Every 1000 rounds a progress indicator is printed. Its format depends on a number of things: (1) whether parallelization is turned on or not, (2) the correlation model [isotropic or separable], (3) whether jumps to the LLM are allowed. Here is an example with the 2-d exp data with parallel prediction under the separable correlation function:

```
(r,l)=(5000,104) d=[0.0144 0.0236] [1.047 0/0.626]; mh=2 n=(59,21)
```

The first part `(r,l)=(5000,104)` is indicating the MCMC round number r=5000 and the number of leaves waiting to be "consumed" for prediction by the parallel prediction thread. When parallelization is turned off (default), the print will simply be `"r=5000"`.

The second part is a printing of the d–(range) parameter to a separable correlation function. For 2 partitions there are two sets of square brackets. Inside the square brackets is the m_X (2 in this case) range parameters for the separable correlation function. Whenever the LLM governs one of the input dimensions a zero will appear. I.e., the placement of `0/0.626` indicates the LLM is active in the 2nd dimension of the 2nd partition. 0.626 is the d–(range) parameter that would have been used if the LLM were inactive. Whenever all dimensions are under the LLM, the d-parameter print is simply `[0]`. This also happens when forcing the LLM (i.e., for `blm` and `btlm`), where `[0]` appears for each partition. These prints will look slightly different if the isotropic instead of separable correlation is used, since there are not as many range parameters.

B.3 Collaboration with `predict.tgp`

In this section I revisit the motorcycle accident data in order to demonstrate how the `predict.tgp` function can be helpful in collaborative uses of `tgp`. Consider a fit of the motorcycle data, and suppose that infer the model parameters only (obtaining no samples from the posterior predictive distribution). The `"tgp"`-class output object can be saved to a file using the `R`–internal `save` function.

```
> library(MASS)
> out <- btgpllm(X = mcycle[, 1], Z = mcycle[, 2],
+     bprior = "b0", m0r1 = TRUE, pred.n = FALSE, verb = 0)
> save(out, file = "out.Rsave")
> out <- NULL
```

Note that there is nothing to plot here because there is no predictive data. (`out <- NULL` is set for illustrative purposes.)

Now imagine e–mailing the "out.Rsave" file to a collaborator who wishes to use your fitted `tgp` model. S/he could first load in the `"tgp"`–class object we just saved, design a new set of predictive locations `XX` and obtain kriging estimates from the MAP model.

```
> load("out.Rsave")
> XX <- seq(2.4, 56.7, length = 200)
> out.kp <- predict(out, XX = XX, pred.n = FALSE)
```

Another option would be to sample from the posterior predictive distribution of the MAP model.

```
> out.p <- predict(out, XX = XX, pred.n = FALSE, BTE = c(0,
+     1000, 1))
```

This holds the parameterization of the `tgp` model *fixed* at the MAP, and samples from the GP or LM posterior predictive distributions at the leaves of the tree.

Finally, the MAP parameterization can be used as a jumping-off point for more sampling from the joint posterior and posterior predictive distribution.

```
> out2 <- predict(out, XX, pred.n = FALSE, BTE = c(0,
+     2000, 2), MAP = FALSE)
```

Since the return–value of a `predict.tgp` call is also a `"tgp"`–class object the process can be applied iteratively. That is, `out2` can also be passed to `predict.tgp`.

Figure 23 plots the posterior predictive surfaces for each of the three calls to `predict.tgp` above. The kriging surfaces are smooth within regions of the partition, but the process is discontinuous across partition boundaries. The middle surface is simply a Monte Carlo–sample summarization of the kriging one above it. The final surface summarizes samples from the posterior predictive distribution when obtained jointly with samples from $\mathcal{T}|\boldsymbol{\theta}$ and $\boldsymbol{\theta}|\mathcal{T}$. Though these summaries are still "noisy" they depict a process with smoother transitions across partition boundaries than ones conditioned only on the MAP parameterization.

The `predict.tgp` function can also sample from the ALC statistic and calculate expected improvements (EI) at the `XX` locations.

C Configuration and performance optimization

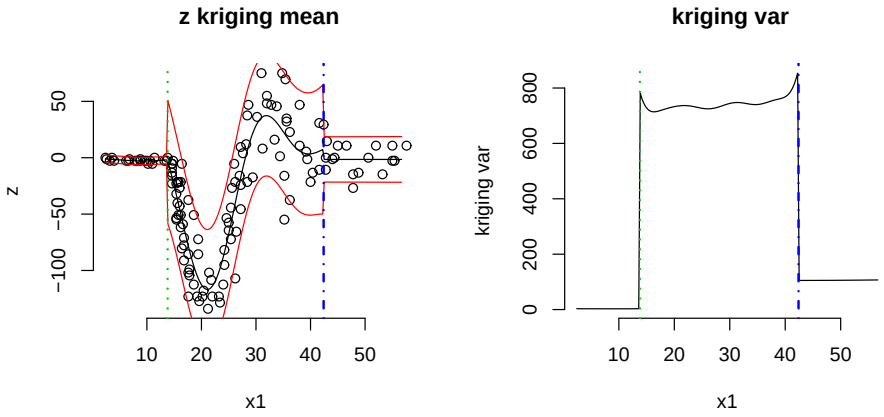
In what follows I describe customizations and enhancements that can be made to `tgp` at compile time in order to take advantage of custom computing architectures. The compilation of `tgp` with a linear algebra library different from the one used to compile `R` (e.g., ATLAS), and the configuration and compilation of `tgp` with parallelization is described in detail.

C.1 Linking to ATLAS

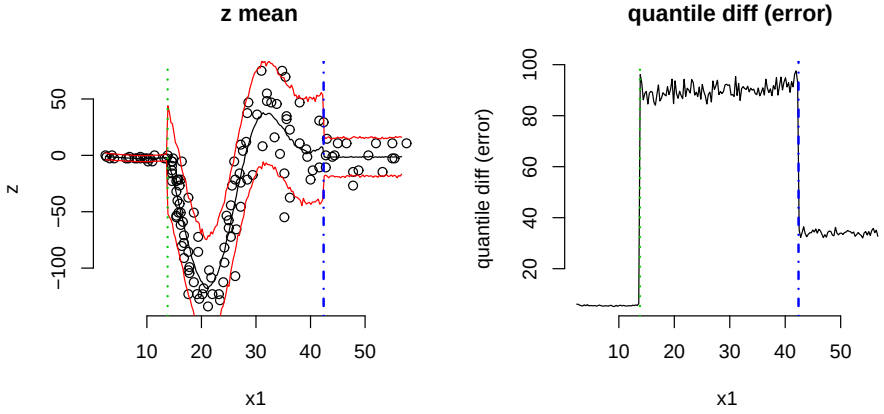
`ATLAS` [30] is supported as an alternative to standard `BLAS` and `LAPACK` for fast, automatically tuned, linear algebra routines. If you know that `R` has already been linked to tuned linear algebra libraries (e.g., on `OSX`), then compiling with `ATLAS` as described below, is unnecessary—just install `tgp` as usual. As an alternative to linking `tgp` to `ATLAS` directly, one could re-compile all of `R` linking it to `ATLAS`, or some other platform–specific `BLAS`/`Lapack`, i.e., `Intel`'s Math Kernel Library, or `AMD`'s Core Math Library, as described in:

`http://cran.r-project.org/doc/manuals/R-admin.html`

```
> plot(out.kp, center = "km", as = "ks2")
```




```
> plot(out.p)
```




```
> plot(out2)
```

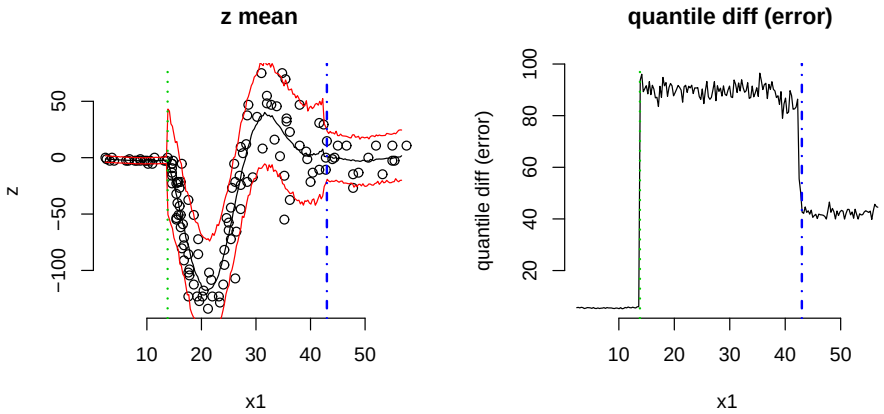


Figure 23: Predictive surfaces (*left*) and error/variance plots (*right*) resulting from three different uses of the `predict.tgp` function: MAP kriging (*top*), sampling from the MAP (*middle*), sampling from the joint posterior and posterior predictive starting from the MAP (*bottom*).