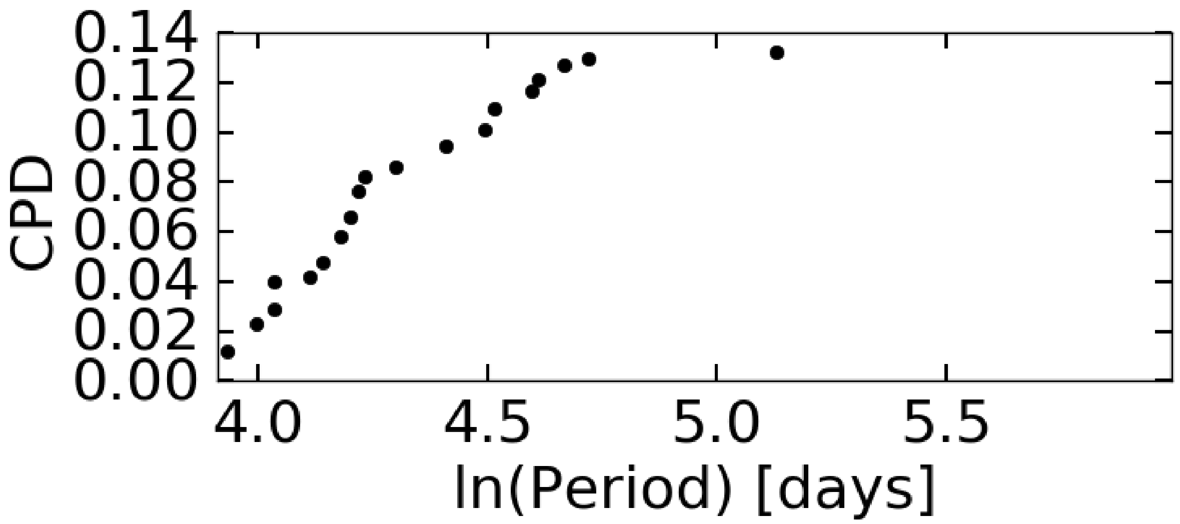
Petigura et al.'s analysis of this small subset of objects is straightforward and outlined below. First, we select the detection efficiency for each entry given our binned representation of the detection efficiency map.

In [9]:
```
w = exp(censor.get_lnprob(data))

figure(figsize=(10, 6))
scatter(data[:, 0], data[:, 1], c=w*1e3, s=50, lw=1.5)
xlabel('ln(Period) [days]')
ylabel('ln(Radius) [$R_\oplus$]')
colorbar(label='Det. Prob. ($10^{-3}$)')
tight_layout()
```



Next we compute the 1-D cumulative distribution of the detection probability over the period (the cumulative period distribution, or "CPD").

In [10]:
```
idx = data[:, 0].argsort() # sorted indices
cpd = w[idx].cumsum() # sorted cumulative sum of probabilities

figure(figsize=(8, 4))
plot(data[idx, 0], cpd, "ko")
xlabel('ln(Period) [days]')
ylabel('CPD')
xlim(lpmn, lpmx)
tight_layout()
```



This represents the cumulative probability of detecting a planet as a function of the period for objects with masses similar to the Earth (a total sample of 19 objects). This looks quasi-linear, which is the expected behavior of a **uniform distribution** over $\ln P$. This just has a constant probability distribution function (PDF) whose amplitude constrains $\Gamma_\oplus$, the occurence rate of planets with Earth-like masses and periods! Fitting a line thus gives access to the derivative,

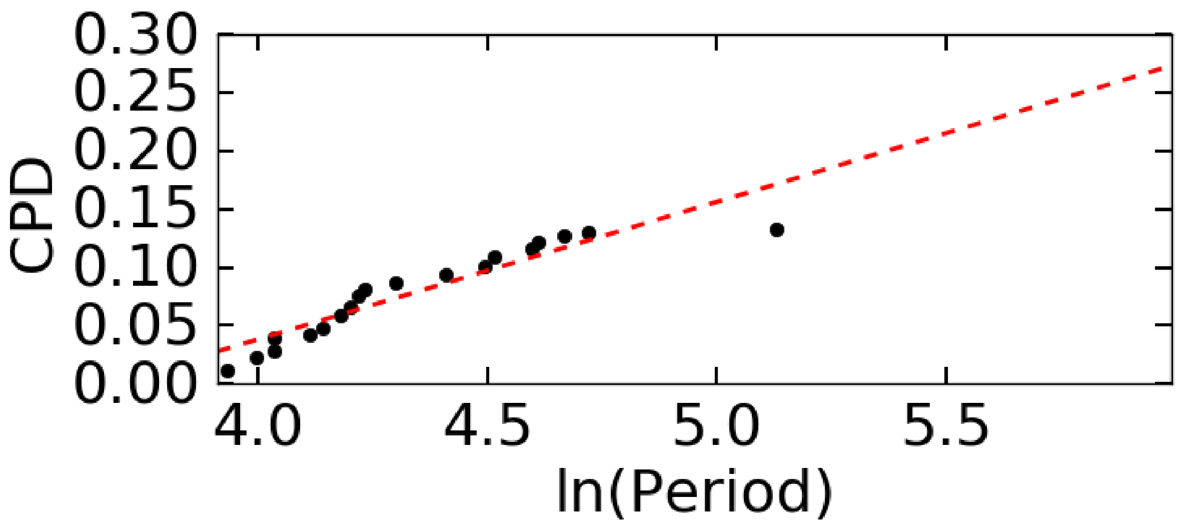
$$\frac{d(\mathrm{CPD})}{dP} = \Gamma_\oplus,$$

and so is a direct probe of $\Gamma_\oplus$ **assuming that the distribution is uniform in $\ln P$**.

In [11]:
```
# linear fit
p = polyfit(data[idx, 0], cpd, 1)
x = linspace(lpmn, lpmx, 5000)

figure(figsize=(8, 4))
plot(data[idx, 0], cpd, "ko")
plot(x, polyval(p, x), "r--",lw=2)
xlabel('ln(Period)')
ylabel('CPD')
xlim(lpmn, lpmx)
tight_layout()

Math(r"\Gamma_\oplus = {0:.3f}".format(p[0]))
```

Out[11]:

$$\Gamma_\oplus = 0.118$$



It is immediately clear that this assumption suffers from small number statistics, ignores measurement uncertainties, and isn't a great fit to the data. However, given we are currently working under the assumption that what we measure is "correct", we can derive some rough error bars around this using bootstrap resampling. This is reasonably well-motivated here where we're not considering formal measurement errors and we're dealing with low-number Poisson statistics.

In [12]:
```
gesamp=empty(10000) # samples

for i in xrange(10000):
    sel = randint(len(data),size=len(data)) # bootstrap resample
    dt, wt = data[sel], w[sel]
    idx = dt[:, 0].argsort() # sorted indices
    cpd = wt[idx].cumsum() # sorted cumulative sum of probabilities
    gesamp[i]=polyfit(dt[idx, 0], cpd, 1)[0] # \Gamma_earth sample

q1 = percentile(gesamp, [16, 50, 84])
e1 = diff(q1)
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q1[1],
e1[0], e1[1]))
```

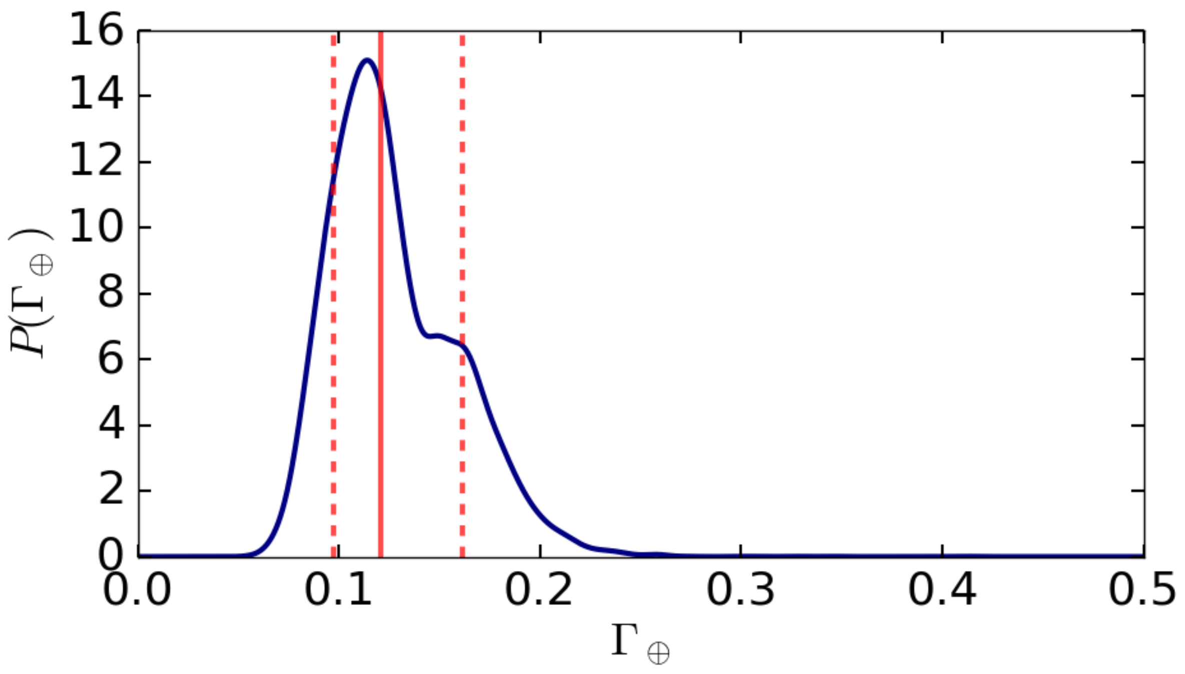
Out[12]:

$$\Gamma_\oplus = 0.121 _{-0.024} ^{+0.041}$$

This reproduces the value from Petigurra et al.

We can visualize this distribution better by plotting up a representation of the full set of posterior draws. Rather than binning the output results using a histogram, we opt to instead use kernel density estimation (KDE) to try and reconstruct the underlying PDF.

In [13]:
```
from sklearn.neighbors import KernelDensity
kde = KernelDensity(kernel='gaussian', bandwidth=0.005).fit(gesamp[:,None]) #
 derive the underlying estimator
x = linspace(0, 0.5, 5000)
log_dens = kde.score_samples(x[:,None]) # return results

# plotting
figure(figsize=(10, 6))
plot(x, exp(log_dens), color='navy', lw=3)
axvline(q1[0], color='r', ls='--', alpha=0.7, lw=3)
axvline(q1[1], color='r', ls='-', alpha=0.7, lw=3)
axvline(q1[2], color='r', ls='--', alpha=0.7, lw=3)
xlabel('$\Gamma_\oplus$')
ylabel('$P(\Gamma_\oplus)$')
tight_layout()
```



It cannot be stressed enough that this linearity (i.e. uniform in $\ln P$) assumption within this bin is **extremely strong** given the perceived quality of the fit. For instance, we can model this result with many other monotonically increasing functional forms, all of which may give fits that are just as good and could have reasonably justified motivations. One example would be the monotonically increasing function

$$\mathrm{CPD}(x) = a \ln(x + b) + c,$$

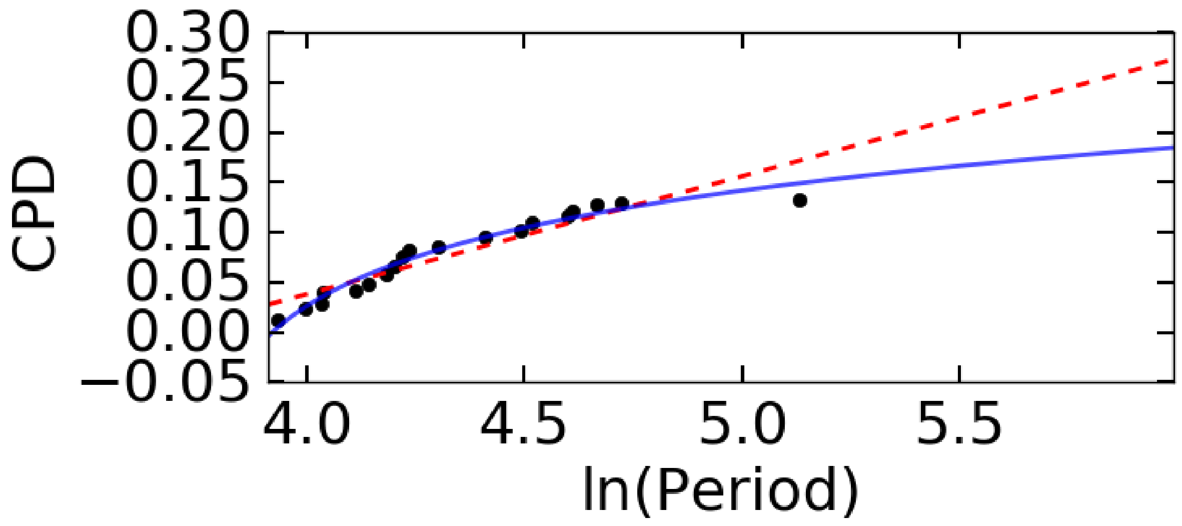
where a, b, and c are free parameters. We present such a fit below for comparison.

In [14]:
```
def logfit(x, a, b, c):
    return a*log(x+b) + c
```

In [15]:
```
idx = data[:, 0].argsort() # sorted indices
cpd = w[idx].cumsum() # sorted cumulative sum of probabilities

# logarithmic fit (for comparison)
from scipy import optimize
p2, cov2 = optimize.curve_fit(logfit, data[idx, 0], cpd)
x = linspace(lpmn, lpmx, 5000)

figure(figsize=(8, 4))
plot(data[idx, 0], cpd, "ko")
plot(x, polyval(p, x), "r--",lw=2)
plot(x, logfit(x, p2[0], p2[1], p2[2]), "blue", lw=2, alpha=0.7)
xlabel('ln(Period)')
ylabel('CPD')
xlim(lpmn, lpmx)
tight_layout()

dcpd = p2[0] / (log(360.) + p2[1])
Math(r"\Gamma_\oplus = {0:.3f}".format(dcpd))
```

Out[15]:

$$\Gamma_\oplus = 0.034$$

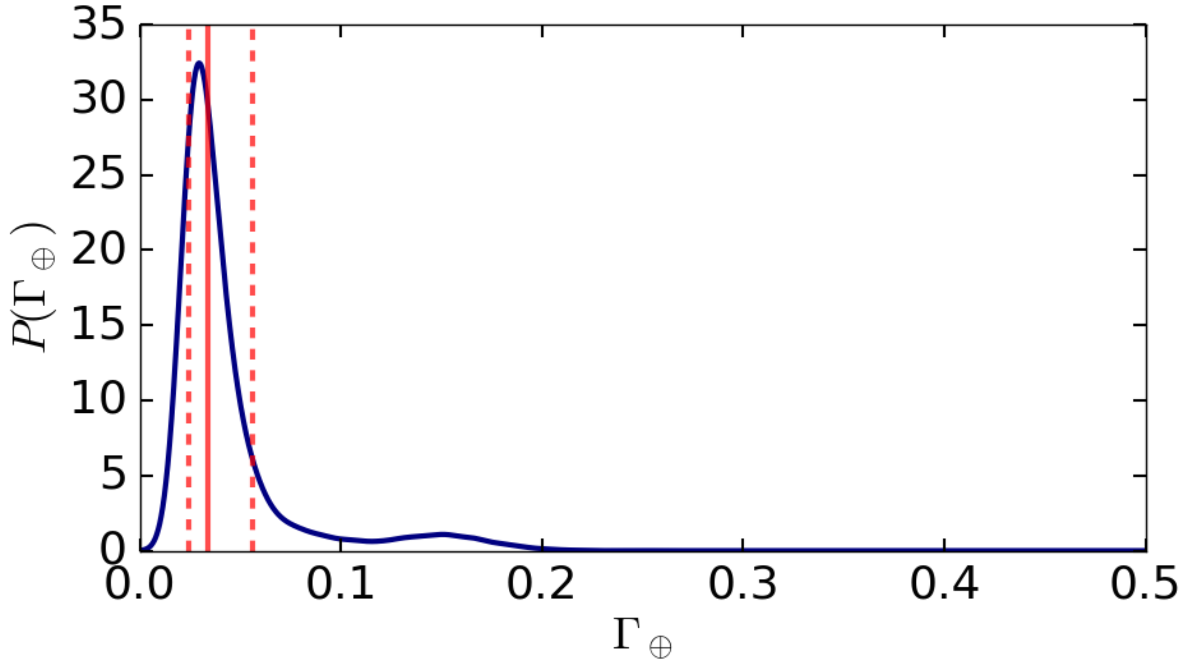


In [16]:
```
gesamp=empty(10000) # samples

for i in xrange(10000):
    sel = randint(len(data),size=len(data))
    dt, wt = data[sel], w[sel]
    idx = dt[:, 0].argsort() # sorted indices
    cpd = wt[idx].cumsum() # sorted cumulative sum of probabilities
    pt = optimize.curve_fit(logfit, dt[idx, 0], cpd, maxfev=100000)[0]
    gesamp[i] = pt[0] / (log(360.) + pt[1])

q2 = percentile(gesamp, [16, 50, 84])
e2 = diff(q2)
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q2[1],
e2[0], e2[1]))
```

Out[16]:

$$\Gamma_\oplus = 0.034 _{-0.009} ^{+0.022}$$

In [17]:
```
kde = KernelDensity(kernel='gaussian', bandwidth=0.005).fit(gesamp[:,None]) #
 derive the underlying estimator
x = linspace(0, 0.5, 5000)
log_dens = kde.score_samples(x[:,None]) # return results

# plotting
figure(figsize=(10, 6))
plot(x, exp(log_dens), color='navy', lw=3)
axvline(q2[0], color='r', ls='--', alpha=0.7, lw=3)
axvline(q2[1], color='r', ls='-', alpha=0.7, lw=3)
axvline(q2[2], color='r', ls='--', alpha=0.7, lw=3)
xlabel('$\Gamma_\oplus$')
ylabel('$P(\Gamma_\oplus)$')
tight_layout()
```



Not only does adding one parameter significantly improve the fit, it also implies an estimate for $\Gamma_\oplus$ lower by a factor of ~ 3.5 with a very different posterior distribution.

Petigura et al.: What "should" have been

Under the assumption of a flat (in log) bin in the range $1\,R_\oplus \leq R < 2\,R_\oplus$ and $50\,\mathrm{days} \leq P < 400\,\mathrm{days}$ (which we assumed above in our linear fit!), the **inverse-detection-efficiency approximation** (see the "Maximum Likelihood Estimation" section for more details) is

$$\Gamma = \frac{1}{\Delta}\sum_k \frac{1}{Q(\mathbf{w}_k)},$$

where $\mathbf{w}_k$ are the physical parameters for object k (i.e. P and R), Δ is the area of the bin, and Q is the total detection efficiency. This is just the discrete estimate computed over our bins weighting every object by the inverse of its detection probability.

Assuming Poisson statistics apply here, we can derive an estimate of:

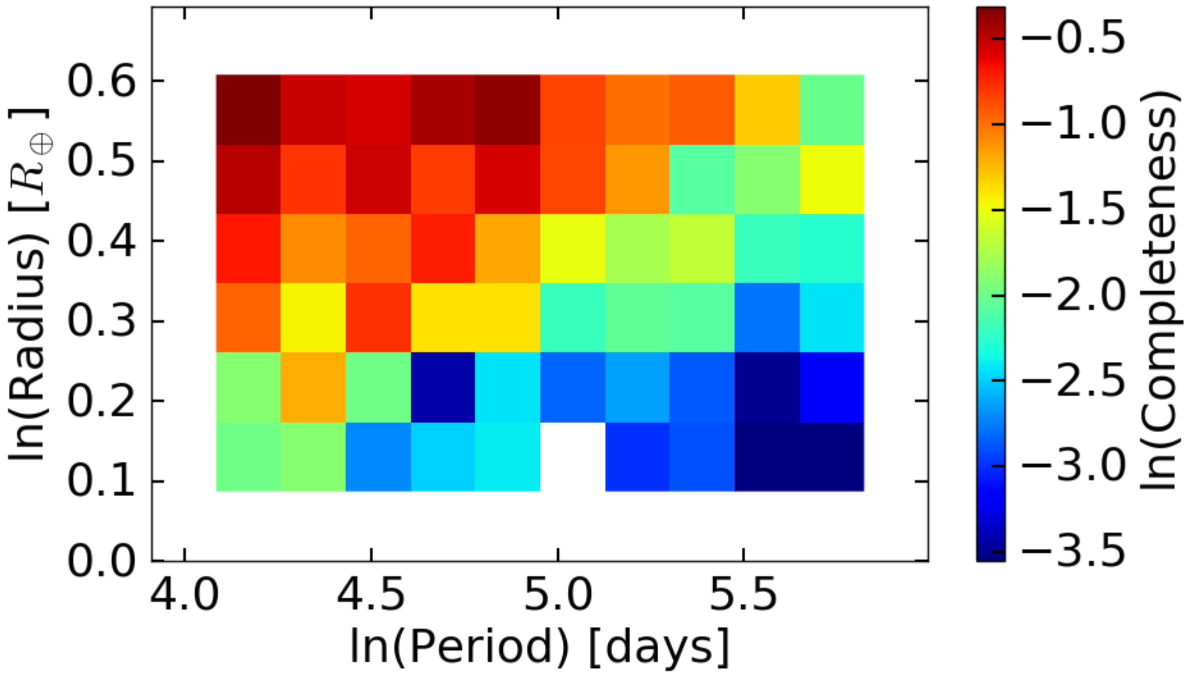
```
In [18]: v = (1./w).sum() # sum of inverse detection probabilities
         v /= ((lpmx - lpmn) * (lrmx - lrmn)) # normalize by bin area
         v /= nstar # normalize by total number of stars in sample
         ve = v/sqrt(len(data))
         Math(r"\Gamma_\oplus = {0:.3f} \pm {1:.3f}".format(v, ve))
```

Out[18]:

$$\Gamma_\oplus = 0.057 \pm 0.013$$

This is not a good estimate though, because the completeness evolves strongly across this bin.

In [19]:
```
m1 = (lpmn < censor.bins[0]) & (censor.bins[0] < lpmx) # bounds (period)
m2 = (lrmn < censor.bins[1]) & (censor.bins[1] < lrmx) # bounds (radius)

figure(figsize=(10, 6))
h = hist2d(xx.ravel(), yy.ravel(), bins=[censor.bins[0][m1],censor.bins[1]
[m2]],
           weights=censor.lncompleteness[1:-1 ,1:-1].swapaxes(0, 1).ravel())
colorbar(label='ln(Completeness)', ticks=arange(-10, 1, 0.5))
xlim([lpmn,lpmx])
ylim([lrmn,lrmx])
xlabel('ln(Period) [days]')
ylabel('ln(Radius) [$R_\oplus$]')
tight_layout()
```



Evaluating the result based on the small amount of planet detections in this bin is thus a Bad Idea. Instead, as shown in Foreman-Mackey et al., the "correct" way to do this is actually integrate across the detection efficiency maps to compute

$$\Gamma = \frac{K}{\int_\Delta Q(\mathbf{w})\,\mathrm{d}\mathbf{w}},$$

where K is the number of objects within the bin. We can estimate $\int_\Delta Q(w)\,\mathrm{d}w$ using Monte Carlo methods as

$$\int_\Delta Q(\mathbf{w})\,\mathrm{d}\mathbf{w} \approx \frac{1}{N}\sum_{i=1}^{N} Q(\mathbf{w}_i)$$

for a set of $\mathbf{w}_i$'s drawn uniformly from within the bin.

```
In [20]: N = 100000 # number of samples
         K = len(data)
         samples = vstack([
                 random.uniform(lpmn, lpmx, size=N),
                 random.uniform(lrmn, lrmx, size=N)]).T # uniform samples in the bin
         Q = exp(censor.get_lnprob(samples)) # detection efficiencies
         Qint = mean(Q)*nstar # integrating and normalizing
```

```
In [21]: # Compute the estimate of \Gamma.
         mu = K / Qint
         std = mu / sqrt(K)

         Math(r"\Gamma_\oplus = {0:.3f} \pm {1:.3f}".format(mu, std))
```

Out[21]:

$$\Gamma_\oplus = 0.153 \pm 0.035$$

This is consistent with the number from Petigura et al. above, but more derived more rigorously.

Relaxing Assumptions

Rather than assuming that the rate in a bin is **flat**, we can assume the next simplest functional form: a **linear model in $\ln P$** (with the caveat that it has to remain non-negative). This no longer gives a simple analytic solution, but the log-likelihood function for the model can be written as (borrowing from Foreman-Mackey):

$$\ln p(\{\ln P_k, \ln R_k\} \mid a, b) = -\int Q(\ln R \ln P)(a \ln P + b) \mathrm{d}(\ln R) \mathrm{d}(\ln P) + \sum_k \left[\ln(a \ln(P_k) + b) + \ln Q(\ln R_k, \ln P_k)\right]$$

over our set of objects indexed by k.

We can sample from this distribution using **emcee**, where a set of uniform priors on a and b can be used to force the rate to always remain non-negative within the confines of our bin. We define these more explicitly below.

In [22]:
```
def model(p, lnp): # linear model
    return polyval(p, lnp - lpmn) # offset by minimum bound

def lnprior(p): # ln-prior
    if len(p) == 1: # for a one-parameter model
        if p[0] <= 0:
            return -inf # set p=0
    elif len(p) >= 2: # for a >two-parameter model
        if model(p, lpmn) < 0.0 or model(p, lpmx) < 0.0:
            return -inf # set p=0
        if len(p) > 2: # if we have a more complicated model with >2 parameter
s
            x = -0.5 * p[1] / p[0]
            if lpmn <= x < lpmx and model(p, x) < 0.0: # if ratio is within bo
unds and model is negative
                return -inf # set p=0
    return 0.0

def lnlike(p): # ln-likelihood
    norm = mean(model(p, samples[:, 0]) * Q) # normalization (relative to prec
omputed Q)
    ll = sum(log(model(p, data[:, 0])) + censor.get_lnprob(data)) # log-likeli
hood
    return ll - norm

def lnprob(p): # ln-posterior
    lp = lnprior(p) # ln-prior
    if not isfinite(lp): # if things blew up
        return -inf # posterior is zero
    ll = lnlike(p) # ln-likelihood
    if not isfinite(ll): # if things blew up
        return -inf # likelihood is zero
    return lp + ll # posterior term
```

We'll now initialize emcee.

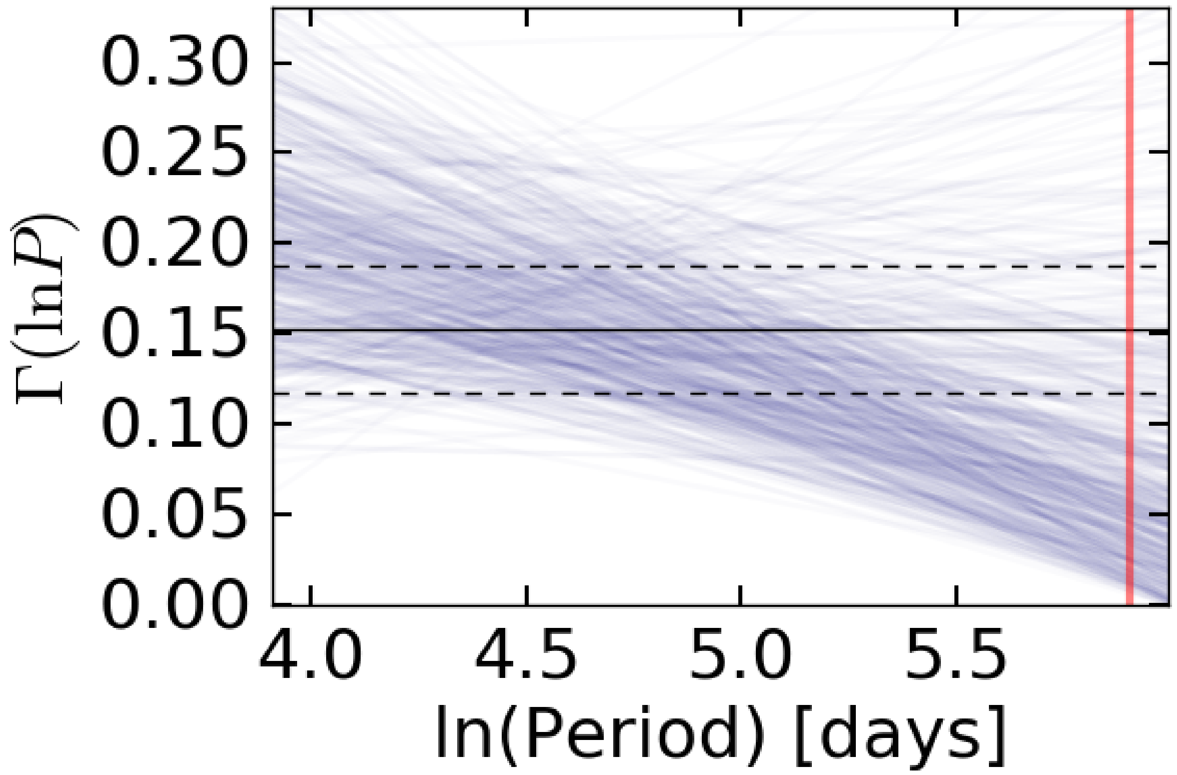
In [23]:
```
nwalkers = 36 # number of walkers
p0 = random.multivariate_normal([0, 5000.], diag([1e-2, 1e-2]), size=nwalkers)
 # intialize walkers
ndim = p0.shape[1] # dimensionality
sampler = emcee.EnsembleSampler(nwalkers, ndim, lnprob) # initialize sampler
```

In [24]:
```
p0, _, _ = sampler.run_mcmc(p0, 500) # burn-in

sampler.reset()
sampler.run_mcmc(p0, 1000); # sample from posterior
```

Our posterior constraints on the output density are shown below, with the uniform estimate and the period of the Earth indicated in dashed black and red, respectively.

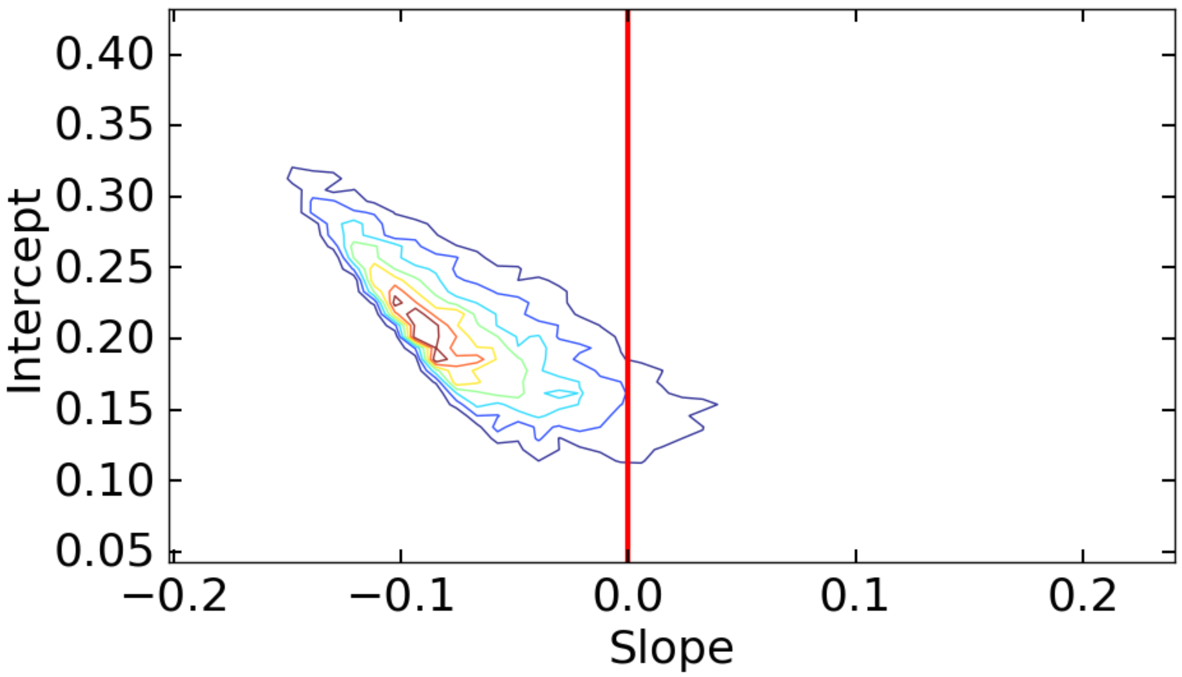
```
In [25]: x = linspace(lpmn, lpmx, 500)
         chain = sampler.flatchain # combine walkers to create single flattened chain

         # plot draws
         for i in random.randint(len(chain), size=500): # draw 500 random samples
             plot(x, model(chain[i], x) / nstar, color="navy", lw=2, alpha=0.02)

         # plot uniform estimate
         axhline(mu, color='k')
         axhline(mu+std, color='k', ls='--')
         axhline(mu-std, color='k', ls='--')

         # plot Earth value
         axvline(log(365.), color='r', alpha=0.5, lw=3)

         xlim(lpmn, lpmx)
         ylim(0, 0.33)
         xlabel('ln(Period) [days]')
         ylabel('$\Gamma(\ln P)$')
```

```
Out[25]: <matplotlib.text.Text at 0xd665f60>
```



At the location of Earth, these two results are in tension, indicating that the data don't fully support a uniform distribution. We quantify this below by examing the distribution of our output fits.

```
In [26]: figure(figsize=(10, 6))
         hh, xx, yy = histogram2d((chain/nstar)[:,0], (chain/nstar)[:,1], bins=50)
         contour((xx[1:]+xx[:-1])*0.5, (yy[1:]+yy[:-1])*0.5, hh.swapaxes(0,1), alpha=0.
         8)
         axvline(0, color='r', lw=3)
         xlabel('Slope')
         ylabel('Intercept')
         tight_layout()
```



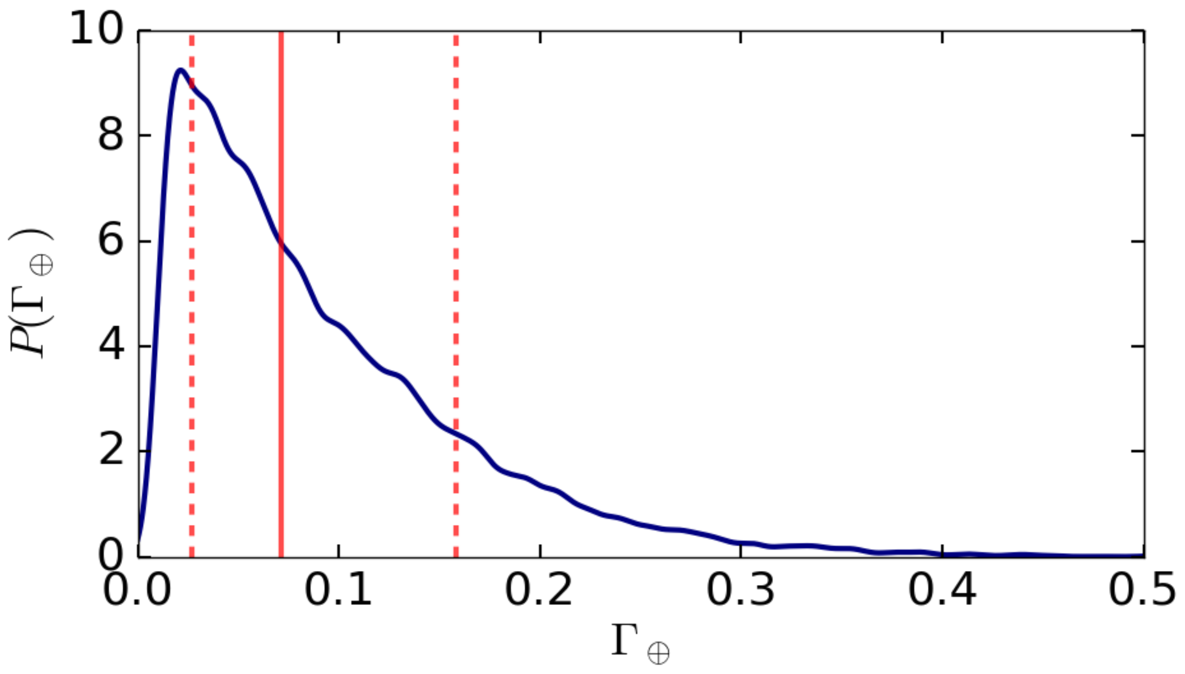
These results strongly disfavor Petigura et al.'s assumption of a uniform distribution across these bins, we can compute the constraint on $\Gamma_\oplus$:

```
In [27]: ge = array([model(p, log(365.)) for p in chain]) # \Gamma_earth from all sampl
         es
         ge /= nstar # normalizing by size of sample

         q3 = percentile(ge, [16, 50, 84]) # compute 16th, 50th, and 84th (i.e. 1-sigm
         a) confidence intervals
         e3 = diff(q3) # grab bounds
         Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q3[1],
         e3[0], e3[1]))
```

Out[27]:

$$\Gamma_\oplus = 0.072\,^{+0.087}_{-0.045}$$

In [28]:
```
from sklearn.neighbors import KernelDensity
kde = KernelDensity(kernel='gaussian', bandwidth=0.005).fit(ge[:,None]) # deri
ve the underlying estimator
x = linspace(0, 0.5, 5000)
log_dens = kde.score_samples(x[:,None]) # return results

# plotting
figure(figsize=(10, 6))
plot(x, exp(log_dens), color='navy', lw=3)
axvline(q3[0], color='r', ls='--', alpha=0.7, lw=3)
axvline(q3[1], color='r', ls='-', alpha=0.7, lw=3)
axvline(q3[2], color='r', ls='--', alpha=0.7, lw=3)
xlabel('$\Gamma_\oplus$')
ylabel('$P(\Gamma_\oplus)$')
tight_layout()
```



For reference, Petigura et al.'s result is:

In [29]:
```
Math(r"\Gamma_\oplus = {0:.3f} \pm {1:.3f}".format(mu, std))
```

Out[29]:

$$\Gamma_\oplus = 0.153 \pm 0.035$$

If we now integrating these results over Petigura et al.'s bin (which ranges from $200

```
In [30]: area = (lrmx - lrmn) * (log(400) - log(200))
         Math(r"\Gamma_{{\oplus,\mathrm{{int}}}} = {0:.3f} \pm {1:.3f} \quad (\mathrm
         {{uniform}})".format(mu*area, std*area))
```

Out[30]:

$$\Gamma_{\oplus,\mathrm{int}} = 0.073 \pm 0.017 \quad (\mathrm{uniform})$$

```
In [31]: q = percentile(ge*area, [16, 50, 84])
         e = diff(q)
         Math(r"\Gamma_{{\oplus,\mathrm{{int}}}} = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}
          \quad (\mathrm{{linear}})"
              .format(q[1], e[0], e[1]))
```

Out[31]:

$$\Gamma_{\oplus,\mathrm{int}} = 0.034 _{-0.022} ^{+0.042} \quad (\mathrm{linear})$$

Dong & Zhu: Parametric Modeling

Dong & Zhu (2013) (https://arxiv.org/abs/1212.4853) assume a parametric form for the underlying occurrence rate density as

$$\Gamma(\log P, \log R) = C\left(\frac{P}{10\,\mathrm{days}}\right)^{\beta}.$$

Over the same range of $1\,R_\oplus \le R < 2\,R_\oplus$, they found that

$$C = 0.66 \pm 0.08, \quad \beta = -0.10 \pm 0.12$$

provided good fits to their data (including selection effects).

For

$$\Gamma(\ln P,\ \ln R) = \frac{1}{(\ln 10)^2}\Gamma(\log P, \log R),$$

$\Gamma_\oplus$ is then:

In [32]:
```
N = 100000
C = 0.66 + 0.08*randn(N)
beta = -0.10 + 0.12*randn(N)
vals = C*(365./10)**beta / log(10)**2
q4 = percentile(vals, [16, 50, 84])
e4 = diff(q4)
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q4[1],
e4[0], e4[1]))
```

Out[32]:

$$\Gamma_\oplus = 0.086\,^{+0.048}_{-0.031}$$

This gives results similar to our linear extrapolation.

Synthetic Data

We now want to generalize our results to the model from Foreman-Mackey et al. Following them, we want to test our results on some synthetic data first before moving onto the "real deal". We start by generating two catalogs from a separable model

$$\Gamma_{\boldsymbol{\theta}}(\ln P,\ \ln R) = \Gamma_{\boldsymbol{\theta}}^{(P)}(\ln P)\,\Gamma_{\boldsymbol{\theta}}^{(R)}(\ln R).$$

Catalog A is generated assuming a smooth(ed) occurrence surface where both distributions are broken power laws.

Catalog B is designed to be exactly the distribution inferred by Petigura et al. in the range that they considered and then smoothly extrapolated outside that range.

In [33]:
```
import simulate_cat
```

In [34]:
```
print 'N(A):', simulate_cat.sim('data/','smooth',smooth=True)
print 'N(B):', simulate_cat.sim('data/','rough',smooth=False)
```

```
N(A): 466
N(B): 456
```

Probabilistic Modeling: Foreman-Mackey et al.

Now it's time to move onto the general analysis that forms the core framework of Foreman-Mackey et al. Let's first start with some basic packages we'll need to manage outputs and make some figures.

In [35]:
```
import h5py
import corner
import cPickle as pickle
```

The meat of this analysis is going to be the underlying probabilistic model: a **Gaussian Process**! We'll use DFM's version for our analysis here.

In [36]:
```
from population import ProbabilisticModel, Dataset, Population
```

Maximum Likelihood Estimation

We will start by computing the maximum-likelihood estimates (MLEs) for $\Gamma_{\oplus}$ from these synthetic data as a control. As Foreman-Mackey et al. show, this reduces to the **inverse-detection-efficiency** method described above (this also ignores measurement errors). This is essentially the (binned) way of doing things without using a GP.

Because we're working fundamentally in a binned space, we want to ensure our bins are large enough to contain a reasonable number of objects (to get better S/N at the cost of decreased resolution in $\ln P$ and $\ln R$). We thus downsample the original map by a factor of 4.

In [37]:
```
lpb, lrb = censor.bins # original bins
x, y = lpb[::4], lrb[::4] # downsample
bins = [x, y] # new bins
pop = Population(bins, censor.bins, 11.0) # initialize our population
print 'Bins:',x.shape[0],'(ln P) x',y.shape[0],'(ln R)'
```

```
Bins: 7 (ln P) x 13 (ln R)
```

Catalog A (smoothed prior)

Let's load in our data.

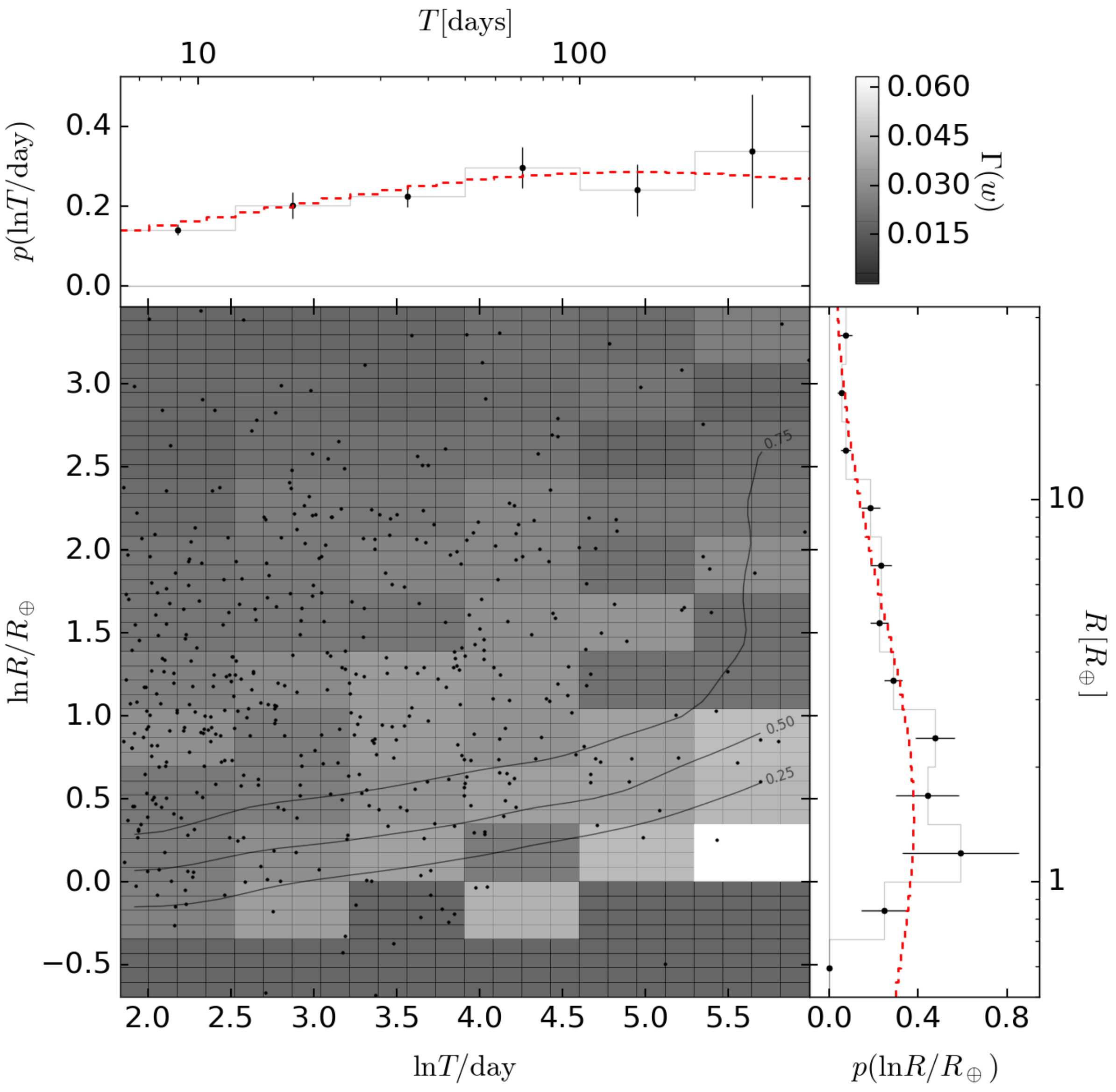
In [38]:
```
catalog, err, truth = pickle.load(open("data/smooth.cat.pkl", 'rb')) # load ca
talog
rerr = [log(catalog[:, 1]) - log(catalog[:, 1]-err[:, 1]),
        log(catalog[:, 1]+err[:, 1]) - log(catalog[:, 1])] # radius error
err = [0, rerr] # period and radius errors
```

We can immediate compute the MLE using the following function:

```
In [39]: from analysis import inverse_detection_efficiency
         v, val, var, literature, mvn, cdf = inverse_detection_efficiency(pop, censor,
         catalog, truth)
```

Let's now visualize these results using a weighted 2-D histogram.

```
In [40]: labels = ["$\ln T/\mathrm{day}$", "$\ln R/R_\oplus$"]
         top_axes = ["$T\,[\mathrm{days}]$", "$R\,[R_\oplus]$"]
         fig1 = pop.plot_2d(v-log(nstar), censor=censor, catalog=log(catalog),
                            err=None, true=truth, labels=labels,
                            top_axes=top_axes, literature=literature)
```

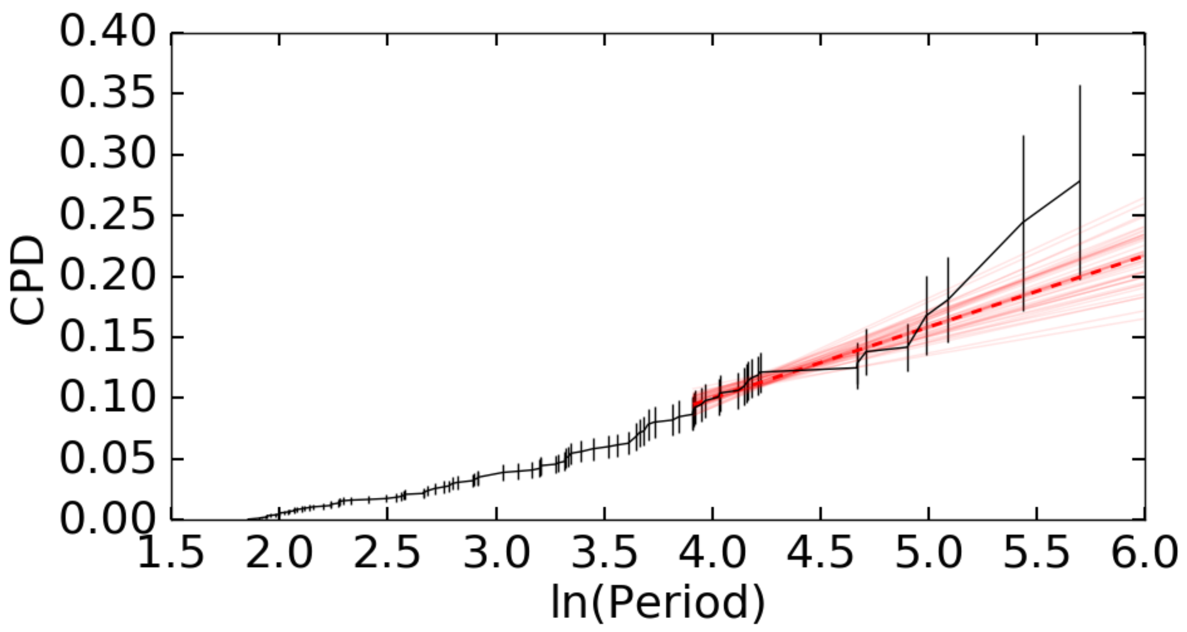


Now let's examine how well we do if we try to extrapolate our fits linearly using the mean and covariance matrices derived from our bins.

In [41]:
```
# predict values
ys = dot(array([[log(200), 1], [log(400), 1]]), # locations to sample
         multivariate_normal(mvn[0], mvn[1], 5000).T) # compute samples from m
ultivariate normal
frac = diff(ys, axis=0) # turn cdf into pdf
q = corner.quantile(frac, [0.16, 0.5, 0.84]) # grab quantiles
e = diff(q)

# plot results
figure(figsize=(10, 5))
a = vander(linspace(log(50), log(400), 500), 2) # compute (x^1, x^2)
y = dot(a, multivariate_normal(mvn[0], mvn[1], 50).T) # compute samples
plot(a[:, 0], y/nstar, "r", alpha=0.1)
plot(a[:, 0], dot(a, mvn[0])/nstar, "--r", lw=2)
errorbar(cdf[0], cdf[1]/nstar, yerr=sqrt(cdf[2])/nstar, fmt="k", capsize=0)
xlabel('ln(Period)')
ylabel('CPD')
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q[1]/nstar,
 e[0]/nstar, e[1]/nstar))
```

Out[41]:

$$\Gamma_\oplus = 0.040 _{-0.008} ^{+0.008}$$



This type of procedure is pretty much what Petigura et al. are attempting to do. As illustrated here, this procedure can be subject to a decent amount of variance and can be systematically biased.

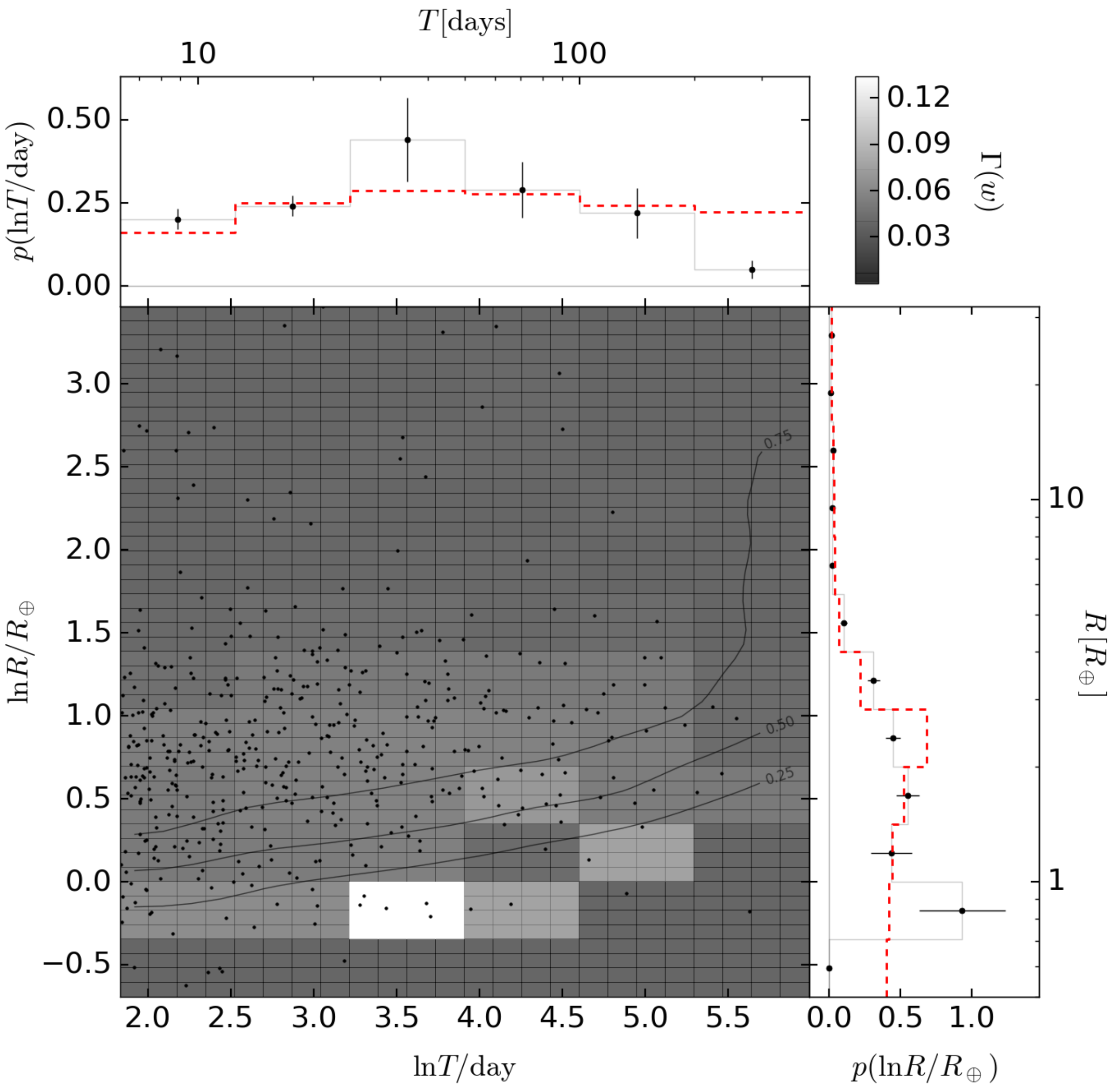
Catalog B (unsmoothed prior)

Let's now do the same for B.

In [42]:
```
catalog, err, truth = pickle.load(open("data/rough.cat.pkl", 'rb')) # Load cat
alog
rerr = [log(catalog[:, 1]) - log(catalog[:, 1]-err[:, 1]),
        log(catalog[:, 1]+err[:, 1]) - log(catalog[:, 1])] # radius error
err = [0, rerr] # period and radius errors
```

In [43]:
```
v, val, var, literature, mvn, cdf = inverse_detection_efficiency(pop, censor,
catalog, truth)
```

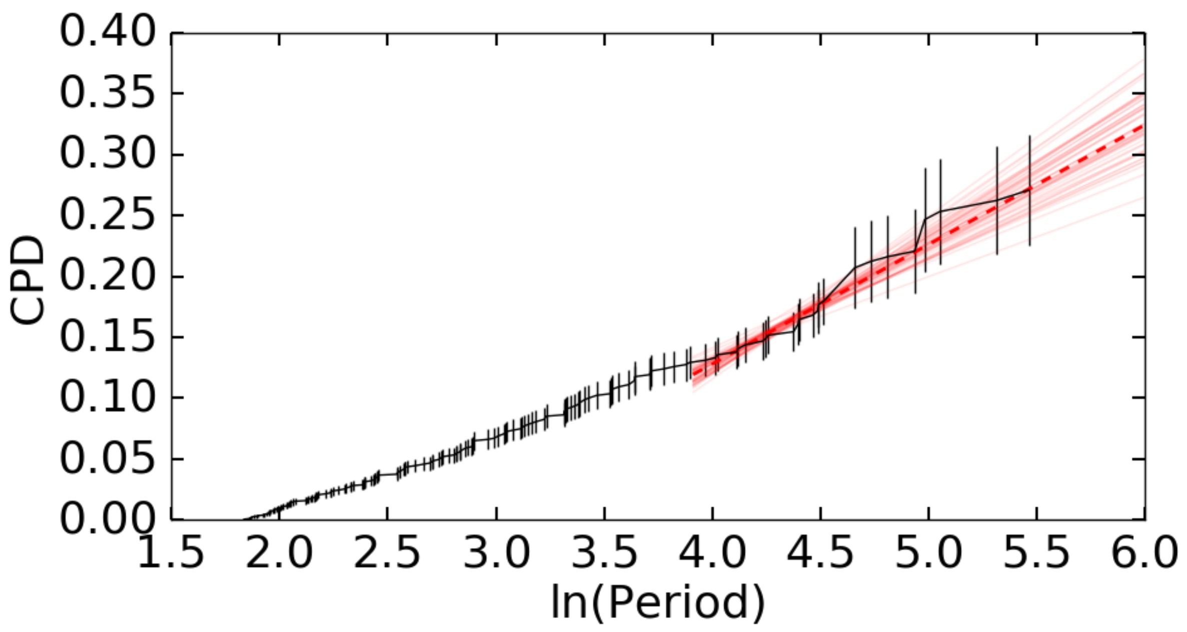
In [44]:
```
fig1 = pop.plot_2d(v-log(nstar), censor=censor, catalog=log(catalog),
                   err=None, true=truth, labels=labels,
                   top_axes=top_axes, literature=literature)
```



In [45]:
```
# predict values
ys = dot(array([[log(200), 1], [log(400), 1]]), # locations to sample
         multivariate_normal(mvn[0], mvn[1], 5000).T) # compute samples from m
ultivariate normal
frac = diff(ys, axis=0) # turn cdf into pdf
q = corner.quantile(frac, [0.16, 0.5, 0.84]) # grab quantiles
e = diff(q)

# plot results
figure(figsize=(10, 5))
a = vander(linspace(log(50), log(400), 500), 2) # compute (x^1, x^2)
y = dot(a, multivariate_normal(mvn[0], mvn[1], 50).T) # compute samples
plot(a[:, 0], y/nstar, "r", alpha=0.1)
plot(a[:, 0], dot(a, mvn[0])/nstar, "--r", lw=2)
errorbar(cdf[0], cdf[1]/nstar, yerr=sqrt(cdf[2])/nstar, fmt="k", capsize=0)
xlabel('ln(Period)')
ylabel('CPD')
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q[1]/nstar,
 e[0]/nstar, e[1]/nstar))
```

Out[45]:

$$\Gamma_\oplus = 0.068 _{-0.010}^{+0.010}$$



The large systematic variation in these two estimates is what motivates going to a fully probabilistic model!

Probabilistic Estimation

Now we want to incorporate measurement uncertainties into our model more explicitly using a GP over the bins. Mathematically, the Gaussian process density is

$$P(\boldsymbol{\theta}) = p(\boldsymbol{\theta} \mid \mu, \boldsymbol{\lambda}) = \mathcal{N}\left[\boldsymbol{\theta};\, \mu\mathbf{1},\, \boldsymbol{\Sigma}(\{\Delta_j\},\, \boldsymbol{\lambda})\right]$$

where $\mathcal{N}(\,\cdot\,;\, \mu\mathbf{1},\, \boldsymbol{\Sigma})$ is a J-dimensional Gaussian over bins Δ_j with a constant mean μ and covariance matrix $\boldsymbol{\Sigma}$, where depends on the bin centers Δ_j and a set of hyperparameters $\boldsymbol{\lambda} = (\lambda_0,\, \lambda_P,\, \lambda_R)$.

The covariance function that we use is an anisotropic, axis-aligned, exponential-squared **stationary kernel**. This means that the coariances between two elements is only a function of their relative distances from each other, such that

$$\Sigma_{ij} = \lambda_0 \exp\left(-\frac{1}{2}\,[\Delta_i - \Delta_j]^{\mathrm{T}}\,\Sigma^{-1}\,[\Delta_i - \Delta_j]\right)$$

where Σ^{-1} is

$$\Sigma^{-1} = \begin{pmatrix} 1/\lambda_P^2 & 0 \\ 0 & 1/\lambda_R^2 \end{pmatrix} \quad .$$

Inference Demonstration

We will not actually execute Foreman-Mackey et al.'s approach here due to time/computational constraints. However, the code that we would use to do this is outlined below.

In [46]:
```
fname="data/smooth"
catalog, err, truth = pickle.load(open(fname+".cat.pkl", 'rb')) # load catalog
K=512 # number of samples
dataset = Dataset.sample(catalog, err, samples=K, censor=censor, functions=[lo
g, log]) # generate realization(s)
rerr = [log(catalog[:, 1]) - log(catalog[:, 1]-err[:, 1]),
        log(catalog[:, 1]+err[:, 1]) - log(catalog[:, 1])] # radius error
err = [0, rerr] # period and radius errors
v, val, var, literature, mvn, cdf = inverse_detection_efficiency(pop, censor,
catalog, truth)
```

We now initialize our probabilistic model and dump it to disk.

In [47]:
```
# initialize model (initial conditions set by DFM)
model = ProbabilisticModel(dataset, pop, censor, [3.6, 2.6, 1.6, 0.0], array([
 0.5, 0.3, 0.3]) / 2.4)

# dump model
pickle.dump((model, catalog, err, truth, labels, top_axes, literature),
            open(fname+".model.pkl", "w"), -1)
```

Now comes to hard part: sampling the underlying distribution. The code that we *can* use to do this is shown below, but I wouldn't run it unless you want to spend a long time waiting for samples. (Note that there's a lot running under the hood here - see the source code and paper for additional details).

In [48]:
```
#nblock = 500
#N, ndim, nhyper = 2000 * nblock, len(pop), 4
#
#samples = empty((nblock, ndim))
#hyper = empty((nblock, nhyper))
#lnprob = empty(nblock)
#
#fn = fname+".results.h5"
#with h5py.File(fn, "w") as f:
#    f.create_dataset("samples", shape=(N, ndim), dtype=float64)
#    f.create_dataset("hyper", shape=(N, nhyper), dtype=float64)
#    f.create_dataset("lnprob", shape=(N,), dtype=float64)
#
#for i, (th, hy, lp, acc) in enumerate(model.sample()):
#    n = i % nblock
#    samples[n, :] = th
#    hyper[n, :] = hy
#    lnprob[n] = lp
#    if n == nblock - 1:
#        print i+1, (i+1.) / N, max(lnprob), acc
#        s = slice(i-n, i+1)
#        with h5py.File(fn, "a") as f:
#            f.attrs["iteration"] = i+1
#            f["samples"][s, :] = samples
#            f["hyper"][s, :] = hyper
#            f["lnprob"][s] = lnprob
#
#    if i >= N-1:
#        break
```

Foreman-Mackey et al.'s Results

Foreman-Mackey et al. have graciously made the results from the paper public (https://zenodo.org/record/11507#.WEtroPkrKUk). In the interests of time and reproducibility, we'll use those instead. These are a set of draws from the occurrence rate bins and hyperparameters, along with the bins used for the analysis. Using these, we can apply our full probabilistic method to our mock data.

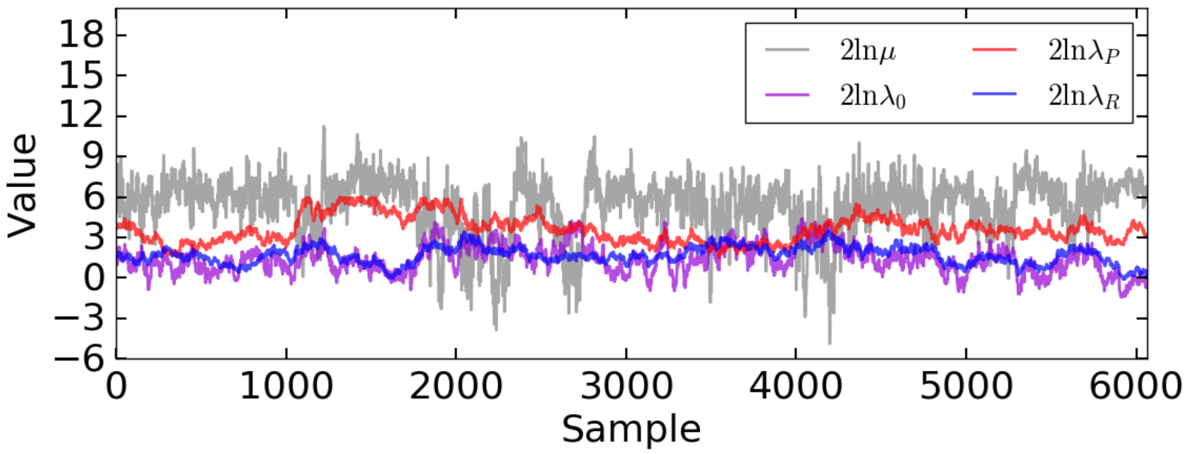
Catalog A

```
In [49]: with h5py.File("data/dfm-exopop-results-7568693/simulated/catalog-a/samples.h
         5") as f:
             samples = f["ln_occurrence_rate_samples"][:, :]
             hyper = f["hyperparameter_samples"][:, :]
             x = f["ln_period_bin_edges"][:]
             y = f["ln_radius_bin_edges"][:]
```

To recap, we have four hyperparameters in our model: the mean $\mu\mathbf{1}$ of the distribution, the correlation amplitude λ_0, and the correlation length scales λ_P and λ_R in period and radius, respectively. Let's see how those samples look.

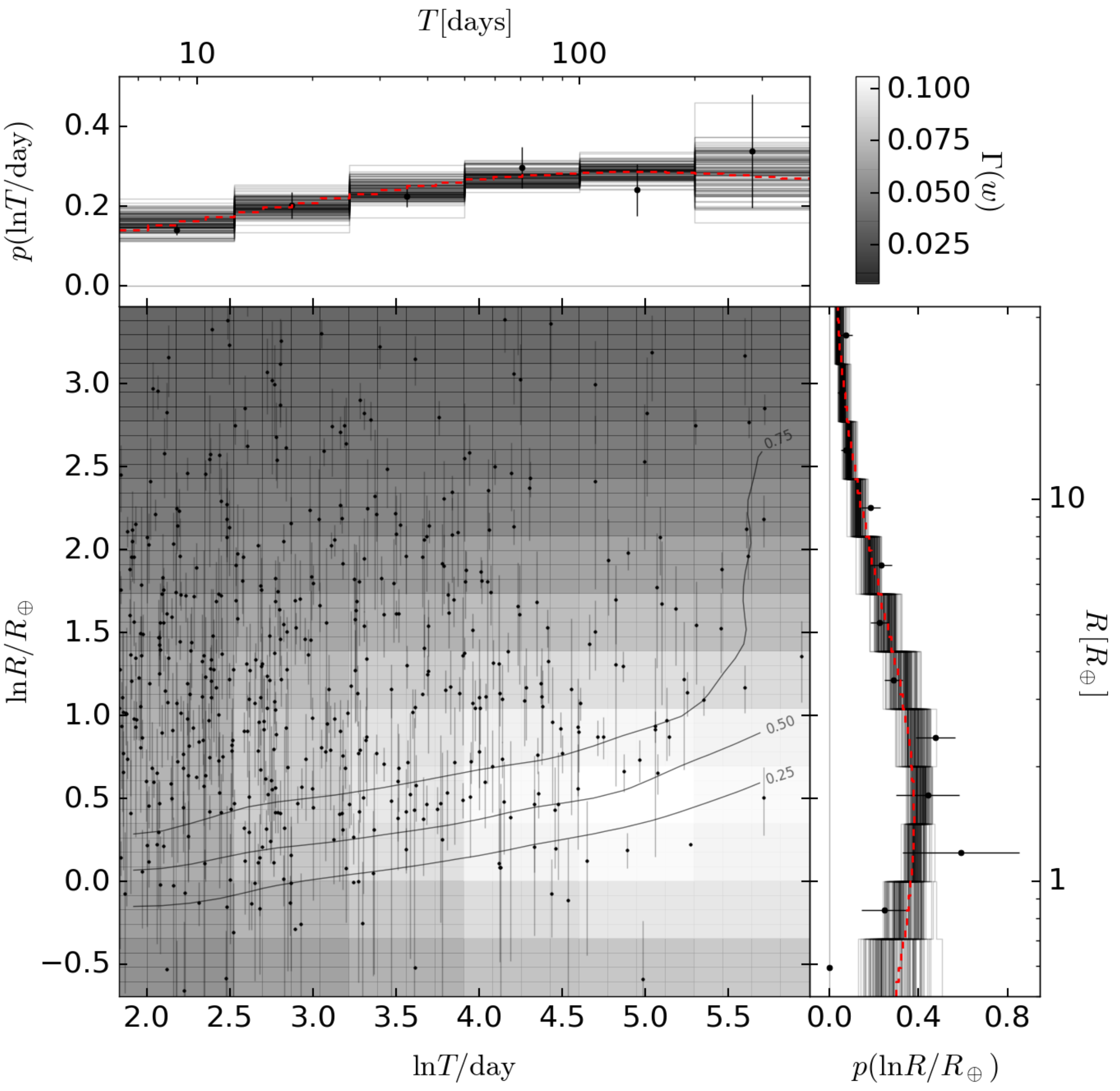
In [50]:
```
def xmap(f, i):
    return (f(*x) for x in i)

hypernames = ['$2\ln\mu$', '$2\ln\lambda_0$', '$2\ln\lambda_P$', '$2\ln\lambda
_R$']
hypercolors = ['gray', 'darkviolet', 'red', 'blue']
figure(figsize=(12, 5))
for i in range(hyper.shape[1]):
    plot(hyper[:, i], label=hypernames[i], color=hypercolors[i], lw=2, alpha=0

xlabel('Sample')
xlim([0, len(hyper)])
yticks(arange(-6, 20, 3))
ylim([-6, 20])
ylabel('Value')
legend(loc="best", fontsize=20, ncol=2)
tight_layout()

print("Hyperparameter values (2ln):")

q=array([corner.quantile(hyper[:, i], [.16, .50, .84]) for i in xrange(hyper.s
hape[1])])
e=diff(q)
print("\n".join(xmap("{0} - {1} + {2}".format, zip(q[:,1], e[:,0], e[:,1]))))

print("\n")
print("Hyperparameter values (linear):")

q=array([corner.quantile(exp(0.5*hyper[:, i]), [.16, .50, .84]) for i in xrang
e(hyper.shape[1])])
e=diff(q)
print("\n".join(xmap("{0} - {1} + {2}".format, zip(q[:,1], e[:,0], e[:,1]))))
```

```
Hyperparameter values (2ln):
5.82237106037 - 2.29818047326 + 1.31855869451
1.3593660634 - 1.04272012809 + 1.05279099171
3.51162724381 - 0.925276485876 + 1.10811068453
1.69742660295 - 0.660306741089 + 0.634341740806


Hyperparameter values (linear):
18.378574011 - 12.5539447749 + 17.1545924537
1.97325217471 - 0.80170766664 + 1.36710776056
5.7881551965 - 2.14381481765 + 4.28495090955
2.33663836769 - 0.657031175678 + 0.872120363421
```



That's our underlying GP. We can now turn those parameters into actual observed occurrence rates by evaluating them at our bin locations, applying our selection function, and sampling from the resulting distribution. Let's now plot up our results!

```
In [51]: data = loadtxt('data/dfm-exopop-results-7568693/simulated/catalog-a/catalog.tx
         t') # period, radius, radius err
         catalog = c_[data[:, 0], normal(data[:, 1], data[:, 2])]
         err=c_[zeros(len(data)), data[:,2]]
         rerr = [log(catalog[:, 1]) - log(catalog[:, 1]-err[:, 1]),
                 log(catalog[:, 1]+err[:, 1]) - log(catalog[:, 1])] # radius error
         err = [0, rerr] # period and radius errors
         cat, _, truth = pickle.load(open("data/smooth.cat.pkl", 'rb')) # Load catalog

         fig1 = pop.plot_2d(samples.reshape(len(samples), (len(bins[0])-1)*(len(bins[1]
         1))[::50] - log(nstar),
                              censor=censor, catalog=log(catalog),
                              err=err, true=truth, labels=labels, top_axes=top_axes, lite
         rature=literature)
```



```
In [52]: rates = pop.get_lnrate(samples.reshape(len(samples), (len(bins[0])-1)*(len(bin
         s[1])-1)), [log(365.), log(1.0)])
         fracs = rates - log(nstar)
         q = corner.quantile(fracs, [0.16, 0.5, 0.84])
         e = diff(q)
         Math(r"\ln\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q[1], e[
          e[1]))
```

Out[52]:

$$\ln\Gamma_\oplus = -2.315 _{-0.363} ^{+0.309}$$

For comparison with the above outputs, we can also convert this to linear scale:

```
In [53]: q = corner.quantile(exp(fracs), [0.16, 0.5, 0.84])
         e = diff(q)
         Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q[1], e[0],
          e[1]))
```

Out[53]:

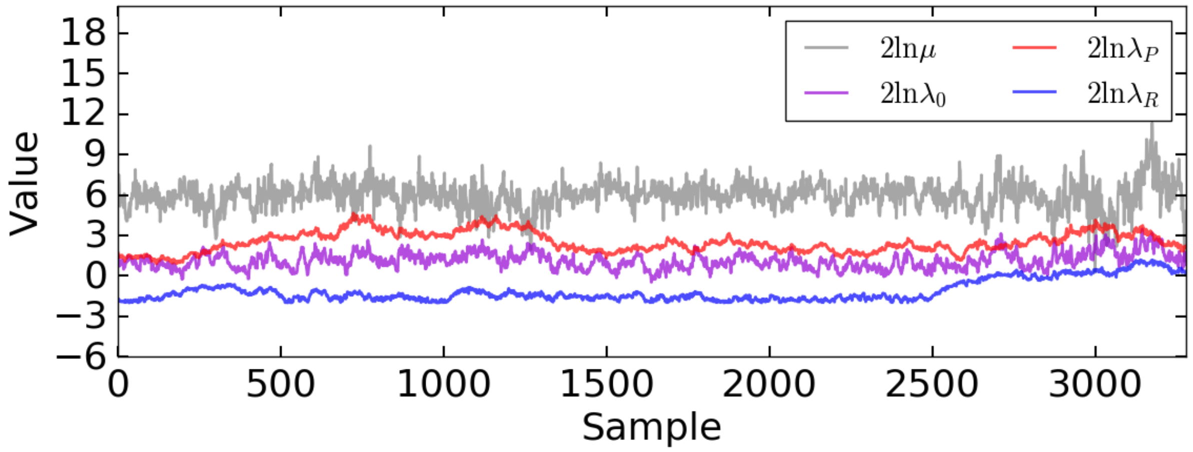
$$\Gamma_\oplus = 0.099 _{-0.030} ^{+0.036}$$

Catalog B

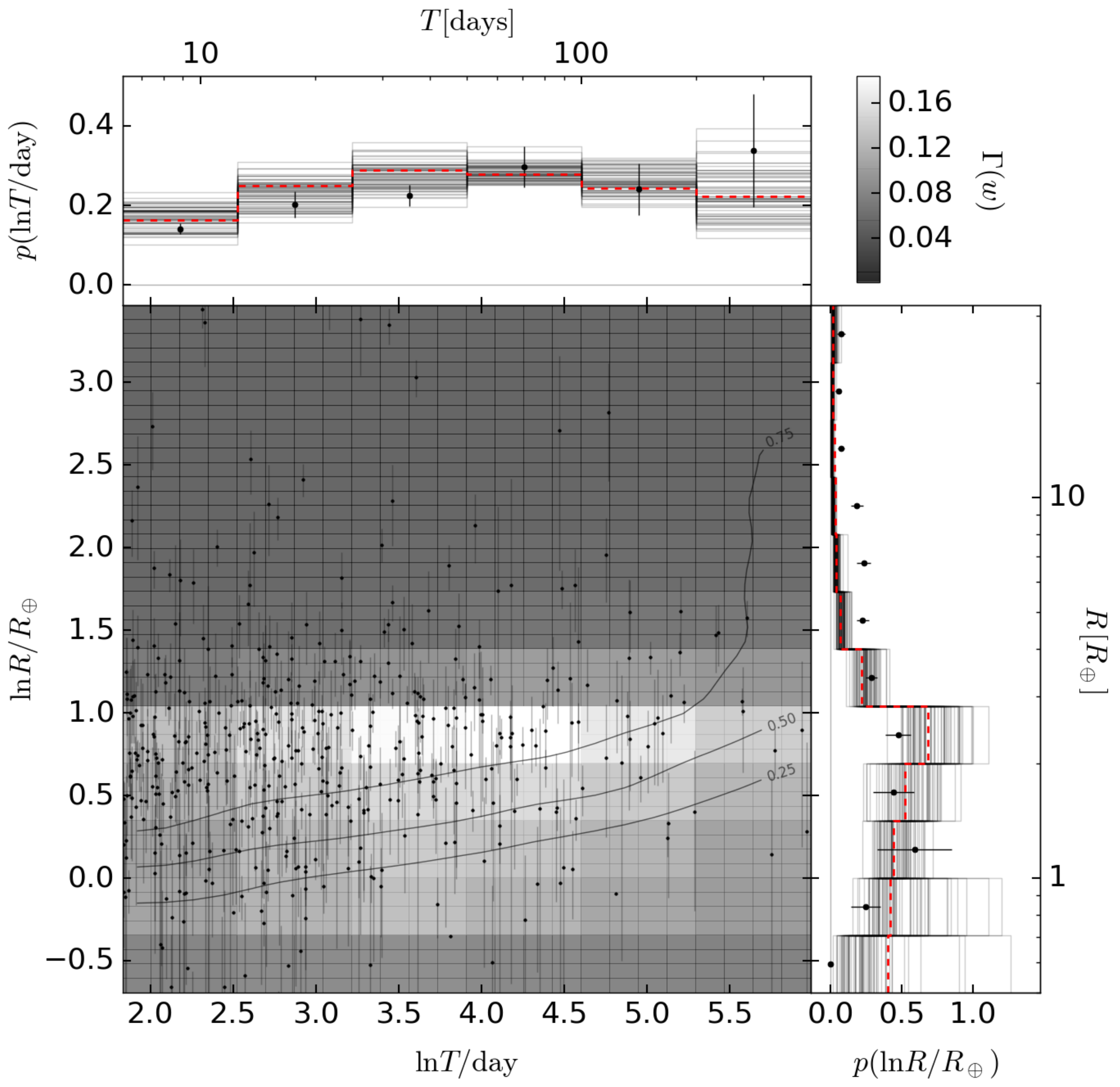
```
In [54]: with h5py.File("data/dfm-exopop-results-7568693/simulated/catalog-b/samples.h
         5") as f:
             samples = f["ln_occurrence_rate_samples"][:,:]
             hyper = f["hyperparameter_samples"][:,:]
             x = f["ln_period_bin_edges"][:]
             y = f["ln_radius_bin_edges"][:]
```

```
In [55]: hypernames = ['$2\ln\mu$', '$2\ln\lambda_0$', '$2\ln\lambda_P$', '$2\ln\lambda
         _R$']
         hypercolors = ['gray', 'darkviolet', 'red', 'blue']
         figure(figsize=(12, 5))
         for i in range(hyper.shape[1]):
             plot(hyper[:, i], label=hypernames[i], color=hypercolors[i], lw=2, alpha=0

         xlabel('Sample')
         xlim([0, len(hyper)])
         yticks(arange(-6, 20, 3))
         ylim([-6, 20])
         ylabel('Value')
         legend(loc="best", fontsize=20, ncol=2)
         tight_layout()

         print("Hyperparameter values (2ln):")

         q=array([corner.quantile(hyper[:, i], [.16, .50, .84]) for i in xrange(hyper.s
         hape[1])])
         e=diff(q)
         print("\n".join(xmap("{0} - {1} + {2}".format, zip(q[:,1], e[:,0], e[:,1]))))

         print("\n")
         print("Hyperparameter values (linear):")

         q=array([corner.quantile(exp(0.5*hyper[:, i]), [.16, .50, .84]) for i in xrang
         e(hyper.shape[1])])
         e=diff(q)
         print("\n".join(xmap("{0} - {1} + {2}".format, zip(q[:,1], e[:,0], e[:,1]))))
```

```
Hyperparameter values (2ln):
6.01043319603 - 0.957077333222 + 0.82307879839
1.10151284966 - 0.568064068363 + 0.616934961441
2.37554504953 - 0.592636448315 + 0.987688419399
-1.45555696009 - 0.322485876485 + 1.43411669934


Hyperparameter values (linear):
20.1905888638 - 7.67871296129 + 10.2798195666
1.73456458947 - 0.428884048379 + 0.626762809553
3.27976746402 - 0.841093772457 + 2.09447073238
0.482980750556 - 0.0719229409033 + 0.506359967591
```



```
In [56]: data = loadtxt('data/dfm-exopop-results-7568693/simulated/catalog-b/catalog.tx
         t') # period, radius, radius err
         catalog = c_[data[:, 0], normal(data[:, 1], data[:, 2])]
         err=c_[zeros(len(data)), data[:,2]]
         rerr = [log(catalog[:, 1]) - log(catalog[:, 1]-err[:, 1]),
                 log(catalog[:, 1]+err[:, 1]) - log(catalog[:, 1])] # radius error
         err = [0, rerr] # period and radius errors
         cat, _, truth = pickle.load(open("data/rough.cat.pkl", 'rb')) # load catalog

         fig1 = pop.plot_2d(samples.reshape(len(samples), (len(bins[0])-1)*(len(bins[1]
         1))[::50] - log(nstar),
                            censor=censor, catalog=log(catalog),
                            err=err, true=truth, labels=labels, top_axes=top_axes, lite
         rature=literature)
```



```
In [57]: rates = pop.get_lnrate(samples.reshape(len(samples), (len(bins[0])-1)*(len(bin
         s[1])-1)), [log(365.), log(1.0)])
         fracs = rates - log(nstar)
         q = corner.quantile(fracs, [0.16, 0.5, 0.84])
         e = diff(q)
         Math(r"\ln\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q[1], e[
          e[1]))
```

Out[57]:

$$\ln\Gamma_\oplus = -2.540_{-0.724}^{+0.648}$$

```
In [58]: q = corner.quantile(exp(fracs), [0.16, 0.5, 0.84])
         e = diff(q)
         Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}}".format(q[1], e[0],
          e[1]))
```

Out[58]:

$$\Gamma_\oplus = 0.079_{-0.041}^{+0.072}$$

These give much more reasonable results than our original inverse-detection-efficiency plus linear extrapolation-based predictions.

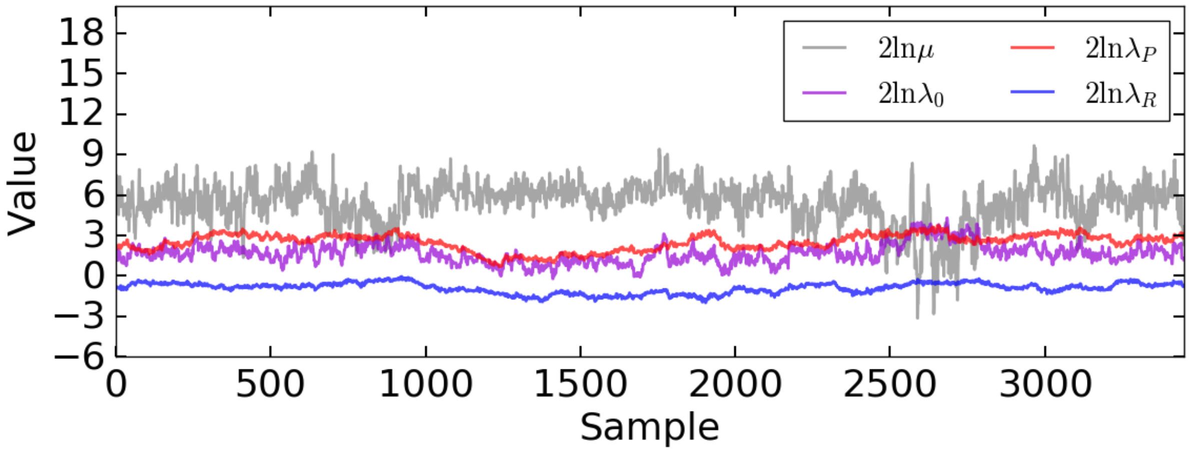
Real Data (Petigura et al.)

Now that we've set everything up, applying this to real data is a breeze!

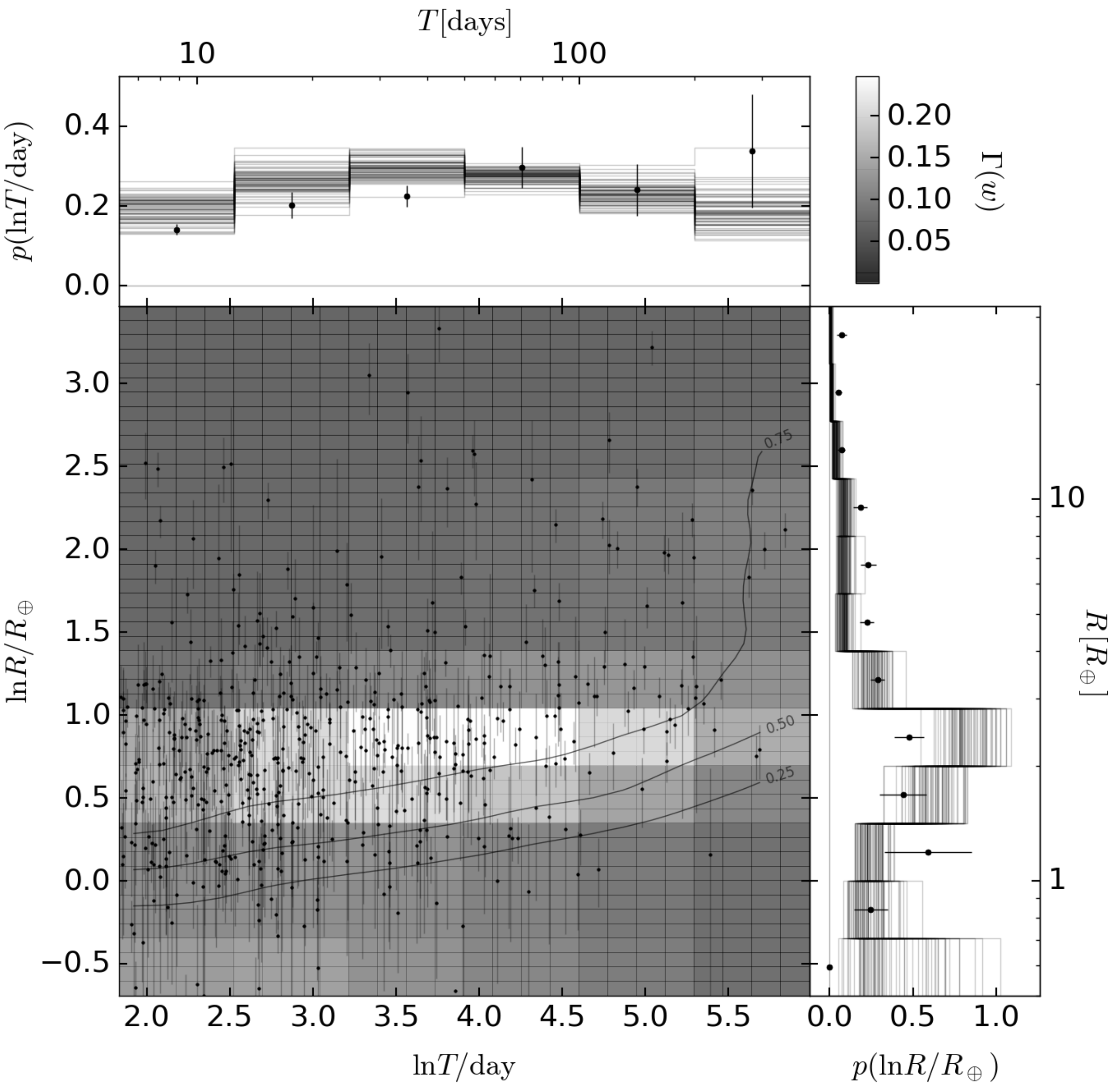
```
In [59]: with h5py.File("data/dfm-exopop-results-7568693/real/samples.h5") as f:
             samples = f["ln_occurrence_rate_samples"][:,:]
             hyper = f["hyperparameter_samples"][:,:]
             x = f["ln_period_bin_edges"][:]
             y = f["ln_radius_bin_edges"][:]
```

```
In [60]: hypernames = ['$2\ln\mu$', '$2\ln\lambda_0$', '$2\ln\lambda_P$', '$2\ln\lambda
         _R$']
         hypercolors = ['gray', 'darkviolet', 'red', 'blue']
         figure(figsize=(12, 5))
         for i in range(hyper.shape[1]):
             plot(hyper[:, i], label=hypernames[i], color=hypercolors[i], lw=2, alpha=0

         xlabel('Sample')
         xlim([0, len(hyper)])
         yticks(arange(-6, 20, 3))
         ylim([-6, 20])
         ylabel('Value')
         legend(loc="best", fontsize=20, ncol=2)
         tight_layout()

         print("Hyperparameter values (2ln):")

         q=array([corner.quantile(hyper[:, i], [.16, .50, .84]) for i in xrange(hyper.s
         hape[1])])
         e=diff(q)
         print("\n".join(xmap("{0} - {1} + {2}".format, zip(q[:,1], e[:,0], e[:,1]))))

         print("\n")
         print("Hyperparameter values (linear):")

         q=array([corner.quantile(exp(0.5*hyper[:, i]), [.16, .50, .84]) for i in xrang
         e(hyper.shape[1])])
         e=diff(q)
         print("\n".join(xmap("{0} - {1} + {2}".format, zip(q[:,1], e[:,0], e[:,1]))))
```

```
Hyperparameter values (2ln):
5.67874964633 - 1.53410463259 + 1.06773512306
1.62704946818 - 0.63000215649 + 0.722368650785
2.61987136158 - 0.763638420549 + 0.484174372443
-0.841039212297 - 0.507972254137 + 0.33428980894


Hyperparameter values (linear):
17.1050685011 - 9.16181853719 + 12.0679064105
2.25584524473 - 0.609556247045 + 0.981355729155
3.70593534171 - 1.17619429787 + 1.01507519701
0.65670550293 - 0.147297361013 + 0.119471492405
```



In [61]:
```
data = loadtxt('data/dfm-exopop-results-7568693/real/catalog.txt') # period, r
adius, radius err
catalog = c_[data[:, 0], normal(data[:, 1], data[:, 2])]
err=c_[zeros(len(data)), data[:,2]]
rerr = [log(catalog[:, 1]) - log(catalog[:, 1]-err[:, 1]),
        log(catalog[:, 1]+err[:, 1]) - log(catalog[:, 1])] # radius error
err = [0, rerr] # period and radius errors

fig1 = pop.plot_2d(samples.reshape(len(samples), (len(bins[0])-1)*(len(bins[1]
1))[::50] - log(nstar),
                   censor=censor, catalog=log(catalog),
                   err=err, true=None, labels=labels, top_axes=top_axes, liter
ature=literature)
```



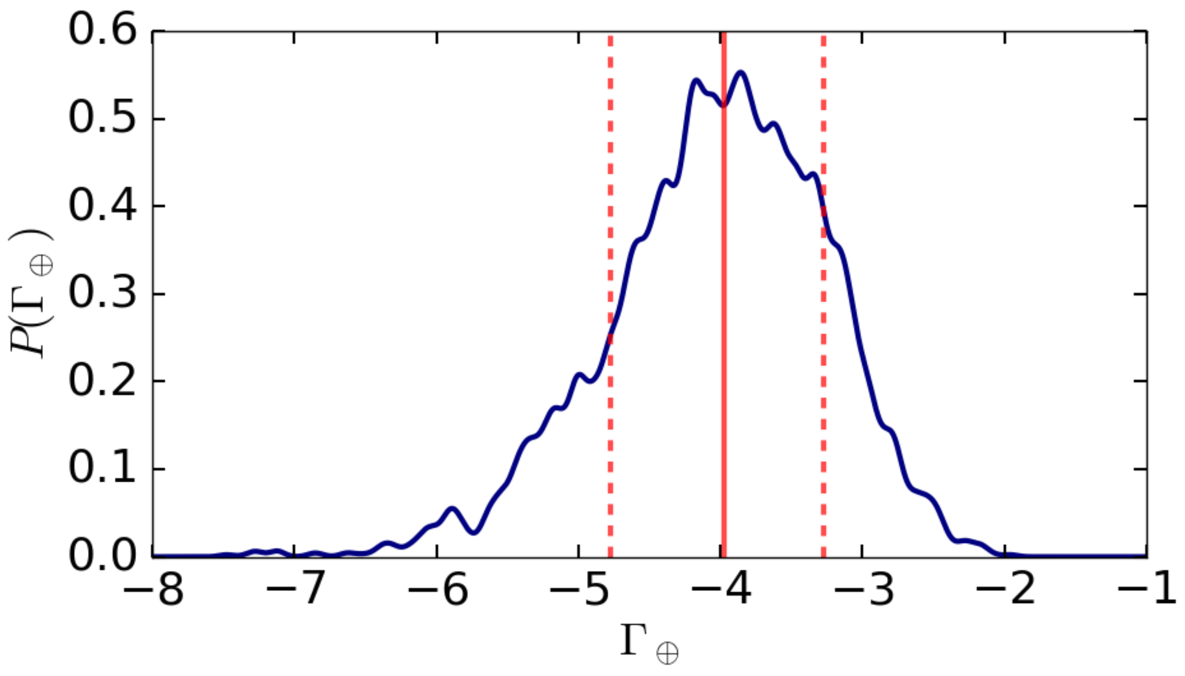
We can now compute and plot $\Gamma_\oplus$ from these realizations!

In [62]:
```
rates = pop.get_lnrate(samples.reshape(len(samples), (len(bins[0])-1)*(len(bin
s[1])-1)), [log(365.), log(1.0)])
fracs = rates - log(nstar)
a, b, c = corner.quantile(fracs, [0.16, 0.5, 0.84])
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}} \quad (\mathrm{{lo
g}})".format(b, b-a, c-b))
```

Out[62]:

$$\Gamma_\oplus = -3.972 _{-0.798} ^{+0.697} \quad (\mathrm{log})$$

In [63]:
```
kde = KernelDensity(kernel='gaussian', bandwidth=0.05).fit(fracs[:,None]) # de
rive the underlying estimator
x = linspace(-8, -1, 5000)
log_dens = kde.score_samples(x[:,None]) # return results

# plotting
figure(figsize=(10, 6))
plot(x, exp(log_dens), color='navy', lw=3)
axvline(a, color='r', ls='--', alpha=0.7, lw=3)
axvline(b, color='r', ls='-', alpha=0.7, lw=3)
axvline(c, color='r', ls='--', alpha=0.7, lw=3)
xlabel('$\Gamma_\oplus$')
ylabel('$P(\Gamma_\oplus)$')
tight_layout()
```

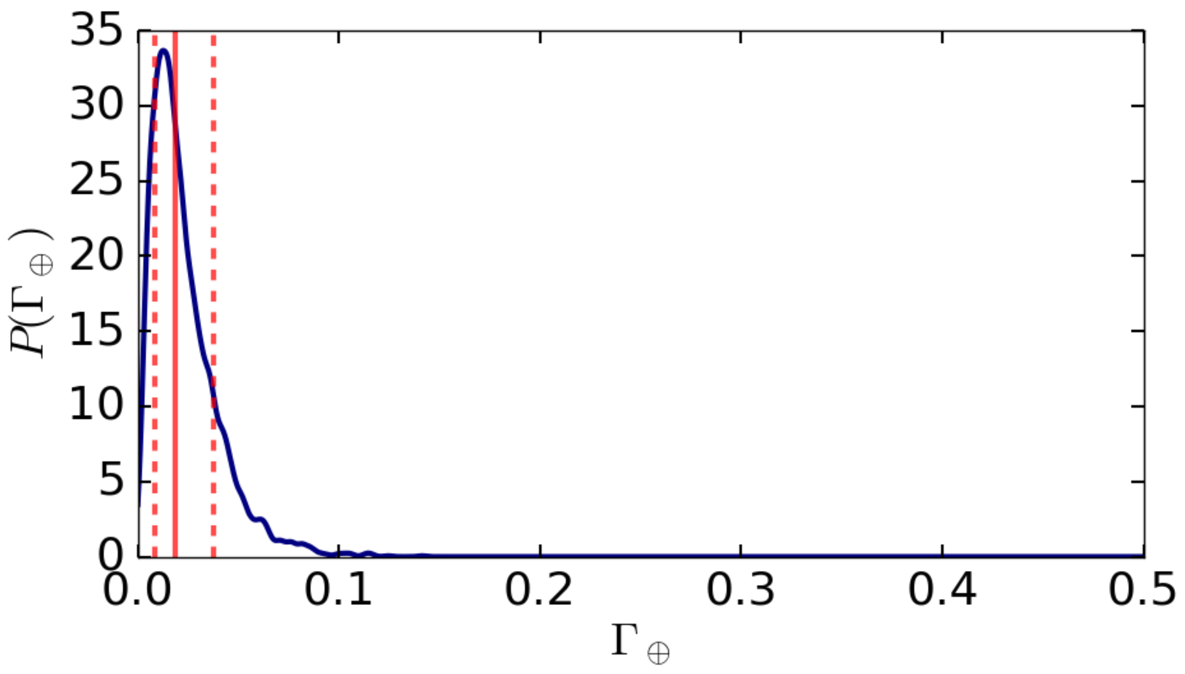


In [64]:
```
al, bl, cl = corner.quantile(exp(fracs), [0.16, 0.5, 0.84])
Math(r"\Gamma_\oplus = {0:.3f} _{{-{1:.3f}}} ^{{+{2:.3f}}} \quad (\mathrm{{lin
ear}})".format(bl, bl-al, cl-bl))
```

Out[64]:

$$\Gamma_\oplus = 0.019 _{-0.010} ^{+0.019} \quad (\mathrm{linear})$$

In [65]:
```
from sklearn.neighbors import KernelDensity
kde = KernelDensity(kernel='gaussian',
bandwidth=0.002).fit(exp(fracs[:,None])) # derive the underlying estimator
x = linspace(0, 0.5, 5000)
log_dens = kde.score_samples(x[:,None]) # return results

# plotting
figure(figsize=(10, 6))
plot(x, exp(log_dens), color='navy', lw=3)
axvline(al, color='r', ls='--', alpha=0.7, lw=3)
axvline(bl, color='r', ls='-', alpha=0.7, lw=3)
axvline(cl, color='r', ls='--', alpha=0.7, lw=3)
xlabel('$\Gamma_\oplus$')
ylabel('$P(\Gamma_\oplus)$')
tight_layout()
```

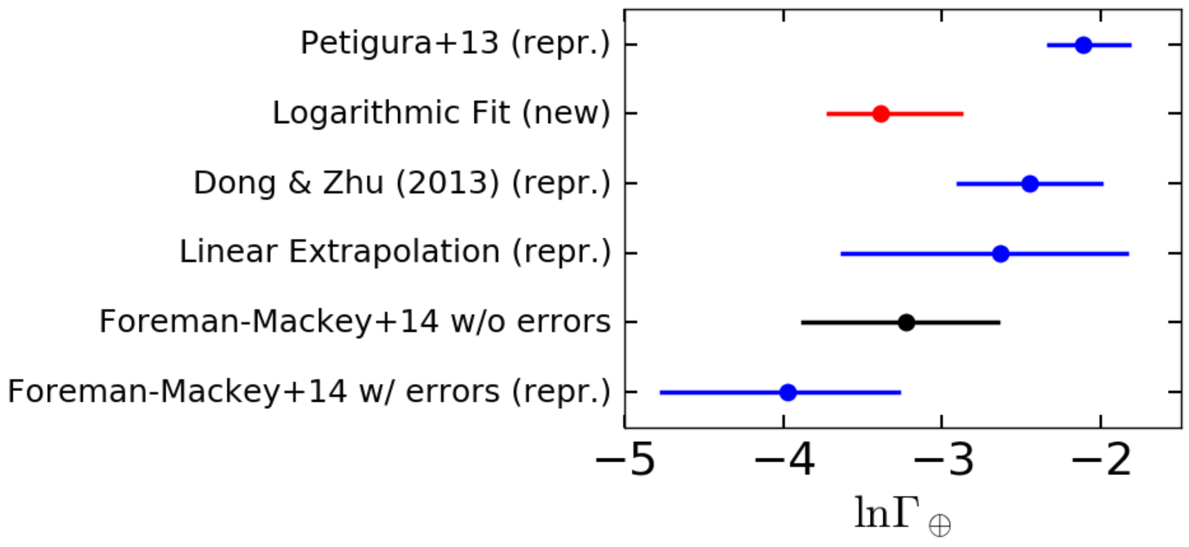


These estimates are significantly lower than the above results, implying that incorporating measurement error and better modeling of the underlying occurence rate (i.e. sampling from the full posterior rather than the MLE) substantially impacts our estimates of $\Gamma_\oplus$.

Final Comparison

We plot all of our calculations together in one final image.

```
In [66]: from matplotlib.ticker import MaxNLocator

         values = [
             ("Petigura+13 (repr.)", q1[1], e1[1], e1[0], 'blue'),
             ("Logarithmic Fit (new)", q2[1], e2[1], e2[0], 'red'),
             ("Dong & Zhu (2013) (repr.)", q4[1], e4[1], e4[0], 'blue'),
             ("Linear Extrapolation (repr.)", q3[1], e3[1], e3[0], 'blue'),
             ("Foreman-Mackey+14 w/o errors", 0.0397591956934, 0.0309881584307, 0.01906
         20520124, 'black'),
             ("Foreman-Mackey+14 w/ errors (repr.)", bl, cl-bl, bl-al, 'blue')
         ]

         fig = figure(figsize=(10, 5))
         for i, v in enumerate(values):
             plot(log(v[1]), i, "o", color=v[4], markeredgecolor='none', markersize=10)
             plot(log([v[1]+v[2], v[1]-v[3]]), [i, i], color=v[4], lw=2.5)

         gca().set_yticklabels([""] + [v[0] for v in values],fontsize=18)
         xlabel(r"$\ln\Gamma_\oplus$")
         fig.subplots_adjust(left=0.48, bottom=0.17, right=0.97, top=0.98)
         ylim(len(values)-.5, -0.5)
         gca().xaxis.set_major_locator(MaxNLocator(5))
         tight_layout()
```


Petigura+13 (repr.)
Logarithmic Fit (new)
Dong & Zhu (2013) (repr.)
Linear Extrapolation (repr.)
Foreman-Mackey+14 w/o errors
Foreman-Mackey+14 w/ errors (repr.)
$\ln\Gamma_\oplus$