Dynamic Systems Simulation and Modelling With R, ctsem, and lme4: Couples' Affect Dynamics Over Time

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Abstract

Understanding how people change is a fundamental goal of psychological science. However, translating complex ideas about psychological dynamics into formal models can be challenging without the right tools. In this tutorial, we introduce a workflow that leverages R and the ctsem package to help researchers build and understand dynamic systems models that capture the complexity of psychological processes. Our workflow emphasizes iterative model-building through simulations, model fitting, and visualizations of the model-implied dynamics alongside their fit to data. We begin with familiar linear models in lme4 and gradually transition to ctsem, which allows us to incorporate complexities such as state-dependent change, random fluctuation distinct from measurement error, covariate effects, interactions, and external inputs. These modelling concepts are illustrated using a running example of affect dynamics in couples therapy, demonstrating how key conceptual and methodological ideas in dynamic systems modelling come together. Our aim is to provide a general framework for understanding dynamic systems modelling and to encourage further exploration of theory-driven statistical approaches in psychological research.

Impact Statement

This tutorial shows how psychological researchers can use R and the ctsem package to build and understand dynamic systems models that capture the complexity of psychological processes. By providing a structured approach to model building, we aim to facilitate the translation of theoretical concepts into empirical models, ultimately enhancing our understanding of psychological concepts and their interrelations over time.

Keywords: dynamic systems, continuous time, hierarchical modeling, longitudinal data analysis, affect dynamics, ctsem, lme4, state-space models

Introduction

Dynamic systems theory provides a framework for understanding how psychological constructs evolve over time (van Geert, 2011). To turn conceptual ideas about dynamic systems into insight about

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The authors have no conflicts of interest to disclose. Author roles were classified using the Contributor Role Taxonomy (CRediT; https://credit.niso.org/) as follows: Charles C. Driver: conceptualization, methodology, software, validation, writing, visualization; Michael Aristodemou: formal analysis, writing, visualization
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mechanisms of change, theory must be translated into empirically testable models, which when combined with data can in turn suggest updates to theory(Borsboom et al., 2021). Yet, this translation from conceptual ideas to testable statistical models can be difficult without tools that make the steps transparent.

This tutorial is designed to help psychological researchers bridge the gap between theoretical concepts in dynamic systems and their practical implementation using statistical modeling. We begin with familiar linear mixed-effects models using the R package lme4 (Bates et al., 2015), then gradually move into the dynamic systems and continuous-time domain using the package ctsem (Driver & Voelkle, 2018a). This progression highlights how modeling choices can evolve alongside theory, allowing increasingly realistic and nuanced representations of psychological change.

A key strength of ctsem is that it can accommodate this full modeling continuum. Starting from basic linear growth models, one can move through discrete- and continuous-time versions of classic frameworks such as the Cross-Lagged Panel Model (Kenny, 2005), the random intercept extension of it (Hamaker et al., 2015), and related forms such as network vector autogression (Epskamp, 2020)). From there, one can extend ctsem to models with considerably more complexity. These extensions include complex variation across individuals, oscillations, and measurement or dynamics parameters that shift over time or in response to moderators and interventions. In this way, ctsem provides a flexible environment for building models up step by step: researchers can begin with simple forms to establish a baseline, then incorporate the dynamics that theory suggests, then perhaps go further with data-driven model and theory development (Borsboom et al., 2021).

Continuous-time representations are particularly valuable for theory-oriented model development, because of the more natural link between continuous-time parameters and typical theoretical interests [aalen2016can, ryan2022time, driver2023formalizing]. Because most psychological processes – such as emotion regulation, stress responses, or cognitive fluctuations – are thought to evolve continuously rather than only when measured, continuous-time models provide a natural representation. Parameters such as drift (state dependence), diffusion (system noise), and external inputs can be interpreted directly as features of the underlying process, instead of as artifacts of the measurement schedule. This interpretability makes continuous-time models especially valuable for theory-oriented research, as it ensures that any constraints imposed on the model (e.g., fixing the effect of one variable on another to zero) are also coherent and meaningfully interpretable (Driver, 2025).

To make these ideas concrete, we present a running example: the impact of couples therapy on affect dynamics over time. This example is grounded in empirical research showing that partners' affective states are dynamically interdependent, becoming synchronized through processes of mutual influence (Butler & Randall, 2013). Such coupling can either amplify or dampen emotional experiences, with implications for individual well-being and relationship stability. Using this context, we progressively build from basic assumptions of linear change to models incorporating feedback loops, random fluctuations, dyadic interdependence, and the effects of therapeutic inputs. Through this step-by-step approach, we introduce different models of affective processes that reflect increasing levels of complexity:

1. **Steady (Linear) Change (Discrete Time)**: an affect process that changes at a steady rate from an initial state of affect during each observation.
2. **Nonlinear Change (Discrete Time)**: an affect process whose growth rate depends on a person's level of affect at the observation before the change happens–creating a nonlinear growth process.
3. **Nonlinear Change with Random Fluctuations (Continuous Time)**: an affect process that changes continuously over time, and whose rate of change depends on a person's level of affect at the moment of change–creating a nonlinear growth process. Here we add the effect of unpredictable endogenous and exogenous events that generate momentary fluctuations in affect. The conceptual shift necessary to understand modeling in continuous time, is explained prior to the introduction of this model.
4. **Couple Dynamics with Self and Partner Effects (Continuous Time)**: an affect process for a couple whose rate of change is dependent on their own level of affect and their partner's level of affect at a given moment.

5. **Couple Dynamics with Individual Differences and Time-Independent Moderation (Continuous Time)**: an affect process for a couple whose rate of change is dependent on their own level of affect and their partner's level of affect at a given moment. In this model, we introduce individual differences in system dynamics and a time-independent moderator (i.e. partner effects are moderated by the time they spend together).
6. **Couple Dynamics with Individual Differences and Time-Dependent Moderation (Continuous Time)**: an affect process for a couple whose rate of change is dependent on their own level of affect and their partner's level of affect at a given moment. In this model, the partner effects are moderated by a time-varying moderator tracking whether the couple is together (time-dependent covariate).
7. **Nonlinear Change with a Transient External Shock (Continuous Time)**: an affect process whose growth rate depends on a person's level of affect at the observation before the change happens–creating a nonlinear growth process. Here the affect process is impacted by a therapy session that only directly impacts affect during the session.
8. **Nonlinear Change with a Persistent External Shock (Continuous Time)**: an affect process whose growth rate depends on a person's level of affect at the observation before the change happens–creating a nonlinear growth process. Here the affect process is instantly impacted by a therapy session with a persistent effect.

By going through the steps to formalize these eight process, researchers will have a structured approach to modeling affect dynamics in a way that captures both within-person change and between-person heterogeneity.

To end this tutorial, we showcase a process of iterative model evaluation and improvement starting from a misspecified model and working toward the data generating mechanism.

Steady (Linear) Change in Affect

Let us start by considering a hypothetical patient named Jill. Jill started going to couples therapy and has agreed to track her affect once every seven days (i.e. at equidistant time intervals), for 21 weeks, through a mobile app. What we want, is to conceptualize possible ways that Jill's affect develops during this time. So we develop some ideas about what Jill's development might look like, and pick the simplest one to start. Our first idea, is that Jill's affect will increase at a steady rate throughout the course of couples therapy.

Now we want to turn our conceptual idea of linear change into a statistical model that we can fit to data. For a steady increase in affect, a linear regression model is an appropriate choice. With our linear regression model, we state that Jill's observed affect (y) changes at a steady rate (B) as a function of time (t) from an initial affect state (η_{t0}), and any deviations from this process are captured by a random noise term (ϵ) to account for the imperfection of our measurements:

$$y(t) = \eta_{t0} + Bt + \epsilon(t)$$

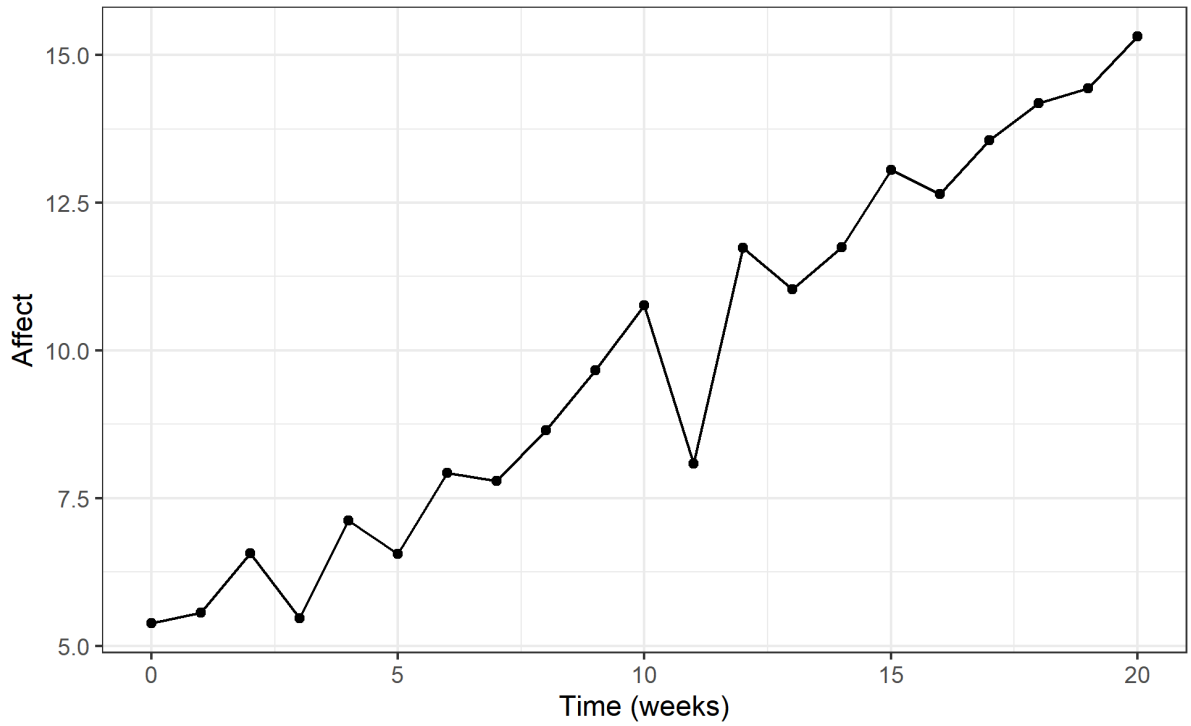
Next, we can obtain a better understanding of the growth process it implies (and whether it matches our conceptual idea) by generating data from the model and visualizing its model-implied trajectory of affect.

Simulation: A linear change model (N = 1)

So let's write some code to generate data from a linear regression model representing a steady rate of change in affect and visualize its model-implied trajectory. First, we specify the number of time points we wish to generate data for (`Time <- 0:20`). Second, we set the initial state of affect at the beginning of the growth process, i.e. the beginning of therapy (`initialAffect <- 5`). Third, we specify the linear regression model that will formalize our linear affect process for a single person, whose affect starts at an initial level (`initialAffect`) of 5 and increases steadily by 0.51 during every weekly observation (`Time*.51`). Fourth, we add random noise to our model by sampling values from a normal distribution

with a mean of 0 and a standard deviation of 1 (`rnorm(n=length(Time), mean = 0, sd = 1)`). These noise values are added to each affect value that is generated by our model. Fifth, we create a data frame to store the number of time points (i.e. weeks) and the affect values we generated for each time point. Finally, we plot the data using a lineplot to illustrate the model-implied affect process over the course of 21 weeks of therapy.

```
Time <- 0:20 # Generate time points for each measurement occasion
initialAffect <- 5 # Initial level of mood at week 0

# Specify a linear model that generates affect data increases by 0.51 each week
Affect <- initialAffect + Time*.51 + rnorm(n=length(Time), mean = 0, sd = 1)

# Create a data frame to store the generated data
data <- data.frame(Time = Time, Affect = Affect)

# Plot the data using a lineplot
ggplot(data, aes(x = Time, y = Affect)) +
  geom_point() + # draw points that show affect during each week
  geom_line() + # line that connects the points to map the trajectory
  theme_bw()+ # set the background for the plot
  labs( x = "Time (weeks)", y = "Affect")+ # add a title and labels to the plot
  theme(legend.position = "none") # remove legend
```



Here we see our linear model provides a good representation of the idea that Jill's affect increases at a steady pace each time we observe her. Albeit with some random fluctuations, which we can attribute to measurement error.

Dealing with individual differences in affect changes

By viewing Jill's model-implied growth process it strikes us that we have no idea whether her rate of change is slow or fast relative to other people who go to couples therapy. That is we may want to know if couples therapy leads to a different amount of change for different people, and if differences in people's rate of change are related to their initial level of affect. For instance, people who have a much lower initial level of affect than Jill may benefit more from couples therapy. To understand where Jill sits relative to other patients, we need to introduce individual differences into our model.

The equation for a linear model which allows people to vary in their initial affect level and rate of change, looks very similar to the linear regression model presented above but includes an i subscript to indicate that each person has their own initial level (η_{t0i}) and rate of change ($B_i t$) of affect:

$$y_i(t) = \eta_{t0i} + B_i t + \epsilon_i(t)$$

This model is commonly termed a linear mixed-effects model (Bates et al., 2015), because it includes both fixed effects (parameters that are assumed to be the same across all subjects, often interpreted as population-level effects) and random effects (parameters that allow for individual variations, such as subject-specific intercepts η_{t0i} or slopes $B_i t$).

Simulation: A linear change model with individual differences

We now generate data from our linear mixed-effects model. The code below is used to generate data for 20 subjects `NSubjects <- 20` whose affect is measured 21 times, once per week for 21 weeks `times <- seq(from=0, to=20, by=1)`. To generate a different initial state for each subject, we sample 20 initial states from a normal distribution of initial affect levels with a mean of 5 and a standard deviation of 2 `initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)`. The values here are arbitrary and can be tweaked to adjust the amount of heterogeneity in initial affect (`sd`), and the sample average initial affect level (`mean`). To match our hypothetical scenario, where people's rate of growth in affect is related to their initial level, we can generate data so that people's rate of change is negatively correlated with people's initial level of affect `timeCoefficients <- rnorm(n = NSubjects, mean = 0.5, sd = 0.1) + scale(initialAffect) * -0.2`. Here we also use the scale function to generate data for the rate of change with a standardized coefficient, which can offer a more intuitive representation of the rate of change.

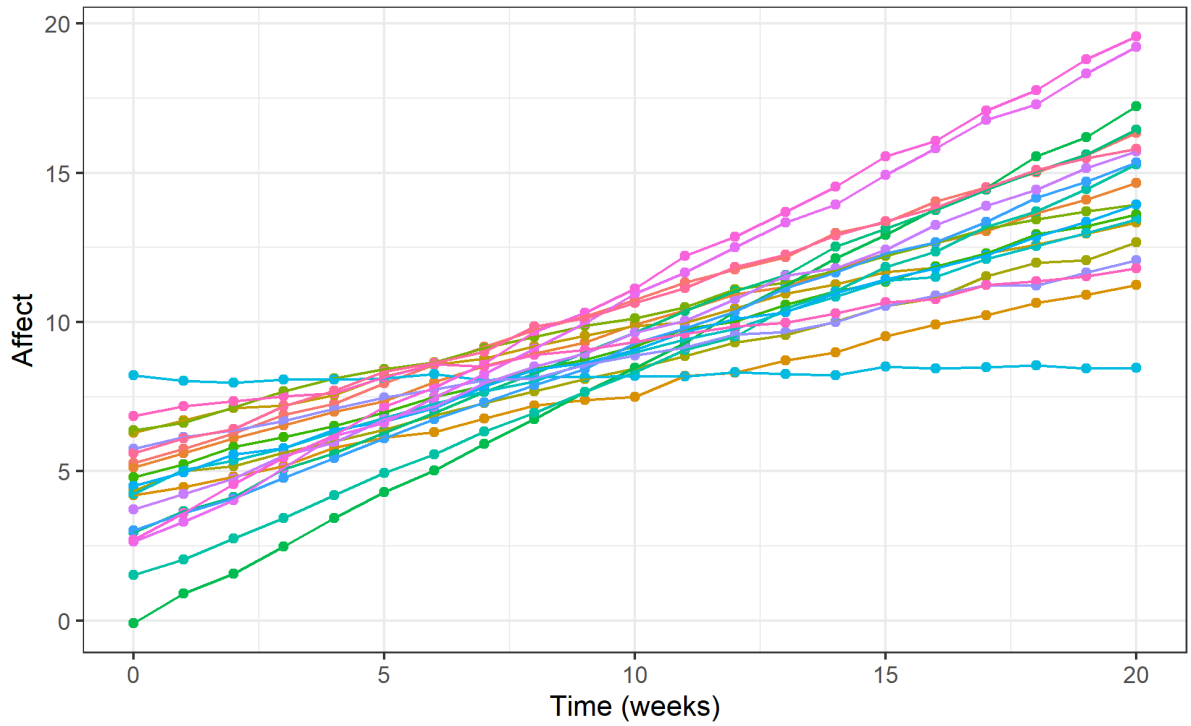
```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=20, by=1) # sequence of time points when subjects are measured
Nobs <- length(times) # number of observations per subject
# sample initial affect for each subject from a normal distribution
initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)
# sample rate of change in affect for each subject
timeCoefficients <- rnorm(n = NSubjects, mean = 0.5, sd = 0.1) +
  scale(initialAffect) * -0.2 # include negative influence of initial affect

cor(initialAffect, timeCoefficients) # check correlation in individual differences
```

```
           [,1]
[1,] -0.8881989
```

We can now create an empty data frame that can later hold the data we generate for each subject and each observation. To fill the data frame, we create two nested loops. The first loop `for(subi in 1:NSubjects)` allows us to go through each subject `subi` one by one. For each subject selected by the first loop, we initialize the second loop `for(obsi in 1:Nobs)` that allows us to go through each observation `obsi`. Within this loop, we fill in each row in our data frame, which corresponds to an observation. For each observation, we generate information about a person's affect level, the current time point (week), and their subject identifier. To keep track of the current observation for each iteration of our loop, we initialize a row count at 0 `row <- 0` and then add 1 to this running row count `row <- row + 1`. To reflect the imperfect measurement of affect, we add some random noise to the affect data that we generated, by sampling random values from a normal distribution with a mean of 0 and a standard deviation of 1 `data$Affect <- data$Affect + rnorm(n=nrow(data), mean = 0, sd = .1)`.

```
#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect = rep(NA,NSubjects*Nobs))
```

```
row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1 # add an integer to the row to keep track of the current observation (row)
    data$Affect[row] <- initialAffect[subi] + # currentt affect is initial affect plus...
      times[obsi] * timeCoefficients[subi] # the effect of time that has passed since.
    data$Time[row] <- times[obsi] # store time point for current observation (row)
    data$Subject[row] <- subi # store subject identifier for current observation (row)
  }
}

# add random noise to the affect data
data$Affect <- data$Affect + rnorm(n=nrow(data), mean = 0, sd = .1)

# plot subject specific trajectories, color-coded by subject
ggplot(data, aes(x = Time, y = Affect, color = as.factor(Subject))) +
  geom_point() + # draw points that show affect during each week
  geom_line() + # line that connects the points to map the trajectory
  theme_bw()+ # set the background for the plot
  labs(x = "Time (weeks)", y = "Affect", color = "Subject")+ # labels for figure axes
  theme(legend.position = "none") # remove legend
```



From our plot, we can see that the correlated initial state and rate of change capture the idea that individuals who start with lower affect levels may improve faster over time.

Fitting a model: A linear mixed-effects model in lme4

We can now fit our model to the data we generated and interpret how well it captures the patterns in our observations. To specify and fit our linear mixed-effects models, we will use the lme4 package in R:

```
# Fit linear mixed-effects model
library(lme4)
lme_model <- lmer(Affect ~ # predict Affect
    1 + # a fixed effect for the intercept
    Time + # with a fixed effect of time
    (1 + Time | Subject), # random intercept and random effect (slope) of time per subject
  data = data) # specify data to fit model to
```

After fitting the model to our data, we can ask for a summary of its parameter estimates.

```
# Summary of model output
summary(lme_model)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: Affect ~ 1 + Time + (1 + Time | Subject)
   Data: data

REML criterion at convergence: -438.9

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.4104 -0.6172  0.0206  0.6602  3.3228

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 Subject  (Intercept) 3.730802 1.93153
          Time        0.044365 0.21063  -0.89
 Residual             0.009718 0.09858
Number of obs: 420, groups:  Subject, 20

Fixed effects:
            Estimate Std. Error t value
(Intercept)   4.4001     0.4320   10.19
Time          0.5042     0.0471   10.71

Correlation of Fixed Effects:
     (Intr)
Time -0.890
```

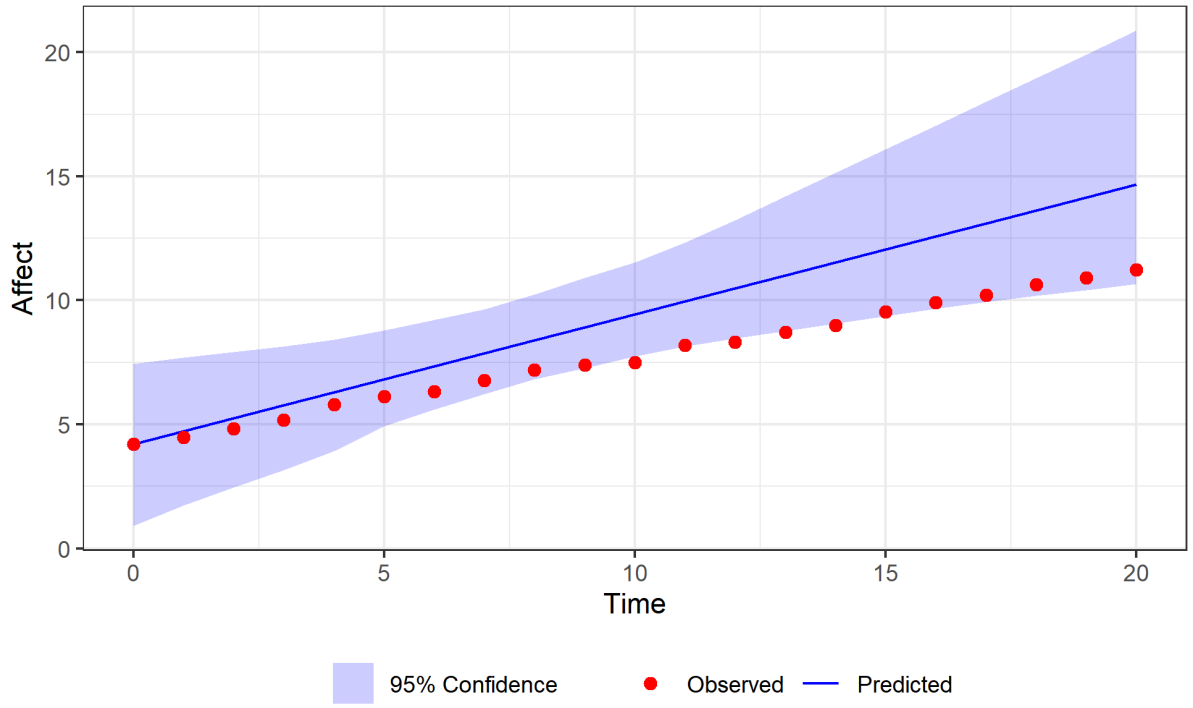
For this simple affect process, we can get a grasp on the model-implied trajectory through the numerical estimates offered by lme4's output table. We can see that our linear mixed-effects model, recovers the parameter values from the data generating model well. We can find the population-level estimates for the intercept and slope values under "Fixed effects". The variance of the subject-specific deviations from the population average can be found under "Random effects". The correlation between the individual differences in the intercept and slope values is under the "Correlation of Fixed Effects" heading. For more information about lme4 and its functionalities we refer the reader to the package documentation (Bates et al., 2015) https://cran.r-project.org/web/packages/lme4/lme4.pdf.

Visualising predictions

Once our models become more complicated, a useful tool to understand their predictions is visualization. Visualization is a great way to build intuition about the affect process our models imply and allows us to detect sources of model misfit that may be difficult to identify by solely relying on numerical fit indices (see Gabry et al. (2019) for examples). For our lme4 model, we can generate two plots showing: (1) the model's predictions (solid line) and its associated uncertainty (shaded ribbon) based only on the estimated model parameters for a single subject (subject 3); (2) predictions based on the model parameters and all data, (past, present, and future) of a single subject (subject 3).

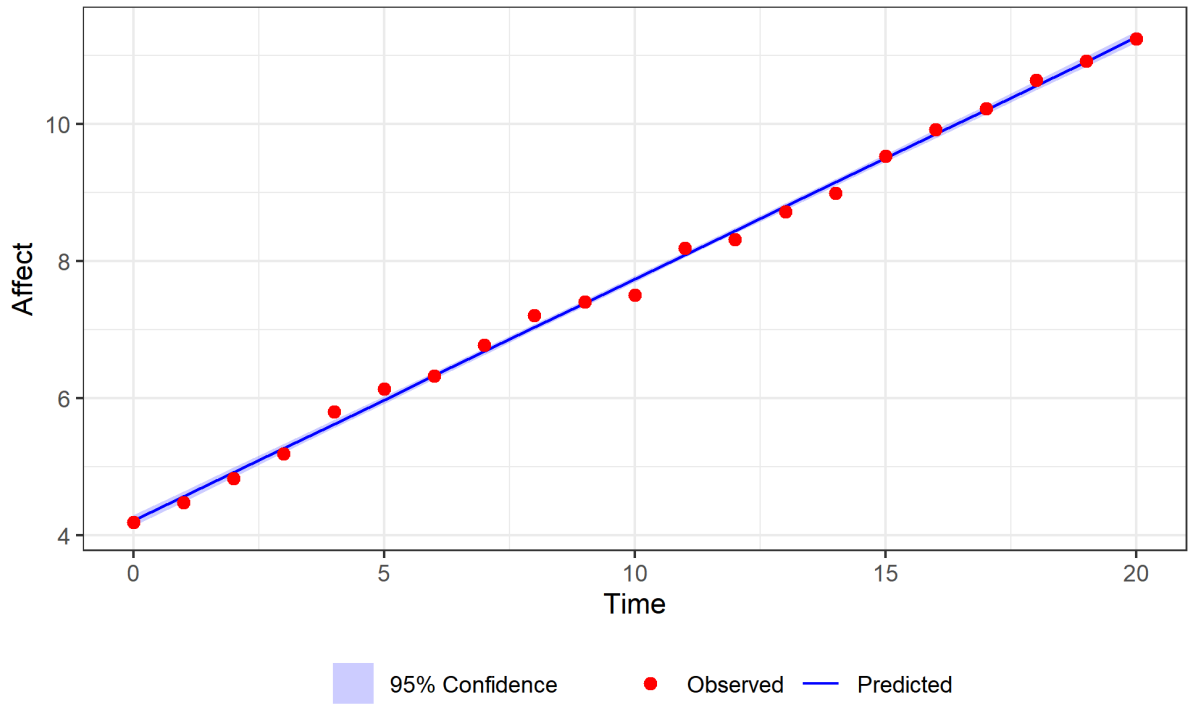
```
# Define a function to extract predictions
pred_fun <- function(model) {
  predict(model, data)
}

# Use bootMer to generate bootstrap (i.e., many) predictions
boot_preds <- bootMer(lme_model, FUN = pred_fun, nsim = 100)

# Extract the predicted values and calculate the mean and confidence intervals
newdata <- data.frame(data, #create a new data frame including original data
  pred = apply(boot_preds$t, 2, mean),
  lower = apply(boot_preds$t, 2, quantile, 0.025),
  upper = apply(boot_preds$t, 2, quantile, 0.975))

# Use ggplot2 to visualize the predictions and uncertainty
```

```
ggplot(newdata[newdata$Subject==3,], aes(x = Time)) +
  geom_line(aes(y = pred, color = "Predicted")) +
  geom_ribbon(aes(ymin = lower, ymax = upper, fill = "95% Confidence"), alpha = 0.2) +
  geom_point(aes(y = Affect, color = "Observed"), size = 2) +
  scale_color_manual(name = "", values = c("Predicted" = "blue", "Observed" = "red")) +
  scale_fill_manual(name = "", values = c("95% Confidence" = "blue")) +
  labs(y = "Affect", x = "Time") +
  theme_bw()+theme(legend.position = "bottom")
```



The first plot, shows how well information solely from the estimated model parameters can reproduce our pattern of observations. The red dots show the observed affect values at each time point. The solid blue line shows the model implied trajectory of affect, with the shaded blue area surrounding the line showing the model's uncertainty about this trajectory. We can see that by solely relying on the model estimates, our model does a poor job of predicting the actual data points. The solid line does not map well onto the observed trajectory of affect, and there is a large amount of uncertainty about the model-implied trajectory.

```
# Define a function to extract predictions
preds <- predict(lme_model,  se.fit = TRUE)

#create a new data frame including original data and predictions
newdata <- data.frame(data, preds,
  lower = preds$fit - 1.96 * preds$se.fit,
  upper = preds$fit + 1.96 * preds$se.fit)

# Use ggplot2 to visualize the predictions and uncertainty
ggplot(newdata[newdata$Subject==3,], #just visualise for subject 3
  aes(x = Time, y = fit)) +
  geom_line(aes(color = "Predicted")) +
  geom_ribbon(aes(ymin = lower, ymax = upper, fill = "95% Confidence"), alpha = 0.2) +
  geom_point(aes(y = Affect, color = "Observed"), size = 2) +
  scale_color_manual(name = "", values = c("Predicted" = "blue", "Observed" = "red")) +
  scale_fill_manual(name = "", values = c("95% Confidence" = "blue")) +
  labs(y = "Affect", x = "Time") +
  theme_bw()+theme(legend.position = "bottom")
```



In the second plot, we visualize the model's predictions after it has learned from all the observations in our dataset. So, data from past, present, and future observations are used by the model to predict each observation. Here the model-implied trajectory does an excellent job at mapping onto our observations and does so with high certainty.

Nonlinear Change (Discrete Time): Adding State Dependence

By formalizing our linear growth process for Jill and other patients, we observe that our simple conceptual idea leads to a surprising prediction. Namely, therapy actually helps people with a lower initial level of affect to have a higher affect level at the end of the 21 weeks of therapy, compared to people who started with higher affect. This means that if Jill entered therapy with more severe affect problems she would come out of therapy with a higher level of affect than if she entered with less severe affect problems. Moreover, if we take our model with a steady rate of growth seriously, then this would imply that Jill could endlessly increase her affect levels by continuing therapy. Both of these predictions seem unrealistic. So we have to rethink our model of affect.

A more defensible prediction could be to expect that people's rate of growth slows down as their affect improves. This would mean that people with a low initial level of affect would increase faster at the start, relative to people with a higher initial level of affect, but their growth rate would slow down as their affect improves. In a statistical model, we can implement such a (nonlinear) growth process by allowing each person's slope to vary not just as a function of where they start, but also as a function of where they are *at every point in time*.

Our statistical model of this nonlinear affect process can still be represented using a regression model. We can achieve our nonlinear growth model by computing the observed level of affect at each time point ($\eta(t)$) as a function of affect at the previous time point ($A\eta_{t-1}$), plus a constant value (B) that is added to each observation:

$$\eta(t) = A\eta_{t-1} + B$$

With this equation we can emulate a process where the rate of growth in affect dampens throughout the course of a therapy session. Our code will do the heavy lifting of computation and allow us to visualize

the model-implied trajectory that our equation creates. But we can also build some intuition by solving this equation for a small number of time points.

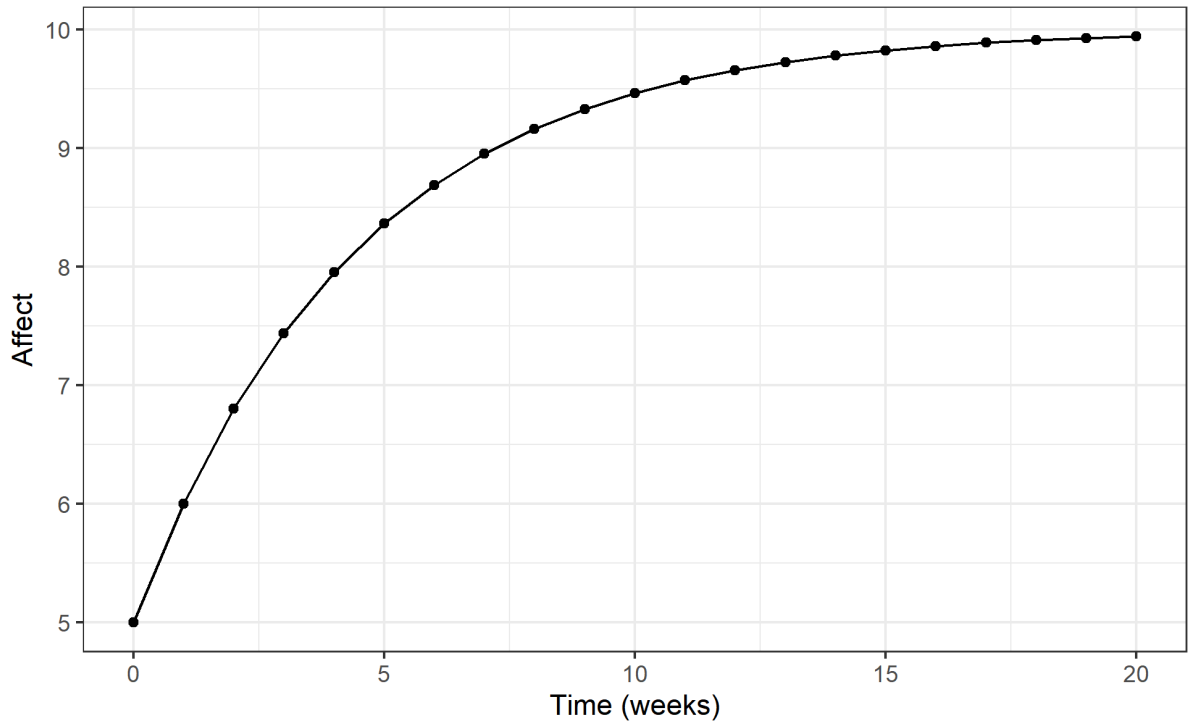
So, let's consider 3 time points T0, T1, and T2. Then let's set the autoregressive coefficient (A) at 0.8, which means that 0.8 of the previous observation will be added to the current observation. Let's also add a constant of 2, as our continuous intercept (B) which is added to every observation.

Then, we can start up our process at T0 by setting an initial level of affect to 5 ($\eta(0) = 5$). At T1, we can see that $0.8 * 5 + 2$ leads to a current level of affect $\eta(1) = 6$. By applying our equation to the next time point, T2, we can see that $0.8 * 6 + 2$ leads to current level of affect equal to 6.8. So from T0 to T1 our affect level grew by 1 unit, but from T1 to T2 it only grew by 0.8. Thus, the rate of growth is dampening as consequence of a change in the prior level of affect.

Simulation: Nonlinear Change (Discrete Time)

Below we provide code that does this computation for all of our 21 weeks, by simply solving the equation we just solved. First we need to set the degree to which the current level of affect is dependent on the prior level of affect (i.e. state dependence, `A <- .8`). Then we add a constant value which is added to each observation generating a consistent rate of growth (`B <- 2`). By adding the state dependence term with the continuous intercept, we generate a nonlinear growth trajectory. We then set an initial affect level which is used to initialize our process (`initialAffect <- 5`). An if-else statement is used so that the first observation is set the initial level of affect (`if(i==1) Affect[i] <- initialAffect`) and each subsequent observation has an affect value that is generated by our model equation (`else Affect[i] <- A*Affect[i-1] + B`).

```
times <- seq(from=0, to=20, by=1) #generate sequence of time points when subjects are measured
A <- .8 #autoregressive coefficient / state dependence
initialAffect <- 5
B <- 2 #continuous intercept
Affect <- rep(NA,length(times)) #create empty affect vector
for(i in 1:length(times)){ #for each measurement occasion
  if(i==1) Affect[i] <- initialAffect #if first time point, set to initial affect
  else Affect[i] <- A*Affect[i-1] + B #otherwise, use autoregression and continuous intercept
}

# Plot the data using a lineplot
ggplot(data.frame(Affect=Affect), aes(x = Time, y = Affect)) +
  geom_line() +
  geom_point() +
  theme_bw()+
  labs(x = "Time (weeks)", y = "Affect")
```



Our figure shows a nonlinear increase in affect over time. This is a better representation of a reality where therapy cannot make you infinitely happy, but it may help you recover from a low point.

A conceptual shift to continuously evolving processes

Our model now provides a more realistic depiction of Jill's growth in affect from week to week. But what happens in between each of our weekly observations? One possibility is that affect stays flat and suddenly jumps during each of our weekly observations. That is, change only happens when we are looking. If we try to imagine such a discretely changing affect process, it would look like a staircase of affect. The alternative possibility is that people's affect changes continuously across time, forming a coherent trajectory. The rate of change that we observe from week to week, is then an aggregate of all the moment-to-moment changes that happen between our weekly observations. If the second option is more akin to our expectation of reality, then we need to shift to a continuous time framework. For issues that arise when modeling continuous processes using discrete-time models we refer the reader to (Driver, 2025).

Differential equations – the mathematics of continuous time

To formally represent continuously changing processes we need to use differential equations. But even without a technical understanding of differential equations researchers can form an intuitive understanding of continuous processes and apply them to their own substantive domain.

Our intuition can be aided by building a mental image of a continuously changing process. To do this we can imagine a discretely changing process where the size of the steps we take in time are extremely small. So small as to give the impression that change between two time points happens almost instantly.

Modeling a growth process in continuous time will be no different than in discrete time, in that we will use symbols to represent different factors and their relationships which add up to generate our growth process. To understand the equation that generates our hypothesized affect process we can again visualize the model-implied process using simulations.

For example, we can model an affect process that changes at a steady rate in continuous time, akin to our first example where we used a linear regression model. But this time using a differential equation.

The major difference here is that our outcome variable (left-hand side of equation) is the rate of change in affect at any given moment in time. Instead of the level of affect, which was used as an outcome in our discrete time (regression) representation. This rate of change in affect (η) at a given moment in time t is denoted by the derivative $\frac{d\eta}{dt}$. We can think of the rate of change at a given moment in time as what we would get if we were to glance at a speedometer in our car. The velocity that we would see, would tell us how fast our current position is changing at a particular moment in time. Since our model is linear, the rate of change at a given moment is given by a constant value B. Thus, the differential equation for a linear model is:

$$\frac{d\eta}{dt} = B$$

If we want to pick up where we left off and represent our nonlinear growth model in continuous time, we can simply add a term that allows the rate of growth at a given time point to depend on the current state of affect (i.e. a state dependency):

$$\frac{d\eta}{dt} = A\eta(t) + B$$

In this equation, the rate at which affect ($\eta(t)$) is changing at a given moment t is a function of the current level of affect ($A\eta(t)$) plus a constant (B), which represents a steady input to the growth process that is independent of the effect that the current level of affect has on its own change.

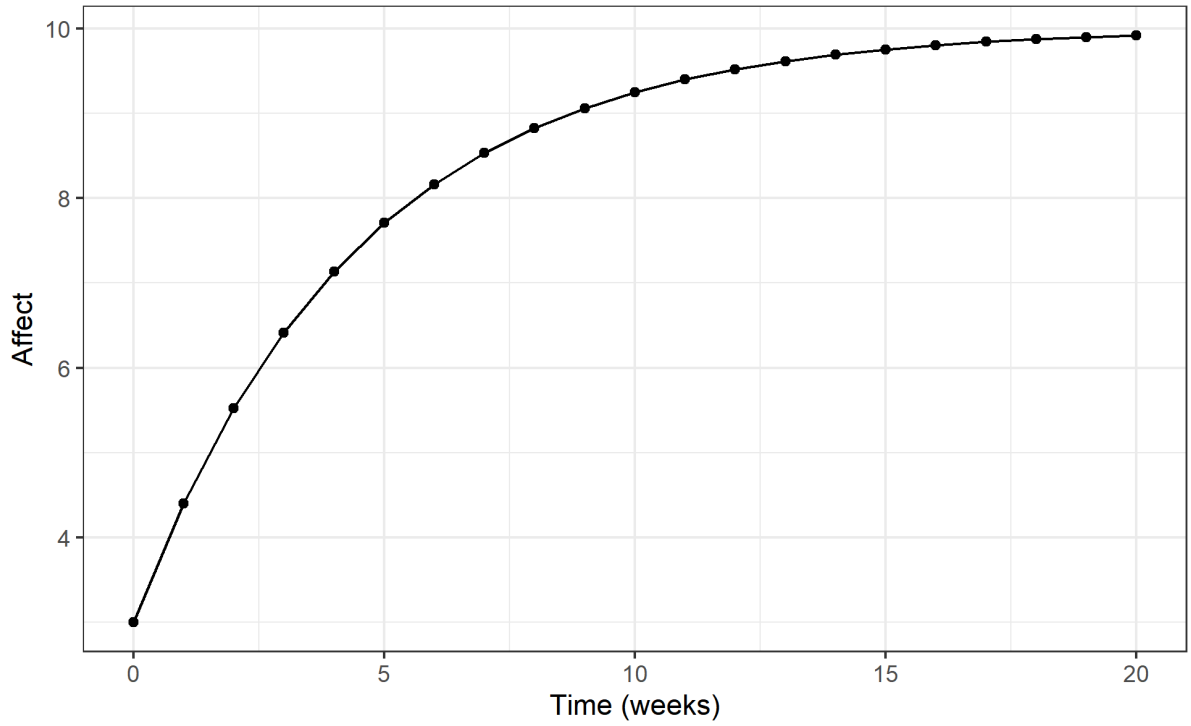
Simulation: Nonlinear Change (Continuous Time)

To generate data for this continuous growth process in R, we can approximate the solution to the differential equation using a 'Euler-Maruyama' method (Higham, 2001). This method works by breaking continuous time into small time slices (steps) and updating the state of our growth process at each step based on the model's dynamics.

To generate data, we first need to define values for our model parameters. This includes: (1) the degree to which the current level of affect influences its own rate of change (`A`, continuous time state-dependence). (2) A constant input to the growth process (`B`, continuous intercept), and an initial level of affect (`initialAffect`). Then we create an empty vector to store the affect values given by our for-loop which implements the 'Euler-Maruyama' method `Affect <- rep(NA,Nobs)`. The for-loop sets the initial level of affect for the first observation (`i=1`) to initialize the process (`if(i==1) Affect[i] <- initialAffect`). For each subsequent observation (`i > 1`), we compute the current level of affect by summing the *rate of change* at the prior time point (`dAffect = A*Affect[i-1] + B`) with level of affect at the prior time point (`Affect[i-1]`). That is, `Affect[i] <- Affect[i-1] + dAffect * 1`. To add the size of the desired time step into the equation, we multiply the rate of change by the size of the time step, in this case `dAffect` is multiplied by 1, meaning that the rate of change is equivalent to the rate of change between each observation.

```
times <- seq(from=0, to=20, by=1) # generate sequence of time points when subjects are measured
Nobs <- length(times) # number of observations per subject
A <- -.2 # continuous time state dependence
initialAffect <- 3 # set initial level of affect
B <- 2 # continuous intercept
Affect <- rep(NA,Nobs) # create empty affect vector

for(i in 1:Nobs){ # for each time point
  if(i==1) Affect[i] <- initialAffect # if first time point, set to initial affect
  else{
    dAffect <- A*Affect[i-1] + B # compute slope of affect at earlier time point
    Affect[i] <- Affect[i-1] + dAffect * 1 # update affect using slope and time step
  }
}

# Lineplot of the approximate continuous trajectory of affect
ggplot(data.frame(Affect=Affect),
  aes(x = Time, y = Affect)) + # Plot the data
```

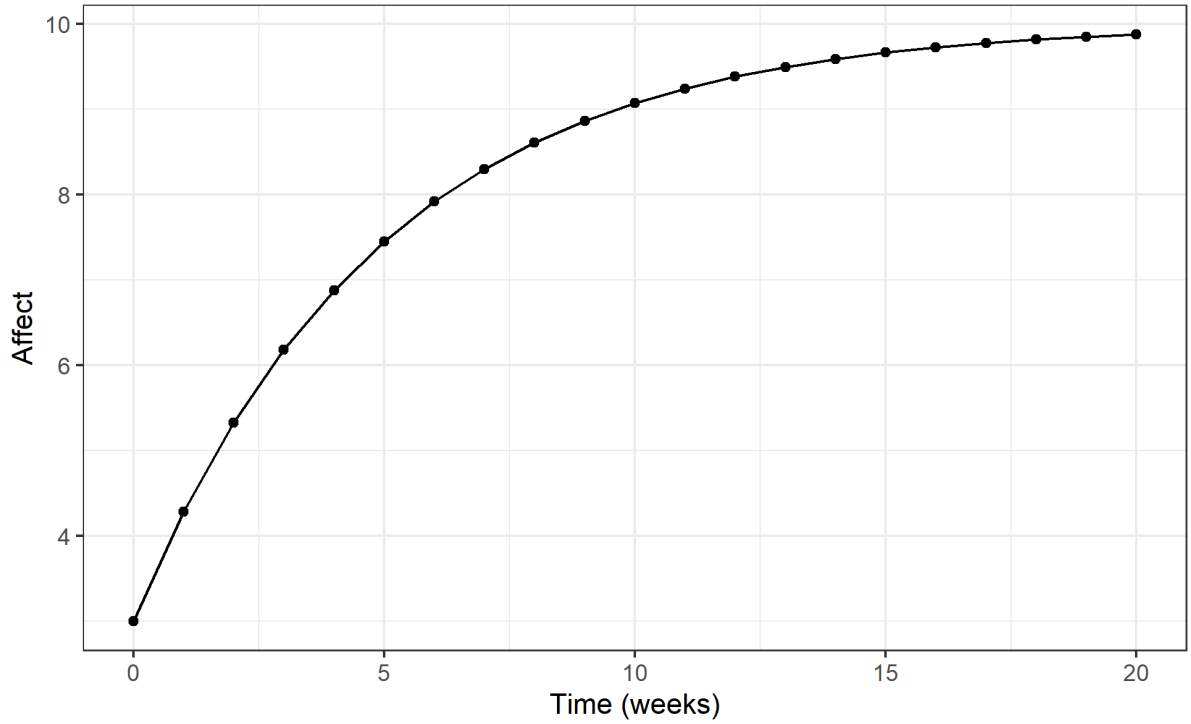
```
  geom_line() +
  geom_point() +
  theme_bw()+
  labs(x = "Time (weeks)", y = "Affect")
```



To better approximate a continuous time solution, we can take smaller steps in time. But more steps means that the necessary computation will be more intensive. So let's start with a small number of intermediary steps, say 10 steps in the time between our observations, to better approximate the continuous time process `Nsteps <- 10`. Now, we introduce another loop, within our previous for-loop, which splits the interval between each observation (e.g. week) into 10 smaller steps (`istep`). The first line within this loop represents the differential equation which gives us the rate of change at the prior time point (`dAffect = A*AffectState + B`). The line below it, updates the current level of affect based on the estimated rate of change at the prior time point multiplied by 1/10 (i.e. `1/Nsteps`). The effect of this multiplication is to give us the rate of change over the smaller step of time we chose. In essence, this scales the rate of change from the full unit of time (e.g. week), given by the preceding equation, to one-tenth, allowing us to better approximate the underlying continuous growth process.

```
times <- seq(from=0, to=20, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
A <- -.2 #continuous time state dependence
B <- .5 #continuous intercept
initialAffect <- 3
B <- 2 #continuous intercept
Affect <- rep(NA,Nobs) #create empty affect vector
Nsteps <- 10 #number of steps in time to compute between each observation (increased precision)

for(i in 1:Nobs){ #for each time point
  if(i==1) Affect[i] <- initialAffect #if first time point, set to initial affect
  else{ #compute new affect state by taking a sequence of small steps in time
    AffectState <- Affect[i-1] #initialise with state at previous time point
    for(stepi in 1:Nsteps){ #take Nsteps in time between each observation
      dAffect <- A*AffectState + B #compute slope of affect at earlier time point
      AffectState <- AffectState + dAffect * 1/Nsteps #update state using slope and time step
    }
    Affect[i] <- AffectState
  }
}
```

```
#Affect <- Affect + rnorm(Nobs,0,.01) #add noise

ggplot(data.frame(Affect=Affect), # Plot the data
  aes(x = Time, y = Affect)) +
  geom_line() +
  geom_point() +
  theme_bw()+
  labs(x = "Time (weeks)", y = "Affect")
```



Nonlinear Change with Random Fluctuations (Continuous Time)

By using our previous model to predict Jill's affect trajectory, we would assume that her affect would change in a smooth deterministic manner. However, real-world affect processes are often subject to unpredictable changes that lead a person's affect trajectory to fluctuate. We can model such fluctuations by adding a system noise term to our differential equation, which generates random fluctuations in affect over time.

Let's work through how this is done. With our current equation, the rate of change in affect $\frac{d\eta}{dt}$ is purely deterministic, meaning that how fast affect changes at a given moment is entirely determined by the terms in the right-hand side of the differential equation $(A\eta(t) + B)$.

To model the impact of random influences on Jill's affect trajectory, we want to add a term that introduces a random "kick" to the rate of change at each moment. Meaning that aside from the deterministic effects there will be some random ups and downs in Jill's growth rate. To add a "kick" to Jill's rate of change we can introduce a noise term that is sampled from a normal distribution. This turns our (ordinary) differential equation into a stochastic differential equation (Kloeden & Platen, 1992), with stochastic denoting the random noise component of our continuous growth process.

Because the random noise term wiggles too erratically to analytically define its rate of change at any point in time, stochastic differential equations are written a bit differently. That is, we model our continuous time process as evolving over infinitesimal (read extremely small) steps in time. At each infinitesimal step in time, our noise term adds a bit to the evolution of change. The amount that it adds is scaled by the system noise term, defining the volatility of the growth process. Thus, our rate of change in affect $d\eta(t)$ evolves via incremental changes, some deterministic $(A\eta(t) + B)$, some random $(GdW(t))$, over each infinitesimal interval dt:

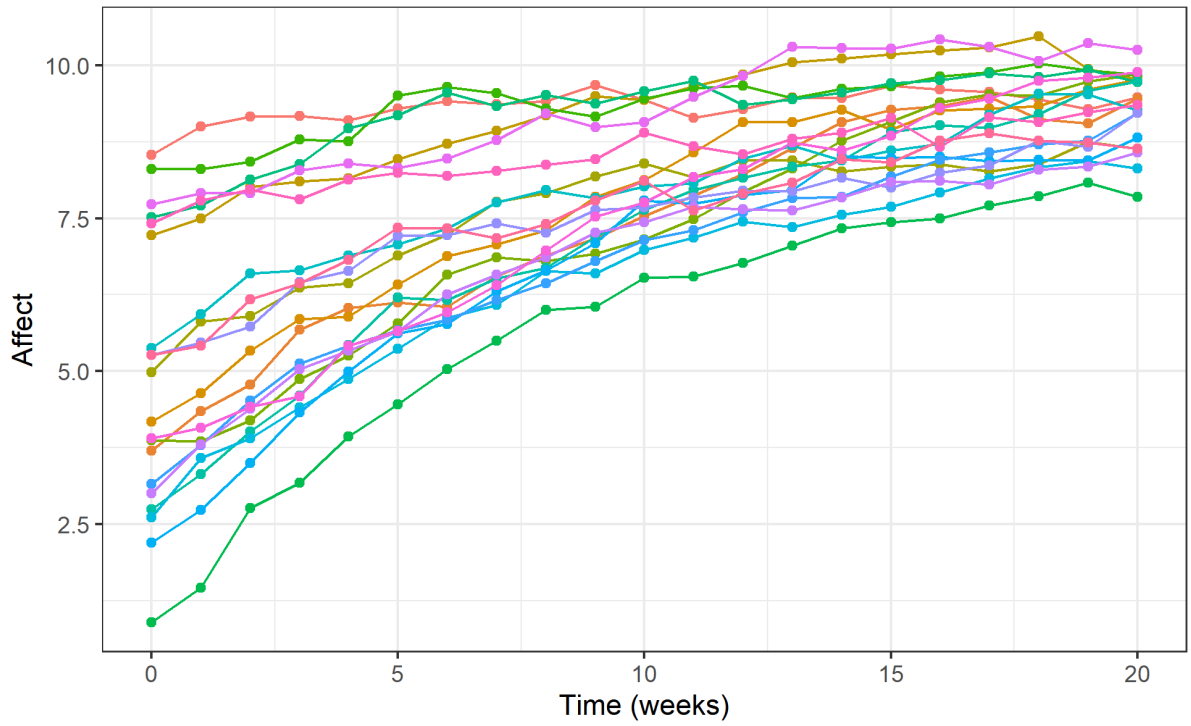
$$d\eta = (A\eta(t) + B)dt + GdW(t)$$

Simulation: Nonlinear Change with Random Fluctuations (Continuous Time)

Adding system noise. To add system noise to our continuous time model, we will update the data generating code using the 'Euler-Maruyama' method (Higham, 2001) (see "Simulation: Nonlinear Change (Continuous Time)" for an explanation of the method). The system noise term will be added to the affect level that is computed for each of our chosen time steps (`istep`). Thus, when we update a person's current affect state at each small time step we add some noise. This noise is sampled from a normal distribution with a mean of 0 and a standard deviation of 1 divided by `Nsteps` (this time 100 steps). Before being added to the function that generates the current affect state, each draw of random noise is multiplied by `G` (the system noise coefficient) to scale the amount of system noise. Thus, the higher the `G` value the more noisy the affect process.

Individual differences. To generate data for multiple individuals we have to make some further tweaks to our code. First, for each participant we sample their initial affect level from a normal distribution with mean 5 and standard deviation of 2 (`initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)`). Second, we add an empty data frame which includes a greater number of rows to fill. Third, we add a loop to repeat the computation of the affect process for each subject `for(subi in 1:NSubjects)`.

```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=20, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)
A <- -.1 #continuous time state dependence
B <- 1 #continuous intercept
G <- 0.2 #system noise coefficient

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect = rep(NA,NSubjects*Nobs))

Nsteps <- 100 #number of steps in time to compute between each observation (more precise)

row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    if(obsi==1) AffectState <- initialAffect[subi] #if first time point, set to initial affect
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation
        dAffect <- A*AffectState + B #compute deterministic slope of affect at earlier time point
        AffectState <- AffectState + dAffect * 1/Nsteps + #update state using slope and time step
          G * rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #and add system noise
      }
    }
    data$Affect[row] <- AffectState #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Subject[row] <- subi #input subject data
  }
}

data$Affect <- data$Affect + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data, # Plot the data
  aes(x = Time, y = Affect, color = as.factor(Subject))) +
  geom_line() +
  geom_point() +
  theme_bw()+
  labs(x = "Time (weeks)", y = "Affect")+
  theme(legend.position = "none")
```



Now we have a somewhat more realistic depiction of affect dynamics, with fluctuations around the smooth, state-dependent increase in affect over time. This model captures the idea that affect processes are subject to both predictable trends and random fluctuations, reflecting some of the complexity of real-world affect dynamics. Note also, that here individuals vary in their initial levels of affect, and the rate of change varies accordingly, such that therapy does not just help everyone at the same rate, and nor does it lead to unrealistic long term projections as we saw in the linear case – there is a limit.

ctsem: A Flexible Tool for Dynamic Systems Modeling

To fit a continuous-time model with state-dependence and system noise we need to shift to a state-space framework (Durbin & Koopman, 2012; Harvey, 1989; Kalman, 1960). The R package `ctsem` (Driver et al., 2017; Driver & Voelkle, 2018a) provides a software framework for specifying and fitting continuous-time (CT) and discrete-time (DT) dynamic models. It enables researchers to model the behavior and evolution of processes over time, and its combination of features can offer some unique advantages for analyzing longitudinal data.

Software Installation

Before starting, ensure your system is ready to use `ctsem`. Follow these steps:

1. **Install R and RStudio**: Download and install R (https://cran.r-project.org/) and RStudio (https://posit.co/products/open-source/rstudio/).
2. **Configure Stan**: `ctsem` relies on Stan (Carpenter et al., 2017) for log likelihood calculations. Ensure you have a compatible C++ compiler installed:

- **Windows**: Install RTools (https://cran.r-project.org/bin/windows/Rtools/).
- **Mac**: Install Xcode command line tools by running `xcode-select --install` in the terminal.
- **Linux**: Install g++ and other build tools using your package manager (e.g., `sudo apt install build-essential`).

3. **Install Required Packages**:

```
install.packages(c("ctsem", "ggplot2", "lme4", "tinytex"))
```

Fitting a model: Nonlinear Change with Random Fluctuations (Continuous Time)

To fit the data we just generated with `ctsem`, we first need to specify our model using the `ctModel` function. The code below is annotated for convenience, for more information about the specification of a continuous-time model using the `ctModel` function please refer to the ctsem manual https://cran.r-project.org/web/packages/ctsem/ctsem.pdf (Driver et al., 2025). Here we will provide a quick description of some of the links between the model equation and the software specification.

Our `ctsem` model can be thought of as linking latent (unobserved) variables that we hypothesize drive the dynamics of affect to observed variables, which we observe directly. Observed variables are treated as indicators of the underlying latent process, and are linked to the latent states via a measurement model.

In this case our latent dynamic model is given by the stochastic differential equation:

$$d\eta = (A\eta(t) + B)dt + GdW(t)$$

Here is how we specify this latent dynamic model using the `ctsem` syntax:

1. The `DRIFT` option specifies the state dependence term A, which we call `stateDependence`, making the rate of growth depend on the current level of affect.
2. The `CINT` option specifies the continuous intercept (B). We call the continuous intercept `B` and only estimate a fixed effect (one value for all subjects). To switch off random effects we need to add `FALSE` behind `B||`, i.e. `B||FALSE`.
3. The `DIFFUSION` option specifies the system noise term (G), which we call `systemNoise`, allowing the model to capture random fluctuations around the model-implied growth trajectory.
4. The initial value of our latent process, is treated as a random variable with its own mean and variance parameters: $\eta_{t0} = \mu_{0i} + \epsilon_{0i}$, where $\epsilon_{0i} \sim \mathcal{N}(0, \sigma^2)$. The `TOMEANS` option, is used to specify the mean parameter for the initial level of affect, which we call `initialAffect`. By adding `TRUE` behind `initialAffect||` we are allowing for random effects (between-subject variance) around the population estimate of the initial level of affect in our sample. The `TOVAR` option specifies the variance parameter (σ^2) to estimate the initial level of affect at T0. By default `TOMEANS` and `TOVAR` are estimated from the data as free parameters.

The latent process model is linked to our observations using a (linear) measurement model:

$$Affect(t) = \Lambda * \eta(t) + \tau + \epsilon_1(t)$$

Where $Affect(t)$ is the observed level of affect. Λ is a matrix of regression weights used to link the latent process to our observations, η is the latent level of affect, τ reflects a constant that can be used to shift the relationship between observations and a latent variable, and ϵ represents measurement error.

1. The `LAMBA` option specifies the Λ matrix. In our case it is a 1x1 matrix with the value 1, meaning that the latent Affect (η) is directly and equally reflected in the observed Affect without any scaling.
2. The `MANIFESTMEANS` option specifies the measurement intercept (τ) which is simply a constant that is added to the measurement model to shift the relationship between observations and a latent variable. In this case it is set to zero, implying that there is no systematic offset in the measurement process.
3. The `MANIFESTVAR` option specifies the measurement error term (ϵ_1), which we call `residualSD`.

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  # Specify features of the data
  manifestNames = "Affect", #names of observed variables in dataset
```

```
latentNames = "Affect", #names of latent processes
time = 'Time', #name of time column in dataset
id = 'Subject', #name of subject column in dataset
type='ct', #use continuous time / differential equation model (dt for discrete-time)
# Specify features of the model
MANIFESTVAR = 'residualSD', #sd of the residual / measurement error
LAMBDA = matrix(1,nrow=1,ncol=1), #relating latent process to observed variables
MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
CINT='B||FALSE', #continuous intercept with *no* random effects
TOMEANS='initialAffect||TRUE', #initial affect with random effects
DRIFT = 'stateDependence',
DIFFUSION = 'systemNoise')
```

For readers that prefer to view the entire model equation, we can generate a LaTeX formatted represention of the equations we just specified by running the `ctModelLatex()` function. To do this we need to install the following package the `tinytex`, if we have not already done so. Sometimes there are difficulties getting LaTeX compilation to work on various systems. For those who have difficulties, generally installing the R package `tinytex` via `install.packages('tinytex')`, then running `tinytex::install_tinytex()`, will be sufficient. In case of errors along the way, restarting R / Rstudio and clearing the workspace can help. For those that do not want the trouble of potential troubleshooting, the output can be found below.

Subject parameter distribution:

$$\underbrace{[\text{initialAffect}_i]}_{\phi(i)} \sim \text{tform}\left\{\text{N}\left([\text{raw\_initialAffect}], [\text{rawPCov\_1\_1}]\right)\right\}$$

Initial latent state:

$$\underbrace{[\text{Affect}]\,(t_0)}_{\boldsymbol{\eta}(t_0)} \sim \text{N}\left(\underbrace{[\text{initialAffect}]}_{\text{T0MEANS}}, \underbrace{UcorSDtoCov\left\{[1e-06]\right\}}_{\mathbf{Q}^*_{t0}\ \text{T0VAR}}\right)$$

Deterministic change:

$$\underbrace{\text{d}\,[\text{Affect}]\,(t)}_{\text{d}\boldsymbol{\eta}(t)} = \left(\underbrace{[\text{stateDependence}]}_{\mathbf{A}\ \text{DRIFT}}\underbrace{[\text{Affect}]\,(t)}_{\boldsymbol{\eta}(t)} + \underbrace{[\text{B}]}_{\mathbf{b}\ \text{CINT}}\right)\text{d}t \quad +$$

Random change:

$$\underbrace{UcorSDtoChol\left\{[\text{systemNoise}]\right\}}_{\mathbf{G}\ \text{DIFFUSION}}\underbrace{\text{d}\,[W_1]\,(t)}_{\text{d}\mathbf{W}(t)}$$

Observations:

$$\underbrace{[\text{Affect}]\,(t)}_{\mathbf{Y}(t)} = \underbrace{[1]}_{\boldsymbol{\Lambda}\ \text{LAMBDA}}\underbrace{[\text{Affect}]\,(t)}_{\boldsymbol{\eta}(t)} + \underbrace{[0]}_{\boldsymbol{\tau}\ \text{MANIFESTMEANS}} \quad +$$

Observation noise:

$$\underbrace{[\text{residualSD}]}_{\boldsymbol{\Theta}\ \text{MANIFESTVAR}}\underbrace{[\epsilon_1]\,(t)}_{\boldsymbol{\epsilon}(t)}$$

System noise distribution per time step: $\Delta[W_{j\in[1,1]}](t-u) \sim \text{N}(0, t-u)$

Observation noise distribution: $[\epsilon_{j\in[1,1]}]\,(t) \sim \text{N}(0,1)$

Note: $UcorSDtoChol$ converts lower tri matrix of standard deviations and unconstrained correlations to Cholesky factor, $UcorSDtoCov =$ transposed cross product of UcorSDtoChol, to give covariance, See Driver & Voelkle (2018) p11. Individual specific notation (subscript i) only shown for subject parameter distribution – pop. means shown elsewhere.

We can now fit the model and ask for a summary of the parameter estimates.

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices= FALSE) # print summary of the fit, some output disabled
```

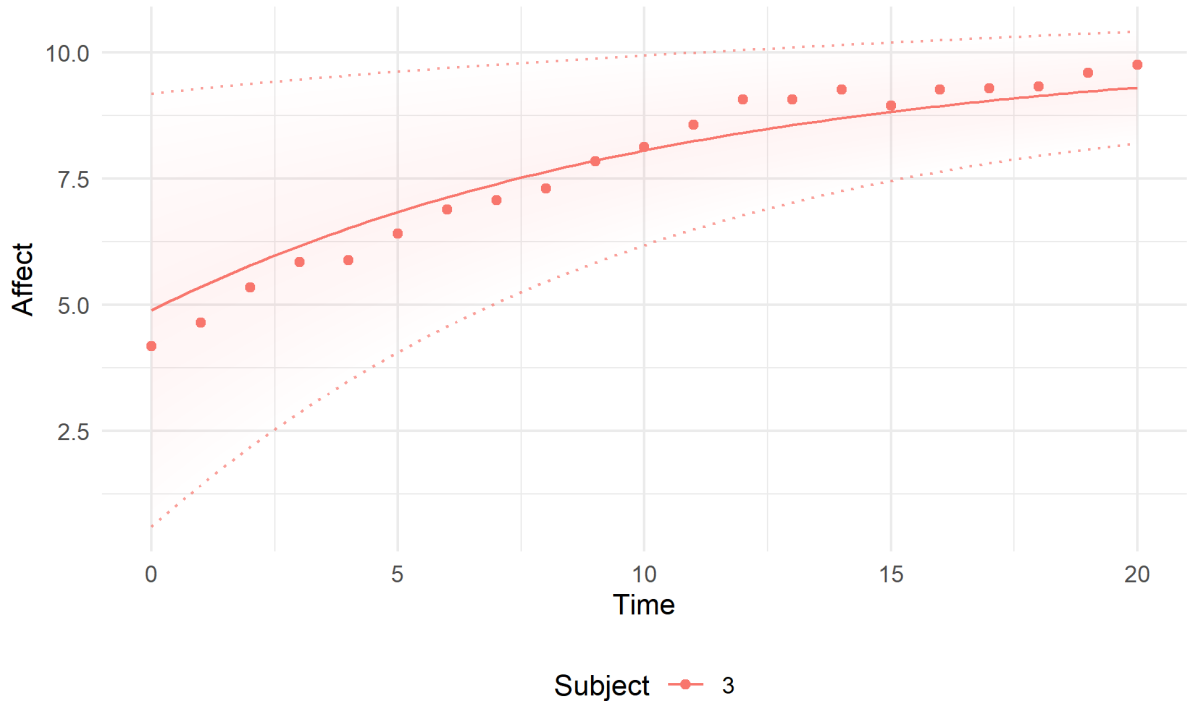
```
$residCovStd
       Affect
Affect  0.082

$resiCovStdNote
[1] "Standardised covariance of residuals"

$popsd
                mean     sd   2.5%    50%  97.5%
initialAffect 2.2151 0.3581 1.5815 2.2007 2.9247

$popmeans
                     mean     sd    2.5%     50%   97.5%
initialAffect     4.8914 0.4917  3.9335  4.9051  5.8865
stateDependence -0.0931 0.0058 -0.1045 -0.0928 -0.0828
systemNoise       0.1961 0.0127  0.1728  0.1956  0.2220
residualSD        0.0585 0.0222  0.0267  0.0546  0.1090
B                 0.9410 0.0457  0.8577  0.9421  1.0307

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] 30.95371

$npars
[1] 6

$aic
[1] -49.90742

$logposterior
[1] 30.95371

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

From our summary table, we can see that the estimated coefficients are not exactly the same as the true values due to the random fluctuations in the data. But the model captures the general trend of affect dynamics over time. The estimated state dependence coefficient is around -0.1, the continuous intercept is approximately 1, and the system noise coefficient is around .2. The random effects standard deviation for initial affect is approximately 2, and the residual standard deviation is around 0.05.

Visualizing predictions

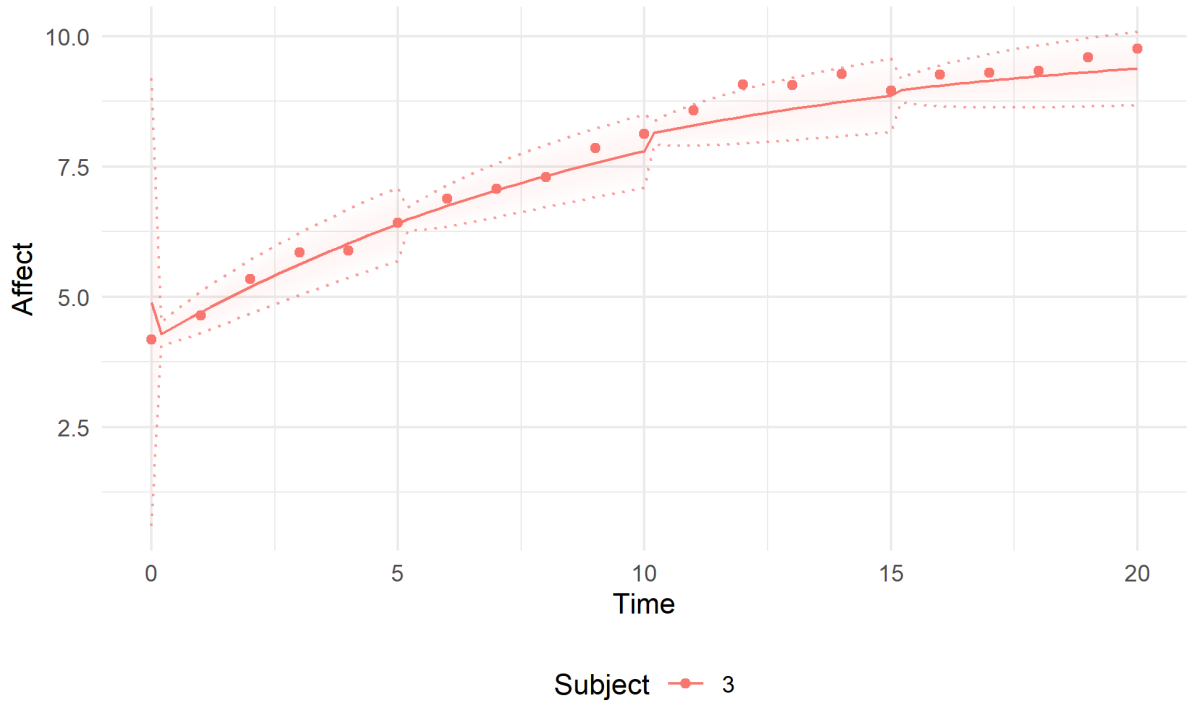
Using `ctsem` we can easily plot the model predictions and associated uncertainty. Our predictions can be conditional on all, none, or some of the individual subjects' observed data. First let's look at the predictions based solely on the parameter estimates.

```
ctKalman(fit= ct_fit, plot = TRUE, subjects = 3, removeObs = TRUE)
```



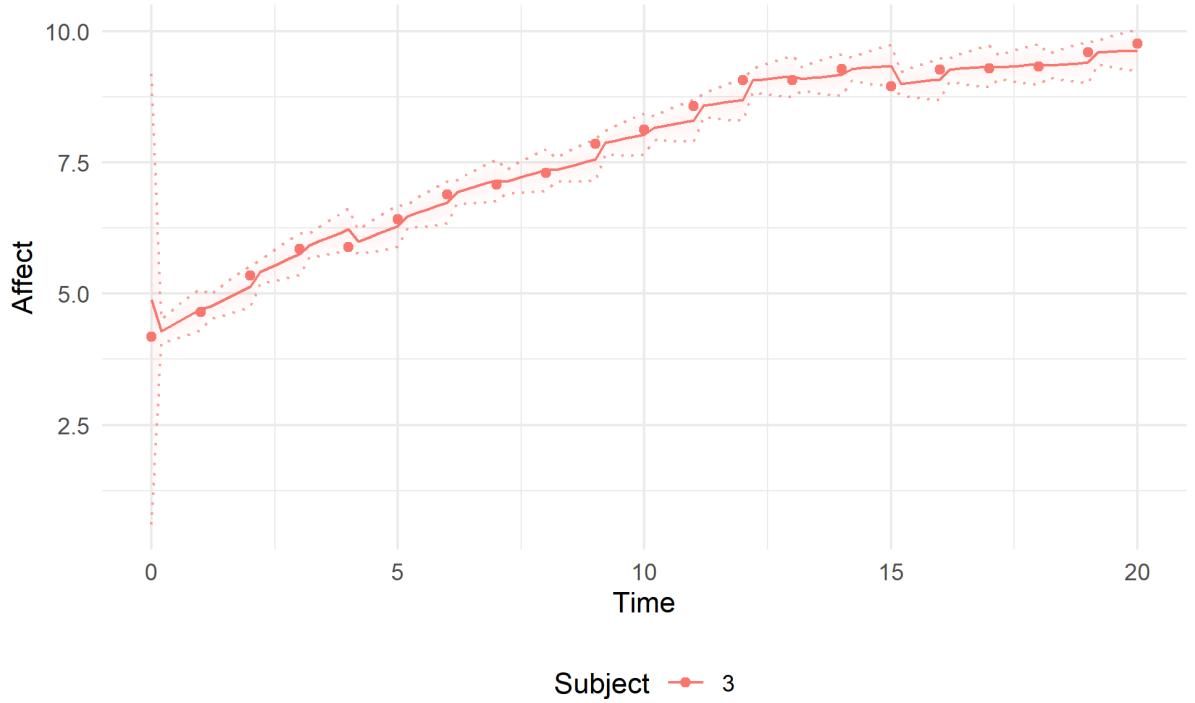
Just like in the case of our simple linear model, we see that the model does a poor job at predicting the observations (red dots) and there is a large degree of uncertainty (shaded red ribbon) around the model-implied trajectory (solid red line). Now let's allow the model to learn from every 5th observation to supplement the predictions it makes using the model estimates alone.

```
ctKalman(fit= ct_fit, plot = TRUE, subjects = 3, removeObs = 5)
```



We can see that the model already does a better job at predicting the observations, and the uncertainty in its predicted trajectory is shrinking. Lastly, let us include all past and present observations and see how our model performs.

```
ctKalman(fit= ct_fit, plot = TRUE, subjects = 3, removeObs = FALSE)
```



Now the model does a fairly good job at predicting the observations, but there is still some uncertainty in its predictions.

Couple Dynamics with Self and Partner Effects (Continuous Time)

Until now, we have looked at Jill's affect in isolation. But she is going to couples therapy, which makes it very likely that how her partner, Bert, feels has a pronounced impact on how Jill feels. In the same way, Jill's affect is also likely to have a reciprocal impact on Bert's affect. This creates an interdependence between Jill and Bert's affect dynamics – a fundamental concept in dyadic data analysis where the behavior or state of one partner influences and is influenced by the other partner, creating a complex system of mutual dependencies. The statistical challenges of dyadic interdependence (Kenny et al., 2006) are particularly relevant here as we transition from modeling individual dynamics to modeling coupled systems where cross-partner effects and shared environmental influences must be explicitly accounted for. We can model this interdependence in two ways:

1. We can introduce *a cross-effect state dependence term*, which captures the extent to which how Jill is feeling at given moment can have a direct effect on how Bert's affect changes at that moment. This is essentially the state dependence we modeled within a person, but now the state (affect level) that drives the rate of change is coming from another person. We can also introduce another cross-effect state-dependence term, capturing the influence of Bert's current state of affect on Jill's rate of change at that moment.

2. *A Common system noise term*, random life events that cause fluctuations in Jill's affect trajectory are also likely to contemporaneously impact Bert's affect (and vice versa). We can model factors that simultaneously shift our couple's rate of change, by adding a correlated noise term.

The revised model which includes Jill and Bert's affect dynamics along with their interdependence is:

$$d\eta_1 = (A_1\eta_1(t) + A_{cross_{12}}\eta_2(t) + B_1)dt + G_{11}dW_1(t) + G_{12}dW_2(t)$$

$$d\eta_2 = (A_2\eta_1(t) + A_{cross_{21}}\eta_1(t) + B_2)dt + G_{21}dW_1(t) + G_{22}dW_2(t)$$

Now we have two equations, one to describe each partner's rate of change in affect. Here Jill's is denoted by 1 and Bert by 2. There are two differences from the prior model equation, within each equation. First, there is an additional term that specifies the effect that Bert's current level of affect has on Jill's rate of change at the same moment ($A_{cross_{12}}\eta_2(t)$). The same goes for Bert's equation ($A_{cross_{21}}\eta_1(t)$). Second, each equation has an additional system noise coefficient, capturing the effect of random fluctuations in Bert's affect on Jill's affect ($G_{12}dW_2(t)$), and the opposite in Bert's case ($G_{21}dW_1(t)$).

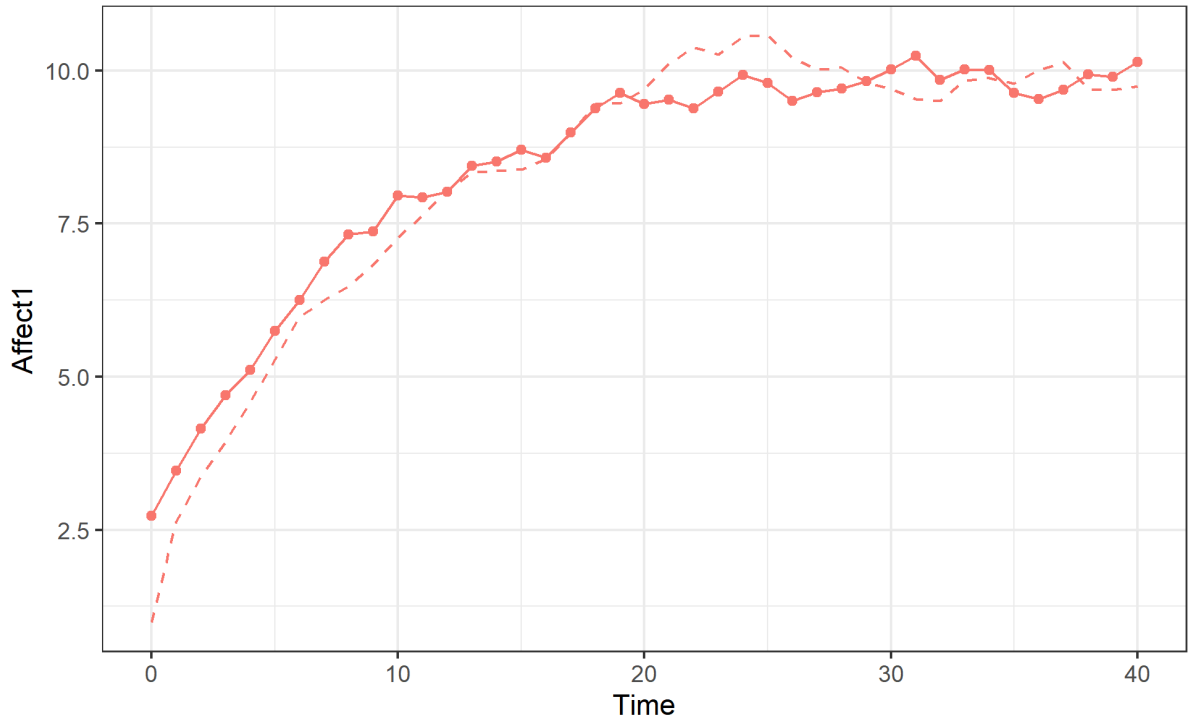
Simulation: Couple Dynamics with Self and Partner Effects (Continuous Time)

We will generate data for Jill and Bert along with another 19 couples (i.e. 20 couples). Each of the 40 people will have their own initial level of affect, but all dynamics and growth terms will be fixed across individuals for now.

Couple dynamics. To generate data for each couple, we can build on the previous model of affect that we used to represent the affect of one person. The first thing we need to add, is an equation to represent the growth process of the additional partner. Then we need to add our cross-effect and common-noise terms to the (differential) equations of both partners. In the code chunk below, we can see that we now have two equations to approximate two continuous affect processes, which are differentiated using `Affect1` (for partner 1) and `Affect2` (for partner 2). Apart from duplicating the equation for one person, each equation has *two* new elements to capture interdependency in affect dynamics. (1) The change in affect for each person depends on their partner's level of affect at the same time point. The coefficient of this cross-effect is denoted by `Across` (e.g. `dAffect1 <- A*Affect1State + Across * Affect2State + B`). (2) We allow the random fluctuations in the couple's affect process to covary. We do this by adding an additional source of random noise `systemNoiseCrossState` to each person's model equation which is scaled by a common system noise coefficient (`Gcross`).

```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=40, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect1 <- rnorm(n = NSubjects, mean = 5, sd = 2)
initialAffect2 <- rnorm(n = NSubjects, mean = 5, sd = 2)
A <- -.2 #continuous time state dependence
Across <- .1 #cross-effect state dependence
B <- 1 #continuous intercept
G <- .2 #unique system noise coefficient
Gcross <- .1 #common system noise coefficient

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect1 = rep(NA,NSubjects*Nobs),
  Affect2 = rep(NA,NSubjects*Nobs)) #now with affect for two individuals

Nsteps <- 100 #number of steps in time to compute between each observation (increased precision)

row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    if(obsi==1){
      Affect1State <- initialAffect1[subi] #if first time point, set to initial affect
      Affect2State <- initialAffect2[subi]
    }
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation
```

```
        # compute deterministic slopes of affect at earlier time point
        dAffect1 <- A*Affect1State + Across * Affect2State + B
        dAffect2 <- A*Affect2State + Across * Affect1State + B

        systemNoiseState1 <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #unique noise for subj 1
        systemNoiseState2 <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #unique noise for subj 2
        systemNoiseCrossState <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #common noise

        Affect1State <- Affect1State + dAffect1 * 1/Nsteps + #update state using slope and time step
          G * systemNoiseState1 + Gcross * systemNoiseCrossState #and add unique and common noise
        Affect2State <- Affect2State + dAffect2 * 1/Nsteps + #update state using slope and time step
          G * systemNoiseState2 + Gcross * systemNoiseCrossState #and add unique and common noise
      }
    }
    data$Affect1[row] <- Affect1State #input affect data
    data$Affect2[row] <- Affect2State #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Subject[row] <- subi #input subject data
  }
}

data$Affect1 <- data$Affect1 + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error
data$Affect2 <- data$Affect2 + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data[data$Subject==1,], # Plot the data for the first couple
  aes(x = Time, y = Affect1, color = as.factor(Subject))) +
  geom_line() +
  geom_line(aes(y = Affect2), linetype = "dashed") +
  geom_point() +
  theme_bw()+
  theme(legend.position = "none")
```



Here we can see the growth process for one couple. Each partner's affect starts from a very different initial affect state, but quite quickly converges to a very similar trajectory. This can be partly attributed to the influence our couple has on each other's rate of growth over time. We can also see a similar pattern of fluctuations in their affect, around their overall level of growth. This is can be due to a set of common experiences the couple goes through, that impact their affect similarly. You can tweak the model parameters to see how each changes the generated trajectory.

Fitting a model: Couple Dynamics with Self and Partner Effects (Continuous Time)

To understand the `ctsem` syntax for our model with variables (one for each partner) is helps to transform the write out the model equation in matrix form to more easily link it with the more compact syntax of `ctsem`. So our latent dynamic model for a couple:

$$d\eta_1 = (A_1\eta_1(t) + A_{cross_{12}}\eta_2(t) + B_1)dt + G_{11}dW_1(t) + G_{12}dW_2(t)$$
$$d\eta_2 = (A_2\eta_1(t) + A_{cross_{21}}\eta_1(t) + B_2)dt + G_{21}dW_1(t) + G_{22}dW_2(t)$$

becomes:

$$\begin{pmatrix} d\eta_1 \\ d\eta_2 \end{pmatrix} = \left(\underbrace{\begin{pmatrix} A_1 & A_{cross_{12}} \\ A_{cross_{21}} & A_2 \end{pmatrix}}_{\text{Drift}} \underbrace{\begin{pmatrix} \eta_1 \\ \eta_2 \end{pmatrix}}_{\eta(t)} (t) + \underbrace{\begin{pmatrix} B_1 \\ B_2 \end{pmatrix}}_{\text{CINT}} \right) dt + \underbrace{\begin{pmatrix} G_{11} & G_{12} \\ G_{21} & G_{22} \end{pmatrix}}_{\text{Diffusion}} \underbrace{d\begin{pmatrix} W_1 \\ W_2 \end{pmatrix}(t)}_{\text{dW(t)}}$$

Now we can connect the matrix form of our latent dynamic model to the `ctsem` syntax:

1. The `DRIFT` option, specifies the auto- (A) and cross-effect (A_{cross}) state-dependence terms. We call them `auto` and `cross`, respectively.
2. The `CINT` option specifies the continuous intercepts ($B1$ and $B2$). We call them continuous intercept `B1` and `B2`, and only estimate a fixed effect (one value for all subjects). To switch off random effects we need to add `FALSE` behind `B||`, i.e. `B||FALSE`.
3. The `DIFFUSION` option specifies the system noise terms ($G_{11}, G_{22}, G_{12}, G_{21}$). The unique system noise is called `systemNoise` and common system noise is called `systemNoiseCross`.
4. The initial values of our latent processes, are treated as random variables with their own mean and variance parameters: $\eta_{t0} = \mu_{0i} + \epsilon_{0i}$, where $\epsilon_{0i} \sim \mathcal{N}(0, \sigma^2)$. The `TOMEANS` option, is used to specify the mean parameter for each partner's initial level of affect, which we call `initialAffect1` and `initialAffect2`. By adding `TRUE` behind `initialAffect||` we are allowing for random effects (between-subject variance) around the population estimate of the initial level of affect in our sample. The `TOVAR` option specifies the variance parameter (σ^2) to estimate the initial level of affect at T0. By default `TOMEANS` and `TOVAR` are estimated from the data as free parameters.

The latent process model is linked to our observations using a (linear) measurement model:

$$\begin{pmatrix} Affect_1 \\ Affect_2 \end{pmatrix}(t) = \underbrace{\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}}_{\Lambda} \underbrace{\begin{pmatrix} \eta_1 \\ \eta_2 \end{pmatrix}}_{\eta(t)} (t) + \underbrace{\begin{pmatrix} 0 \\ 0 \end{pmatrix}}_{\tau} + \underbrace{\begin{pmatrix} \sigma_1 & 0 \\ 0 & \sigma_2 \end{pmatrix}}_{\Theta} \underbrace{\begin{pmatrix} \epsilon_1 \\ \epsilon_2 \end{pmatrix}(t)}_{\epsilon(t)}$$

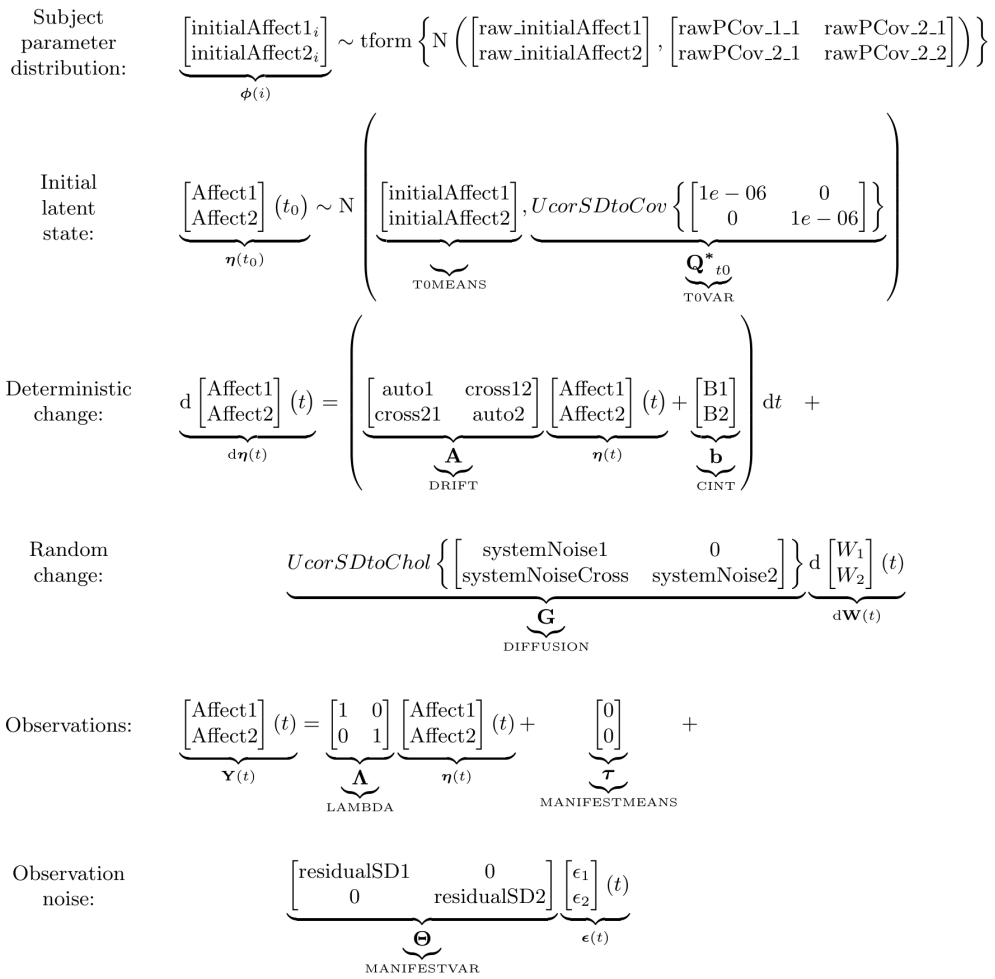
Where $Affect(t)$ is the observed level of affect. Λ is a matrix of regression weights used to link the latent process to our observations, $\eta(t)$ is the latent level of affect, τ reflects a constant that can be used to shift the relationship between observations and a latent variable, and ϵ represents measurement error.

1. The `LAMBA` option specifies the Λ matrix. Now it is a 2x2 matrix with the value 1 on the diagonal, meaning that the latent Affect (η) is directly and equally reflected in the observed Affect without any scaling.
2. The `MANIFESTMEANS` option specifies the measurement intercept (τ) which is simply a constant that is added to the measurement model to shift the relationship between observations and a latent variable. In this case it is set to zero, implying that there is no systematic offset in the measurement process.

3. The `MANIFESTVAR` option specifies the standard deviation (Θ) of the measurement error terms (ϵ_1), which we call `residualSD1` and `residualSD2`.

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  manifestNames = c("Affect1",'Affect2'), #names of observed variables in dataset
  latentNames = c("Affect1",'Affect2'), #names of latent processes
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  MANIFESTVAR = c(
    'residualSD1',0,
    0, 'residualSD2'), #sd of the residual / measurement error
  LAMBDA = diag(1,2), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT=c('B1||FALSE','B2||FALSE'), #continuous intercept with *no* random effects
  TOMEANS=c('initialAffect1||TRUE','initialAffect2||TRUE'), #initial affect with random effects
  DRIFT = c(
    'auto1', 'cross12', #auto effect for subj 1 and cross-effect from 2 to 1
    'cross21','auto2' ), #cross-effect from 1 to 2 and auto effect for subj 2
  DIFFUSION = c(
    'systemNoise1', 0, #system noise for subj 1, 0 in upper triangle (correlation only needs 1 par)
    'systemNoiseCross', 'systemNoise2')) #correlation in system noise, and sd for subj 2

ctModelLatex(ct_model) #generate LaTeX representation of the model
```

Below we generate the model equations, for a clearer view of the entire model structure.



Note: *UcorSDtoChol* converts lower tri matrix of standard deviations and unconstrained correlations to Cholesky factor, *UcorSDtoCov* = transposed cross product of UcorSDtoChol, to give covariance, See Driver & Voelkle (2018) p11. Individual specific notation (subscript i) only shown for subject parameter distribution – pop. means shown elsewhere.

Fit and Summarise ctsem Model

Then we fit our model and summarize its output. However, since it is difficult to get a feeling for the nonlinear model-implied trajectory of a system composed of multiple interdependent process through numerical values, we will focus on a visual representation of our system instead.

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #print summary of the fit, some output disabled
```

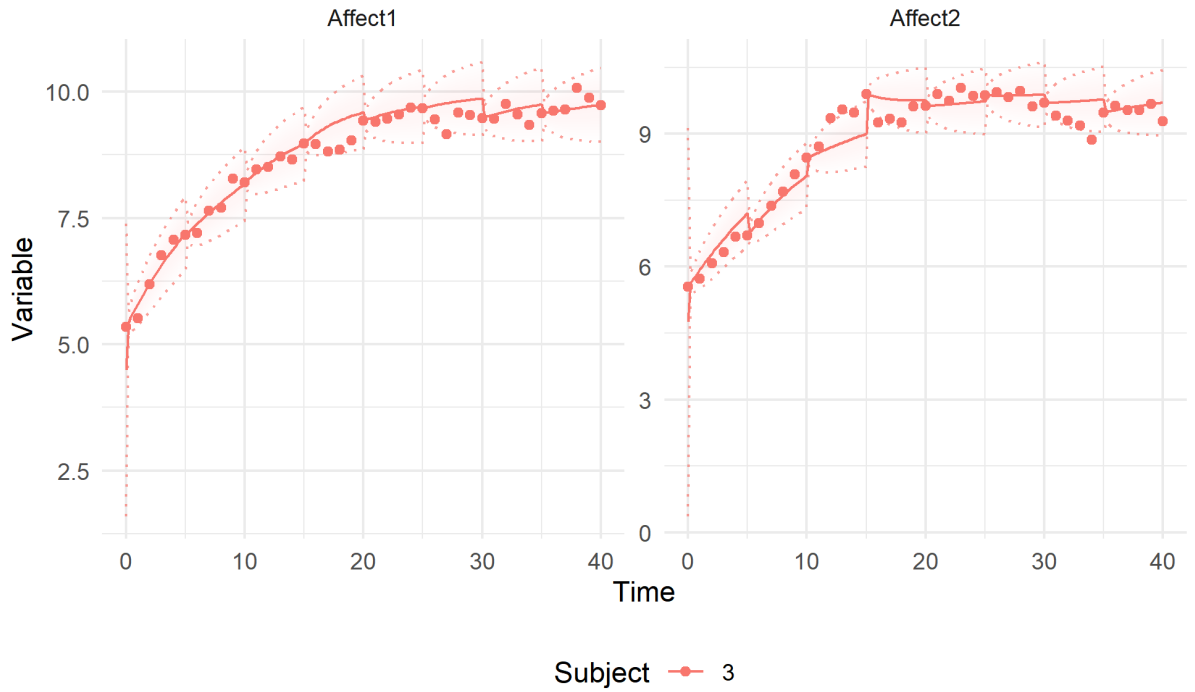
```
$residCovStd
        Affect1 Affect2
Affect1   0.039   0.002
Affect2   0.002   0.063

$resiCovStdNote
[1] "Standardised covariance of residuals"

$rawpopcorr
                                mean     sd    2.5%     50%  97.5%       z
```

```
initialAffect2__initialAffect1 -0.0574 0.2271 -0.4681 -0.0581 0.3852 -0.2526

$popsd
                 mean     sd   2.5%    50%  97.5%
initialAffect1 1.5371 0.3992 0.8957 1.4913 2.4588
initialAffect2 2.3589 0.8774 1.0939 2.2008 4.4829

$popmeans
                     mean     sd    2.5%     50%   97.5%
initialAffect1    4.5024 0.4306  3.7144  4.5074  5.3325
initialAffect2    4.7427 0.5508  3.6556  4.7583  5.8537
auto1            -0.2153 0.0085 -0.2320 -0.2156 -0.1988
cross12           0.1178 0.0079  0.1014  0.1180  0.1324
cross21           0.1116 0.0068  0.0986  0.1115  0.1253
auto2            -0.2068 0.0062 -0.2194 -0.2067 -0.1956
systemNoise1      0.2378 0.0071  0.2240  0.2379  0.2515
systemNoiseCross  0.0714 0.0168  0.0399  0.0714  0.1037
systemNoise2      0.2398 0.0105  0.2204  0.2396  0.2606
residualSD1       0.0000 0.0000  0.0000  0.0000  0.0000
residualSD2       0.0000 0.0000  0.0000  0.0000  0.0000
B1                0.9803 0.0723  0.8378  0.9799  1.1224
B2                0.9528 0.0325  0.8890  0.9529  1.0155

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] 109.9812

$npars
[1] 16

$aic
[1] -187.9623

$logposterior
[1] 109.9812

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

Visualise Predictions

Just like before, we can look at how well the model predicts our observations based on the estimated model parameters plus every 5th data point for our 3rd dyad (subject 3). When we visualize predictions from our model, now including multivariate dynamics, state dependence, and random fluctuations, we see a very different picture to the earlier linear models. Our model is able to capture a reality where there is a complex interplay between the nonlinear affect dynamics of two individuals. The uncertainty in the predictions reflects two sources: The first, is that there are inherently unpredictable fluctuations in affect due to factors we have not observed or modeled. So our model is inevitably imperfect. The second, is that each measurement of affect is likely an imperfect indicator of the underlying affect state, so we can't be sure of the true state of the system even at the moment where we measure it (via e.g., a survey on a smartphone).

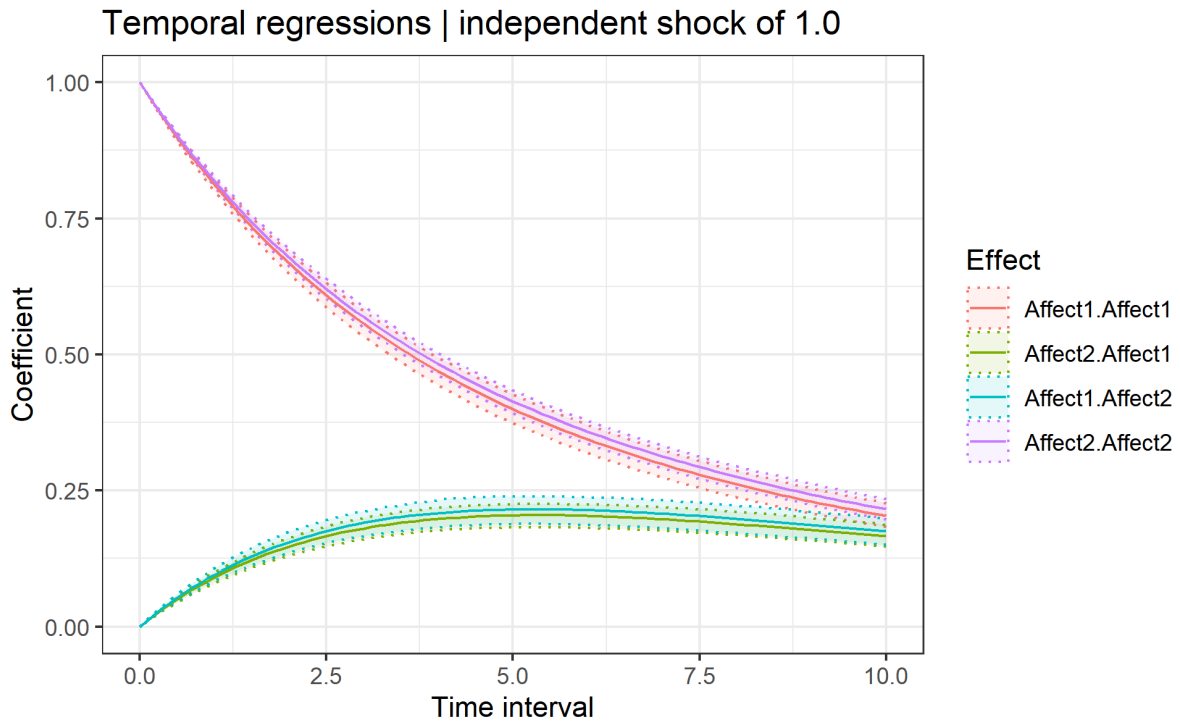
```
ctKalman(fit = ct_fit, plot=TRUE, subjects = 3, kalmanvec=c('y','yprior'), removeObs = 5)
```



Visualise Dynamics – independent shocks

We can also use visualizations to build intuition about the model-implied dynamics (i.e. auto-effect and cross-effect state dependencies). To do this, we can create a plot that tracks the results of an imaginary experiment. In this experiment, we take both Jill and Bert, and place them in a completely controlled setting, where no external factors can impact their affect. That is, their affect remains at baseline unless we do something about it. Second, we intervene on Jill's affect to increase it by 1 at time 0. Third, we plot how Jill's and Bert's affect would be expected to change over 10 weeks following the shock to Jill, as a function of their individual auto-effects and the cross-effects they have on each other. For example, if we increase Jill's affect by 1, her affect is expected to change by approximately 0.40 from baseline after 5 weeks (red solid line, `Affect1.Affect1` in the plot at time interval = 5) because of her auto self-dependency and the bidirectional cross-effects between her and Bert. Instead, Bert's affect is expected to increase by 0.20 by week 5 (green solid line, `Affect2.Affect1` in the plot at time interval = 5). We can also visualize what happens if we increase Bert's affect by 1 *instead* by viewing the blue and purple solid lines. This plot is known as an impulse response function plot (Lütkepohl, 2005).

```
ctStanDiscretePars(ct_fit,plot=T) #plot dynamics
```

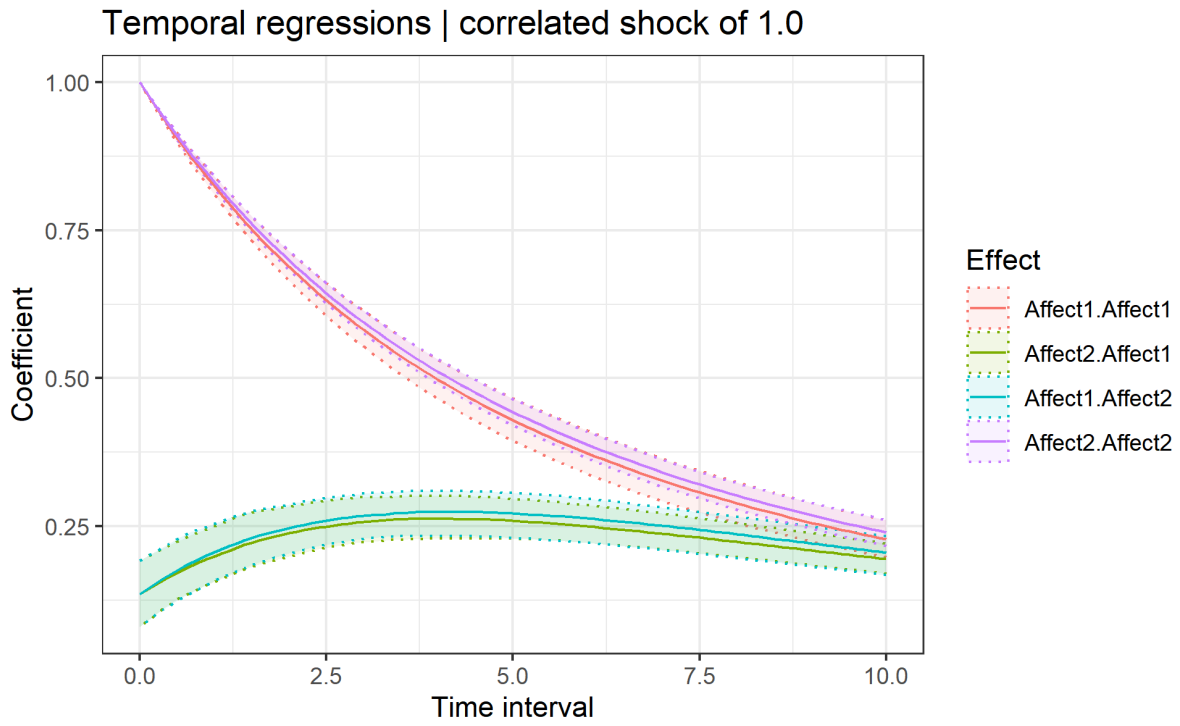


Visualise Dynamics – Correlated shocks

Our hypothetical experiment with independent shocks, may have low generalizability to real world dynamic systems. This is because often a shock that happens to one partner can also affect the other partner (see Driver and Voelkle (2018b), for more on the combined interpretation of system noise and dynamics).

To solve this issue, we can create a plot where we consider the estimated correlation in the system noise, which tells us to what extent Jill and Bert's fluctuations are related. This essentially means that when Jill experiences a random fluctuation in affect, Bert is also likely to experience a fluctuation in the same (or opposite) direction. Instead of plotting an impulse response function based solely on an independent 1-unit shock, we modify the impulse response function to reflect that a shock to one partner comes with a correlated fluctuation in the other partner's affect. For example, if the system noise correlation is estimated at 0.25, then when Jill's affect increases by 1 unit, Bert's affect is expected to change by approximately 0.25 units as a result of that shared noise component. With `ctsem` we can simulate and plot the impulse response function, such that when one partner is shocked by 1 unit the response in the other partner is scaled by the system noise correlation. This gives a more realistic picture of the dynamic interplay between the partners.

```
ctStanDiscretePars(ct_fit,plot=T, observational=TRUE) #plot dynamics
```



From this plot we see that when Jill's affect increases by 1 at T0, Bert's affect is expected to contemporaneously fluctuate in the same direction as well (positive system noise correlation). The positive cross-effect coefficients also show that there is a positive bidirectional relationship between the two partners. Such that when one partner's affect increases we can expect that to cause a subsequent increase in the other partner's affect. Here, we can be sure that this reflects a causal effect because we generated the data with such an effect. But in a real-world scenario, we would need to consider the possibility of confounding variables that could explain the observed relationship. The system noise correlation can account for confounders that change very quickly (compared to the speed of change of affect), but is unlikely to sufficiently account for confounders that change at a similar speed to affect. For instance, a sudden loud noise that startles both partners will lead to a very brief fluctuation in affect for both partners, which will be absorbed into the system noise. However, a prolonged period of gloomy weather might cause a gradual systematic shift in the affect of both partners that can be misinterpreted as evidence that one partner's affect directly impacts the other's affect. Such slowly changing confounders are not accounted for in this model, but individual differences in the continuous intercept could be added to account for some such effects. More sophisticated individual-differences models could also be used. We will consider these later.

Individual Differences in System Dynamics

In the above models, we have generally assumed that all individuals have the same system dynamics. In reality, people will have highly heterogeneous system dynamics. This is because there are likely to be an immense number of factors that contribute to what we might consider as the individual's dynamic system. Factors that change slowly or not at all, with respect to our observed time window, can reasonably be treated as stable individual differences. Such individual differences may exist in the magnitude of random fluctuations, with some people having more stable affect systems while others have a more volatile affect. Alternatively, in the case of couples, some dyads may have more interdependent affect dynamics with stronger coupling, while other dyads are more independent.

Couple Dynamics with Individual Differences and Time-Independent Moderation (Continuous Time)

For our case, we are going to consider two sources of individual differences. First, we are going to assume that individuals have differences in their long-term, post therapy baseline affect. This will be done by allowing individual differences in the continuous intercept. Second, we will assume that couples who have been together longer have a stronger influence on each others' affect. This will be incorporated by allowing for individual differences in the strength of our cross-effect state-dependence terms, and by allowing the size of each couple's cross-effect to depend on the average time they spend together.

Simulation: Couple Dynamics with Individual Differences and Time-Independent Moderation (Continuous Time)

The code chunk to run this simulation, builds on the code we used earlier. To generate a continuous intercept for each person we sample from a normal distribution, e.g., `B1 <- rnorm(n = NSubjects, mean = 2, sd = .3)`. We assume that people with a higher affect are more likely to get in a relationship, thus we add a common value sampled from a normal distribution to the value for each person in a dyad. That is, `Bcommon <- rnorm(n = NSubjects, mean = 1, sd = .2)` is added to the sampled values of B1 and B2 (e.g., `B1 <- Bcommon + rnorm(n = NSubjects, mean = 2, sd = .3)`).

To add individual differences in the continuous intercept parameter, we index the parameter to denote that it is specific to the denoted subject. So `B1` becomes `B1[subi]` where `subi` refers to the subject identifier.

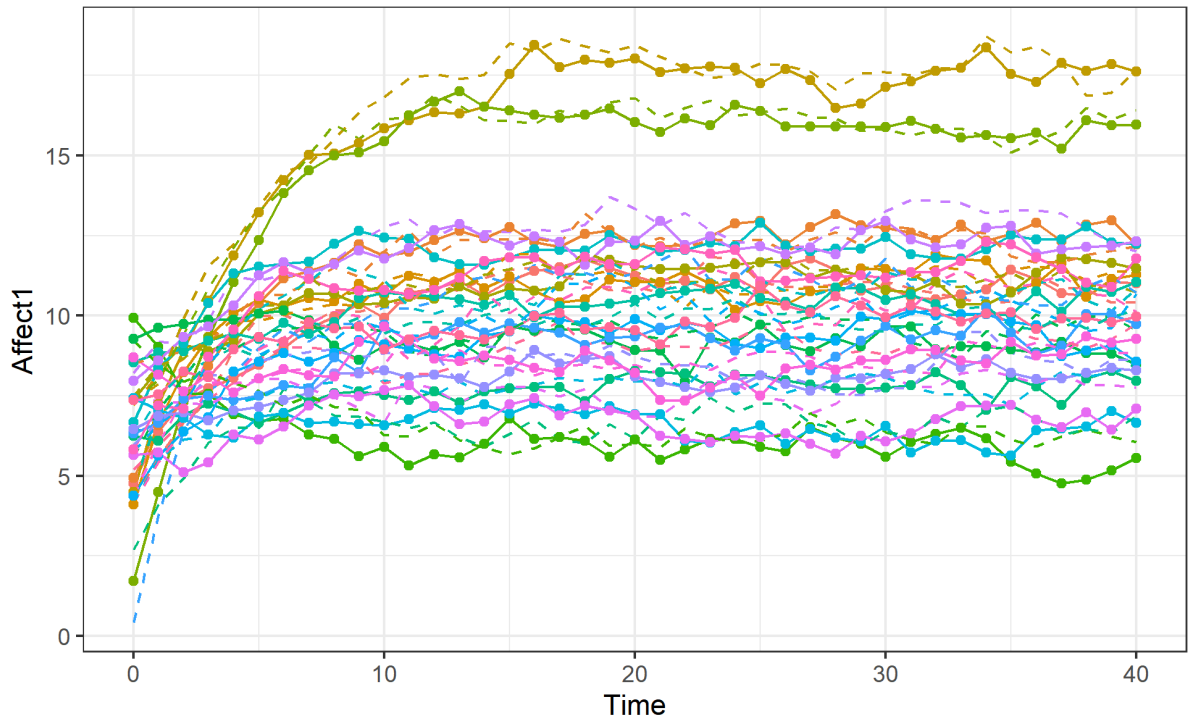
A similar process is used to generate data for our heterogeneous cross effects. We sample a cross-effect for each couple from a normal distribution and then add the time the couple has spent together, scaled by a coefficient that determines the degree of influence time spent together has on each couple's cross effects `Across <- rnorm(n= NSubjects, mean = .1, sd=.05) + .05*TimeTogetherZ`. The cross-effect parameter is also indexed in our data generating loop to generate a subject-specific parameter, e.g. `Across[subi] * Affect2State`.

```r
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=40, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect1 <- rnorm(n = NSubjects, mean = 5, sd = 2)
initialAffect2 <- rnorm(n = NSubjects, mean = 5, sd = 2)
TimeTogether <- runif(n=NSubjects, min = 0, max = 20) #time together in years
TimeTogetherZ <- scale(TimeTogether) #standardise time together
A <- -.4 #continuous time state dependence
Across <- rnorm(n= NSubjects, mean = .1, sd=.05) + .05*TimeTogetherZ #cross-effect state dependence

# generate continuous intercepts for each individual,
# assuming high affect individuals may partner with high affect individuals
Bcommon <- rnorm(n = NSubjects, mean = 1, sd = .2) #common continuous intercept variance
B1 <- Bcommon + rnorm(n = NSubjects, mean = 2, sd = .3) #unique continuous intercept for subj 1
B2 <- Bcommon + rnorm(n = NSubjects, mean = 2, sd = .3) #continuous intercept for subj 2
cor(B1,B2) #check if people with higher affect tend to couple
```

```
[1] 0.4183134
```

```r
G <- .4 #unique system noise coefficient
Gcross <- .1 #common system noise coefficient

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect1 = rep(NA,NSubjects*Nobs),
  Affect2 = rep(NA,NSubjects*Nobs)) #now with affect for two individuals

Nsteps <- 100 #number of steps in time to compute between each observation (increased precision)
```

```
row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    if(obsi==1){
      Affect1State <- initialAffect1[subi] #if first time point, set to initial affect
      Affect2State <- initialAffect2[subi]
    }
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation

        #compute deterministic slope of affect at earlier time point
        dAffect1 <- A*Affect1State + Across[subi] * Affect2State + B1[subi]
        dAffect2 <- A*Affect2State + Across[subi] * Affect1State + B2[subi]

        systemNoiseState1 <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #unique noise for subj 1
        systemNoiseState2 <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #unique noise for subj 2
        systemNoiseCrossState <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #common noise for both

        #update states using slope and time step, and add unique and common system noise
        Affect1State <- Affect1State + dAffect1 * 1/Nsteps +
          G * systemNoiseState1 + Gcross * systemNoiseCrossState

        Affect2State <- Affect2State + dAffect2 * 1/Nsteps +
          G * systemNoiseState2 + Gcross * systemNoiseCrossState
      }
    }
    data$Affect1[row] <- Affect1State #input affect data
    data$Affect2[row] <- Affect2State #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Subject[row] <- subi #input subject data
    data$TimeTogetherZ[row] <- TimeTogetherZ[subi] #input time together data
  }
}

data$Affect1 <- data$Affect1 + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error
data$Affect2 <- data$Affect2 + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data, # Plot the data for all couples
  aes(x = Time, y = Affect1, color = as.factor(Subject))) +
  geom_line() +
  geom_line(aes(y = Affect2), linetype = "dashed") +
  geom_point() +
  theme_bw()+
  theme(legend.position = "none")
```



Fitting a model: Couple Dynamics with Individual Differences and Time-Independent Moderation (Continuous Time)

These individual differences can be accommodated in `ctsem` using both 'fixed' and 'random' effect approaches. In the fixed effect approach, we rely on observed covariates (time-independent predictors in `ctsem`) to moderate the system parameters and explain the individual differences. In `ctsem` these are at present largely restricted to linear effects. For alternative forms, the usual approach of including higher order terms (e.g., age and age squared) is possible. Creative use of `ctsem`'s modeling flexibility could also be used to estimate other nonlinear effects.

In the random effect approach, we assume that the individual differences are at least partly due to unobserved factors, and estimate the variance and correlations in these factors, relying purely on the observed data (without covariates) to estimate where each individual's parameter(s) sit with respect to their distribution of subject-specific deviations from the average population estimate.

By combining fixed and random effects, we try to improve the estimated model for each individual by allowing individuals to have unique system dynamics, but not 'completely unique' – we still rely to some extent on how other individuals behave (for more on hierarchical modeling see Driver and Voelkle (2018a)). In `ctsem` we can either decide to automatically specify random effects (preferable in most cases), or manually add random effects (for details on the manual method see the (Driver & Tomasik, 2023)). For our example, we will leave the specification of the random effects to the `ctsem` back-end.

So, let's go over the new syntax in our `ctsem`. In terms of data that we fit our model on, we add the time couples spent together (`TimeTogetherZ`) as a stable source of individual differences (time-independent predictor). This is done using the argument `TIpredNames = c('TimeTogetherZ')`. By default when covariates are included in `ctsem` they moderate all parameters of the system. Thus, we turn the default moderation off using `tipredDefault = FALSE`. Now if we want our time-independent predictor to moderate a specific parameter, we need to explicitly specify the moderation. The moderation of a cross-effect (e.g. `cross21`) by `TimeTogetherZ` can be specified within the DRIFT matrix by inserting the name of the predictor to the fifth slot (slots are denoted by the pipe `|` operator, where each `|` defines 1 slot). Thus, we write `cross21||TRUE||TimeTogetherZ`. This would estimate the `cross21` parameter, allow it to vary as a linear function of `TimeTogetherZ`, and allow for random effects (done by adding `TRUE` to the third slot, `cross21||TRUE`) to account for any individual differences that could

not be explained by `TimeTogetherZ`. It is important to note that moderators in `ctsem` can dramatically influence the interpretation of parameters and lead to confusion if care is not taken – usually centering, and possibly scaling, the moderator(s) is a good idea. Since we also want random effects for the continuous intercept of each partner we specify these using `CINT=c('B1||TRUE','B2||TRUE')`. All the other arguments are explained in prior sections of this tutorial, or can be found in the `ctsem` manual (https://cran.r-project.org/package=ctsem/vignettes/hierarchicalmanual.pdf).

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  tipredDefault = FALSE, #moderation disabled unless explicitly specified
  TIpredNames = c('TimeTogetherZ'), #names of time independent predictors in dataset
  manifestNames = c("Affect1",'Affect2'), #names of observed variables in dataset
  latentNames = c("Affect1",'Affect2'), #names of latent processes
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  MANIFESTVAR = c(
    'residualSD1',0,
    0, 'residualSD2'), #sd of the residual / measurement error
  LAMBDA = diag(1,2), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT=c('B1||TRUE','B2||TRUE'), #continuous intercept with random effects
  TOMEANS=c('initialAffect1||TRUE','initialAffect2||TRUE'), #initial affect with random effects
  DRIFT = c(
    'auto1', 'cross21||TRUE||TimeTogetherZ', #auto effect for subj 1 and cross-effect from 2 to 1
    'cross21||TRUE||TimeTogetherZ','auto2' ), #cross-effect from 1 to 2 and auto effect for subj 2
  DIFFUSION = c(
    'systemNoise1', 0, #system noise sd for subj 1, 0 in upper triangle (1 par for correlation)
    'systemNoiseCross', 'systemNoise2')) #correlation in system noise, and sd for subj 2 noise
```

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
s = summary(ct_fit, parmatrices=FALSE) #store summary of the fit
```

Now if we look at the `$tipreds` (time-independent predictors) section of the summary, we have an estimated value for the effect of time together on the cross-effect state dependence. We can see that the cross-effect state dependence increases by approximately .05 for each increase of 1 in standardized time together. Thus, partner's who spent more time together have more tightly coupled affect.

```
print(s$tipreds)
```

```
                            mean     sd   2.5%   50%  97.5%      z
tip_TimeTogetherZ_cross21 0.0315 0.0165 -7e-04 0.031 0.0653 1.9017
```

The `$rawpopcorr` section of the summary shows the estimated correlations between the random effects of the model – the initial states and the continuous intercepts. We can see that the correlation between the random effects for the continuous intercepts is approximately the true correlation we used to generate the data.

```
print(round(s$rawpopcorr,2))
```

```
                                mean   sd  2.5%   50% 97.5%     z
initialAffect2__initialAffect1 -0.04 0.21 -0.45 -0.06  0.39 -0.21
cross21__initialAffect1        -0.08 0.34 -0.67 -0.10  0.61 -0.25
B1__initialAffect1             -0.36 0.29 -0.75 -0.42  0.36 -1.25
B2__initialAffect1             -0.41 0.31 -0.81 -0.50  0.39 -1.31
cross21__initialAffect2         0.25 0.36 -0.57  0.33  0.80  0.70
B1__initialAffect2             -0.15 0.26 -0.61 -0.16  0.39 -0.60
B2__initialAffect2             -0.15 0.29 -0.67 -0.17  0.52 -0.51
B1__cross21                     0.12 0.40 -0.72  0.21  0.75  0.31
B2__cross21                     0.28 0.47 -0.80  0.42  0.90  0.61
B2__B1                          0.45 0.25 -0.18  0.49  0.84  1.78
```

Visualise Individual Differences

We can plot the trajectory of affect implied by the estimated model parameters, conditional on values of -1, 0, and 1 on any time-independent predictors included in the model.

The first set of plots (`Effect of TimeTogetherZ on observed trajectory`), show the observed trajectory of partner 1 (Affect1) and partner 2 (Affect2) based on the three cutoffs of `TimeSpentTogetherZ` (-1.28, 0.01, 1.06). We can see that couples that spent more time together have a faster rate of growth in affect and also plateau at a higher affect value. The second set of plots (`Effect of TimeTogetherZ on latent trajectory`), shows the same information but for the latent trajectories of affect.

The third set of plots, (`Temporal regressions | independent shock of 1.0`) show an impulse response function for an independent 1-unit shock, but this time separated by our cutoffs of time spent together. Here we can visualize the fact that when a person experiences a shock to their affect (increase of 1) their partner is expected to change more over time if they spend more time together, on average. The fourth set of plots (`Temporal regressions | correlated shock of 1.0`), shows the impulse response function but this time taking into consideration the estimated correlated system noise.

```
tipredplots <- ctPredictTIP(ct_fit, plot=T, tipreds = c('TimeTogetherZ'))
```

Couple Dynamics with Individual Differences and Time-Dependent Moderation (Continuous Time)

We may feel uncomfortable relying on people's retrospective estimate of how much time they spend together to moderate their degree of interdependence. However, we also do not want to assume that couples continuously affect each other even when they are not in each other's presence. For instance, according to our model, if Jill gets fired, her change in affect would immediately influence Bert's affect, even if Bert is completely unaware of this event. If we have information about Jill and Bert's proximity, we can use this information to tell our model to only allow Jill's affect to impact Bert's rate of change when the couple is together. This can be done by moderating our couple's cross-effect parameter by a time-dependent moderator of presence.

Simulation: Couple Dynamics with Individual Differences and Time-Dependent Moderation (Continuous Time)

To generate data for a model with a time-dependent moderator of cross-effect state dependence, we first need to generate a time-dependent moderator that indicates when a couple is communicating (0 no communication, 1 = communication). To do this, we will sample a value of 0 or 1 from a binomial distribution, where the probability of communication at each observation is given by the time couples spend together `Comm <- rbinom(n = NSubjects, size = 1, prob = TimeTogether / 20)`. Such that couples that spend more time together will have more observations when they are communicating. To sample a value for each observation `Nobs` per subject `Nsubjects`, we use the lapply function which is essentially a loop over each `TimeTogetherValue` (`t`), `Comm <- lapply(TimeTogether, function(t) rbinom(n = Nobs, size = 1, prob = t / 20))`. Then the communication value `comm_val` we use at each time step is simply the the observed `Comm` value during the current observation, `comm_val <- Comm[[subi]][obsi]`.

Second, we add the time-dependent moderator in our model of affect dynamics. Which makes the rate of change for partner 1 `dAffect1 <- A*Affect1State + Across[subi] * Affect2State * comm_val + B1[subi]`, where `Across` is multiplied by the time-dependent moderator `comm_val` at each time step. This makes it so there is no cross-effect when the couple is not communicating (`comm_val` = 0).

```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=40, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect1 <- rnorm(n = NSubjects, mean = 5, sd = 2)
initialAffect2 <- rnorm(n = NSubjects, mean = 5, sd = 2)
TimeTogether <- runif(n=NSubjects, min = 0, max = 20) #time together in years
TimeTogetherZ <- scale(TimeTogether) #standardise time together
A <- -.4 #continuous time state dependence
Across <- rnorm(n= NSubjects, mean = .1, sd=.05) #cross-effect state dependence

# Sample from a binomial distribution with prob based on time spent together
Comm <- lapply(TimeTogether, function(t) rbinom(n = Nobs, size = 1, prob = t / 20))

# Check the relationship: compute the mean interaction for each subject and correlate with TimeTogetherZ
Comm_means <- sapply(Comm, mean)
print(cor(Comm_means, TimeTogetherZ))
```

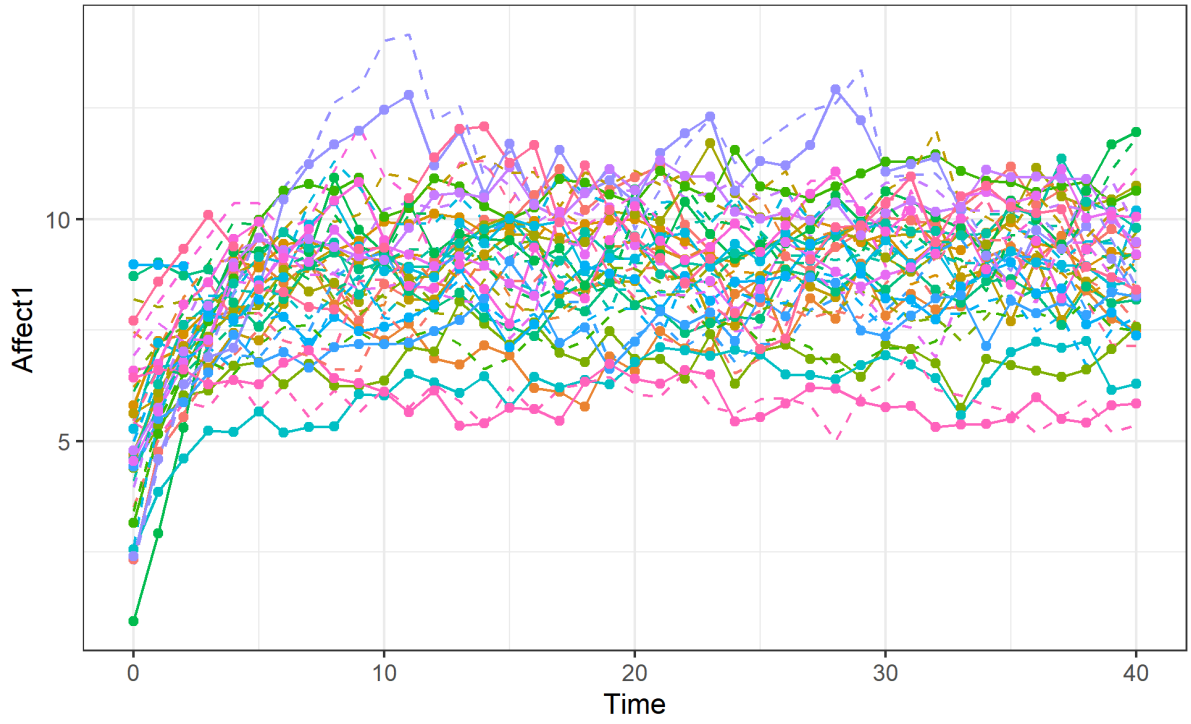
```
          [,1]
[1,] 0.9627666
```

```
# generate continuous intercepts for each individual,
# assuming high affect individuals may partner with high affect individuals
Bcommon <- rnorm(n = NSubjects, mean = 1, sd = .2) #common continuous intercept variance
B1 <- Bcommon + rnorm(n = NSubjects, mean = 2, sd = .3) #unique continuous intercept for subj 1
B2 <- Bcommon + rnorm(n = NSubjects, mean = 2, sd = .3) #continuous intercept for subj 2
cor(B1,B2) #check if people with higher affect tend to couple
```

```
[1] 0.2747585
```

```
G <- .4 #unique system noise coefficient
Gcross <- .1 #common system noise coefficient

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect1 = rep(NA,NSubjects*Nobs),
  Affect2 = rep(NA,NSubjects*Nobs)) #now with affect for two individuals

Nsteps <- 100 #number of steps in time to compute between each observation (increased precision)

row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    comm_val <- Comm[[subi]][obsi]
    if(obsi==1){
      Affect1State <- initialAffect1[subi] #if first time point, set to initial affect
      Affect2State <- initialAffect2[subi]
    }
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation

        #compute deterministic slope of affect at earlier time point
        dAffect1 <- A*Affect1State + Across[subi] * Affect2State * comm_val + B1[subi]
        dAffect2 <- A*Affect2State + Across[subi] * Affect1State * comm_val + B2[subi]

        systemNoiseState1 <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #unique noise for subj 1
        systemNoiseState2 <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #unique noise for subj 2
        systemNoiseCrossState <- rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #common noise for both individuals

        #update states using slope and time step, and add unique and common system noise
        Affect1State <- Affect1State + dAffect1 * 1/Nsteps +
          G * systemNoiseState1 + Gcross * systemNoiseCrossState

        Affect2State <- Affect2State + dAffect2 * 1/Nsteps +
          G * systemNoiseState2 + Gcross * systemNoiseCrossState

      }
    }
    data$Affect1[row] <- Affect1State #input affect data
```

```
    data$Affect2[row] <- Affect2State #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Comm[row] <- comm_val
    data$Subject[row] <- subi #input subject data
    data$TimeTogetherZ[row] <- TimeTogetherZ[subi] #input time together data
    data$const[row] <- 1 # add constant for ctsem spec
  }
}

data$Affect1 <- data$Affect1 + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error
data$Affect2 <- data$Affect2 + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data, # Plot the data for all couples
  aes(x = Time, y = Affect1, color = as.factor(Subject))) +
  geom_line() +
  geom_line(aes(y = Affect2), linetype = "dashed") +
  geom_point() +
  theme_bw()+
  theme(legend.position = "none")
```



Fitting a model: Couple Dynamics with Individual Differences and Time-Dependent Moderation (Continuous Time)

To specify a model with a time-dependent moderator in `ctsem` we need to take four new steps. First, we need to specify the name of our time-dependent predictor using `TDpredNames = c("Comm")` where `Comm` is the name we give to our moderator. Second, we need to define the main effect of our predictor using the `TDPREDEFFECT` argument. By default this is set to freely estimate a main effect for a time-dependent predictor. However, in our case we only want an interaction effect so we are going to set this to 0, `TDPREDEFFECT = 0`. Third, we need to modify our drift matrix. Here we are going to specify the interaction between our cross-effect state dependence terms and our time-dependent moderator, by specifying that our cross-effect state dependence is a function of an intercept (capturing a baseline cross-effect, i.e., when our moderator is 0) and an interaction term capturing the current level of our cross-effect which is moderated (multiplied) by the value of our moderator at a given time point, e.g., our cross-effect becomes `cross12int + cross12level*Comm`. To specify our cross-effect as a function of multiple elements, we need to use the `PARS` argument. Here we can also specify random effects, in our baseline cross-effects, e.g., `cross12int||TRUE`.

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  #TIpredNames = c('TimeTogetherZ'), #names of time independent predictors in dataset
  manifestNames = c("Affect1",'Affect2'), #names of observed variables in dataset
  latentNames = c("Affect1",'Affect2'), #names of latent processes
  TDpredNames = c('Comm'), #names of time dependent predictors in dataset
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  MANIFESTVAR = c(
    'residualSD1',0,
    0, 'residualSD2'), #sd of the residual / measurement error
  LAMBDA = diag(1,2), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT=c('B1||TRUE','B2||TRUE'), #continuous intercept with random effects
  TOMEANS=c('initialAffect1||TRUE','initialAffect2||TRUE'), #initial affect with random effects
  TDPREDEFFECT = 0,
  DRIFT = c( #auto effects on diagonal, cross effects on off diagonal
    'auto1', '(cross12int + cross12level*Comm)', #auto effect for subj 1 and cross-effect from 2 to
    '(cross21int + cross21level*Comm)','auto2'), #cross-effect from 1 to 2 and auto effect for subj 2
  DIFFUSION = c(
    'systemNoise1', 0, #system noise person 1, 0 in upper triangle (correlation needs 1 par)
    'systemNoiseCross', 'systemNoise2'), #correlation in system noise, system noise person 2
  PARS = c('cross12int||TRUE','cross21int||TRUE',
    'cross12level','cross21level'))
ctModelLatex(ct_model) #generate LaTeX representation of the model
```

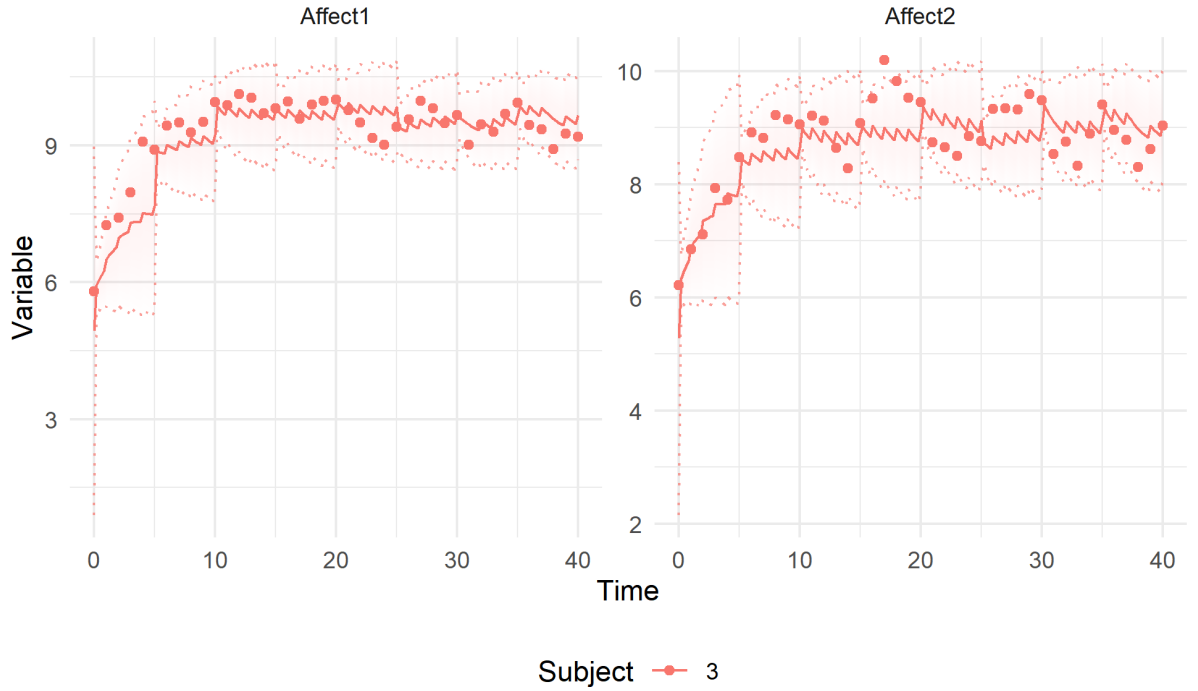
```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #print summary of the fit, some output disabled
```

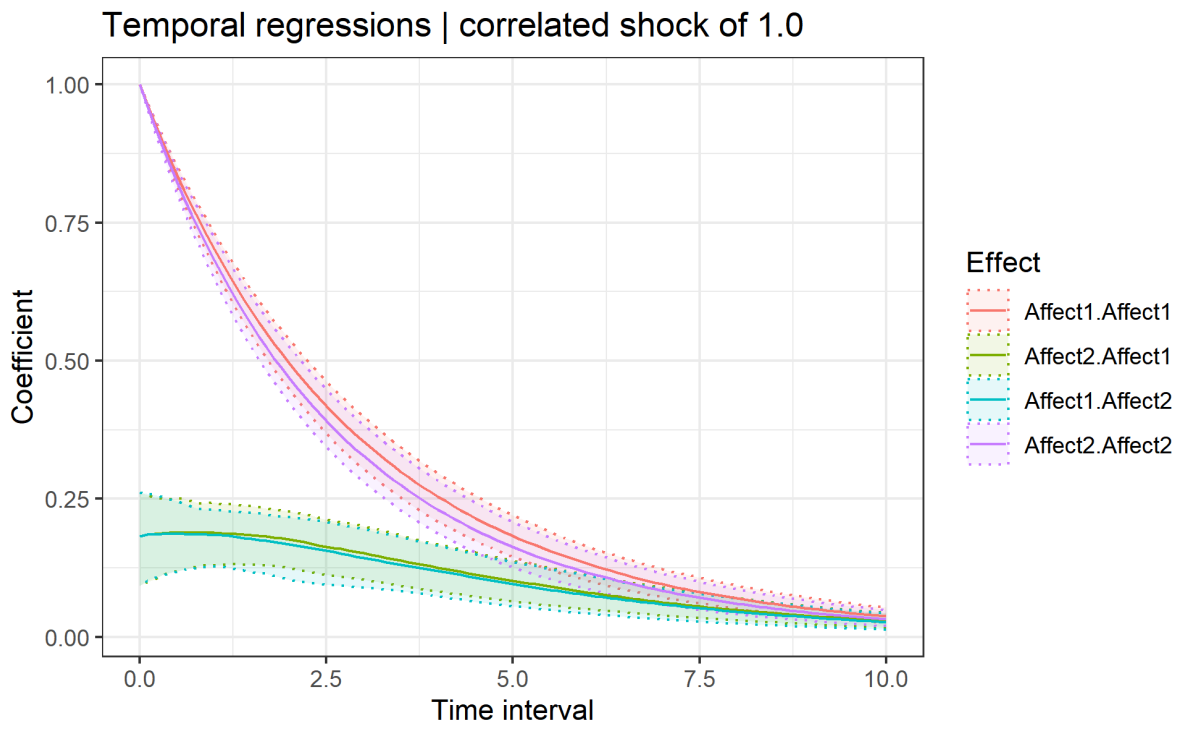
```
$residCovStd
        Affect1 Affect2
Affect1   0.084   0.018
Affect2   0.018   0.087

$resiCovStdNote
[1] "Standardised covariance of residuals"

$rawpopcorr
                                   mean     sd    2.5%     50%  97.5%       z
initialAffect2__initialAffect1   0.0652 0.4127 -0.7985  0.0601 0.8746  0.1579
B1__initialAffect1              -0.2637 0.3639 -0.8375 -0.3231 0.5708 -0.7248
B2__initialAffect1               0.1377 0.3384 -0.5616  0.1362 0.7548  0.4070
cross12int__initialAffect1      -0.0068 0.4215 -0.7841 -0.0733 0.8945 -0.0162
cross21int__initialAffect1      -0.1529 0.4583 -0.7958 -0.2962 0.8440 -0.3337
B1__initialAffect2               0.0845 0.4177 -0.7894  0.1595 0.7884  0.2024
B2__initialAffect2               0.0599 0.4347 -0.8788  0.1535 0.7274  0.1378
cross12int__initialAffect2       0.2618 0.5306 -0.6790  0.1574 0.9901  0.4934
cross21int__initialAffect2      -0.0225 0.5238 -0.7298 -0.1971 0.9420 -0.0429
B2__B1                           0.4070 0.4754 -0.7269  0.5754 0.9583  0.8562
cross12int__B1                   0.0058 0.4672 -0.8627  0.0809 0.7822  0.0124
cross21int__B1                  -0.1356 0.4080 -0.7956 -0.1750 0.6914 -0.3324
cross12int__B2                   0.0485 0.4358 -0.8550  0.1365 0.7503  0.1113
cross21int__B2                  -0.2517 0.3904 -0.8260 -0.3245 0.6190 -0.6446
cross21int__cross12int           0.0268 0.5123 -0.6608 -0.1242 0.9532  0.0524

$popsd
                 mean     sd   2.5%    50%  97.5%
initialAffect1 2.0714 0.3219 1.5130 2.0480 2.7762
initialAffect2 1.6187 0.2540 1.1670 1.6004 2.1730
B1             0.3688 0.2242 0.0960 0.3107 0.9291
B2             0.4481 0.1704 0.2065 0.4202 0.8642
cross12int     0.0450 0.0229 0.0147 0.0403 0.1068
cross21int     0.0360 0.0209 0.0106 0.0314 0.0881

$popmeans
                    mean     sd    2.5%     50%   97.5%
initialAffect1    4.9521 0.4539  4.0753  4.9412  5.7969
initialAffect2    5.2639 0.3546  4.5380  5.2717  5.9343
auto1            -0.3761 0.0284 -0.4342 -0.3747 -0.3241
```

```
auto2            -0.4038 0.0326 -0.4698 -0.4026 -0.3403
systemNoise1      3.7771 0.1426  3.5004  3.7713  4.0673
systemNoiseCross -0.0453 0.0115 -0.0670 -0.0458 -0.0222
systemNoise2      0.4359 0.0121  0.4129  0.4360  0.4613
residualSD1       0.1388 0.0287  0.0905  0.1364  0.1988
residualSD2       0.0000 0.0000  0.0000  0.0000  0.0000
cross12level      0.1282 0.0042  0.1202  0.1282  0.1362
cross21level      0.1312 0.0042  0.1229  0.1314  0.1391
B1                3.1174 0.1824  2.7547  3.1184  3.4659
B2                3.3194 0.2002  2.9474  3.3114  3.7339
cross12int       -0.0359 0.0327 -0.1033 -0.0360  0.0273
cross21int       -0.0297 0.0317 -0.0881 -0.0306  0.0360

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] -796.8785

$npars
[1] 36

$aic
[1] 1665.757

$logposterior
[1] -796.8785

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

```
ctKalman(fit = ct_fit, plot=TRUE, subjects = 3, kalmanvec=c('y','yprior'), removeObs = 5)
```



```
ctStanDiscretePars(ct_fit,plot=T, observational=TRUE) #plot dynamics
```



Nonlinear Change with a Transient External Shock (Continuous Time)

The last element we will consider in this tutorial is how to explicitly model an external influece at a specific time point with a specific form. So let's return to our example of Jill to make things more concrete.

Let's say Jill is going through therapy and improving at a rate given by her dynamic system parameters that we used so far. What happens if she encounters a traumatic event in the midst of her 21 weeks of therapy? Such an event could have a pronounced effect on Jill's affect dynamics, which a realistic model of her growth needs to consider. We can incorporate this into our dynamic systems model using an input effect that captures the influence of an external intervention on the system dynamics.

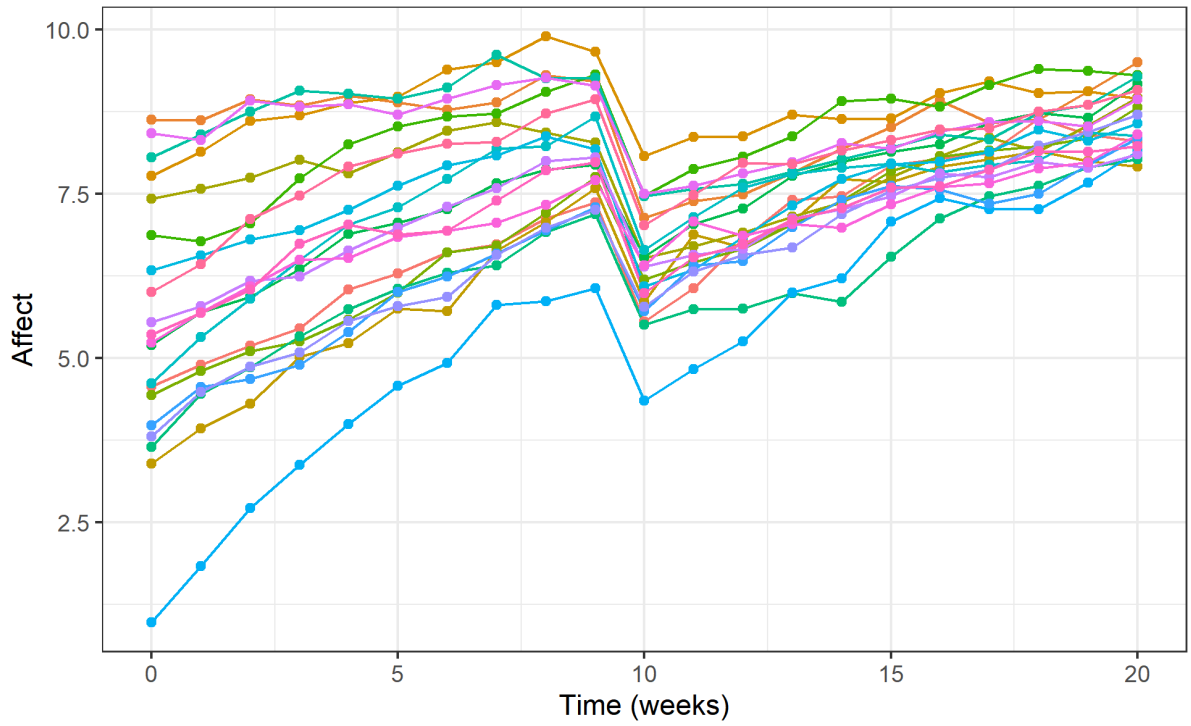
Simulation: Nonlinear Change with a Transient External Shock (Continuous Time)

To add an input effect to our data generating model, we will make use of an `ifelse` statement within our data generating loop. We need to take two steps to make this work. First, we need to define the precise time point where we want our input to occur. In our case, we choose to intervene after half of our time window has passed `inputTime <- times[ceiling(length(times)/2)]`. Second, for each iteration in our loop, we evaluate the time point at each observation to see if it matches the time of the intervention we have specified (i.e. `inputTime`). When the answer becomes yes, then we add our input effect to the model that generates the rate of change in affect during that observation. This is done by adding `M` to the generated rate of change (`dAffect + M`) during the given observation, where M is the input effect coefficient determining the effect size of our intervention.

To save the input variable in our data frame, we add a column called input where the value is 1 when `inputTime` matches `Time`, and 0 otherwise.

```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=20, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)
```

```
A <- -.1 #continuous time state dependence
B <- 1 #continuous intercept
G <- .2 #system noise coefficient
M <- -2 #input effect coefficient
inputTime <- times[ceiling(length(times)/2)] #intervention after ~ 1/2 of time window passed

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect = rep(NA,NSubjects*Nobs))

Nsteps <- 100 #number of steps in time to compute between each observation (increased precision)

row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    if(obsi==1) AffectState <- initialAffect[subi] #if first time point, set to initial affect
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation
        dAffect <- A*AffectState + B #compute deterministic slope of affect at earlier time point
        if(times[obsi]==inputTime) dAffect <- dAffect + M #add input effect if intervention time
        AffectState <- AffectState + dAffect * 1/Nsteps + #update state using slope and time step
          G * rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #and add system noise
      }
    }
    data$Affect[row] <- AffectState #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Subject[row] <- subi #input subject data
    data$Input <- ifelse(data$Time == inputTime, 1, 0) #input effect data
  }
}

data$Affect <- data$Affect + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data, # Plot the data
  aes(x = Time, y = Affect, color = as.factor(Subject))) +
  geom_line() +
  geom_point() +
  theme_bw()+
    labs(x = "Time (weeks)", y = "Affect")+
  theme(legend.position = "none")
```



Now we have a depiction of affect dynamics with an input effect, which decreases affect by 2 units at the moment it is applied to our system.

Fitting a model: Nonlinear Change with a Transient External Shock (Continuous Time)

To specify a ctsem model with an intervention effect, we simply need to specify a time-dependent predictor `TDpredNames = Input`. This adds a within-person covariate that has the same effect on each person in our dataset.

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  manifestNames = "Affect", #names of observed variables in dataset
  latentNames = "Affect", #names of latent processes
  TDpredNames = 'Input', #names of time dependent predictors in dataset
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  MANIFESTVAR = 'residualSD', #sd of the residual / measurement error
  LAMBDA = matrix(1,nrow=1,ncol=1), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT='B||FALSE', #continuous intercept with *no* random effects
  TOMEANS='initialAffect||TRUE', #initial affect with random effects
  DRIFT = 'stateDependence',
  DIFFUSION = 'systemNoise')

ctModelLatex(ct_model) #generate LaTeX representation of the model
```

Subject parameter distribution:

$$\underbrace{[\text{initialAffect}_i]}_{\phi(i)} \sim \text{tform}\left\{\text{N}\left([\text{raw\_initialAffect}], [\text{rawPCov\_1\_1}]\right)\right\}$$

Initial latent state:

$$\underbrace{[\text{Affect}]\,(t_0)}_{\boldsymbol{\eta}(t_0)} \sim \text{N}\left(\underbrace{[\text{initialAffect}]}_{\text{T0MEANS}}, \underbrace{UcorSDtoCov\left\{[1e-06]\right\}}_{\underbrace{\mathbf{Q}^*_{t0}}_{\text{T0VAR}}}\right)$$

Deterministic change:

$$\underbrace{\text{d}\,[\text{Affect}]\,(t)}_{\text{d}\boldsymbol{\eta}(t)} = \left(\underbrace{[\text{stateDependence}]}_{\underbrace{\mathbf{A}}_{\text{DRIFT}}}\underbrace{[\text{Affect}]\,(t)}_{\boldsymbol{\eta}(t)} + \underbrace{[\text{B}]}_{\underbrace{\mathbf{b}}_{\text{CINT}}} + \underbrace{[\text{td\_Affect\_Input}]}_{\underbrace{\mathbf{M}}_{\text{TDPREDEFFECT}}}\underbrace{[\text{Input}]}_{\boldsymbol{\chi}(t)}\right)\text{d}t \;+$$

Random change:

$$\underbrace{UcorSDtoChol\left\{[\text{systemNoise}]\right\}}_{\underbrace{\mathbf{G}}_{\text{DIFFUSION}}}\underbrace{\text{d}\,[W_1]\,(t)}_{\text{d}\mathbf{W}(t)}$$

Observations:

$$\underbrace{[\text{Affect}]\,(t)}_{\mathbf{Y}(t)} = \underbrace{[1]}_{\underbrace{\boldsymbol{\Lambda}}_{\text{LAMBDA}}}\underbrace{[\text{Affect}]\,(t)}_{\boldsymbol{\eta}(t)} + \underbrace{[0]}_{\underbrace{\boldsymbol{\tau}}_{\text{MANIFESTMEANS}}} \;+$$

Observation noise:

$$\underbrace{[\text{residualSD}]}_{\underbrace{\boldsymbol{\Theta}}_{\text{MANIFESTVAR}}}\underbrace{[\epsilon_1]\,(t)}_{\boldsymbol{\epsilon}(t)}$$

System noise distribution per time step: $\Delta\left[W_{j\in[1,1]}\right](t-u) \sim \text{N}(0, t-u)$

Observation noise distribution: $\left[\epsilon_{j\in[1,1]}\right](t) \sim \text{N}(0,1)$

Note: *UcorSDtoChol* converts lower tri matrix of standard deviations and unconstrained correlations to Cholesky factor, *UcorSDtoCov* = transposed cross product of UcorSDtoChol, to give covariance, See Driver & Voelkle (2018) p11. Individual specific notation (subscript i) only shown for subject parameter distribution – pop. means shown elsewhere.

Looking at the model, note that we now have a time dependent predictor effect – this is the input effect `td_Affect_Input`.

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #summary of the fit, some output disabled
```

```
$residCovStd
       Affect
Affect  0.113

$resiCovStdNote
[1] "Standardised covariance of residuals"

$popsd
                mean     sd   2.5%    50%  97.5%
initialAffect 1.9269 0.3125 1.3817 1.9069 2.5964

$popmeans
                    mean     sd    2.5%     50%   97.5%
initialAffect     5.5194 0.4233  4.6754  5.5050  6.3197
stateDependence -0.0938 0.0079 -0.1105 -0.0934 -0.0798
systemNoise       0.1949 0.0136  0.1709  0.1943  0.2222
residualSD        0.0562 0.0287  0.0192  0.0494  0.1284
B                 0.9454 0.0594  0.8363  0.9442  1.0623
td_Affect_Input -1.9076 0.0468 -1.9952 -1.9099 -1.8185

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] 40.36664

$npars
[1] 7

$aic
[1] -66.73327

$logposterior
[1] 40.36664

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

Different Types of Inputs

The model above implies that the input effect is immediate and has a lasting effect on the system, as we can see in the plot where the level takes time to recover. But there is also the assumption that the effects transmit through time with the same dynamics as the rest of the system. This is probably the simplest approach to thinking about such effects, but in reality, the effects of an intervention may be more complex, and may depend on the individual, the context, may induce other changes in the system, and may persist or transfer through the system in different ways to the typical system behavior. For example, while the regular ups and downs of life may dissipate relatively quickly, a traumatic event may have direct effects that last over a long period and may require more consideration.

Nonlinear Change with a Persistent External Shock (Continuous Time)

For our example, we can a model an intervention that has a persistent effect on all future instances of our system. For more examples of intervention effects and how to specify them in `ctsem` we refer the reader to (Driver & Voelkle, 2018b).

The simplest way to add a persistent external shock would be to just use a dummy variable that applies a 0 to all observations prior to the intervention and a 1 to all observations post (and including) the time of the intervention. However, this would lead to a spike in the rate of change in affect during

our observation time, followed by a gradual decay in the rate of change back to baseline in the time in-between observations. This can cause problems when used with specific study designs (e.g. unequal time intervals). Thus, a solution that is more generally appropriate is desirable.

To do this, we need to specify a latent (intervention) process which is impacted by our observed intervention variable. In turn, the latent intervention process will direclty impact our affect process *during and in-between our observations*. This latent intervention process, can have its own autoregressive parameter which allows us to specify an accelerating, dissipating, or stable effect across continuous time. That is, if the autoregressive parameter is set to 0, our latent intervention process will remain at a stable value and exert a stable effect on a person's rate of change over time. If the autoregressive parameter is set to negative value (e.g. -0.1), then the effect of the our intervention will dissipate over time. If it is set to a value greater than 0, the effect of our intervention will accumulate over time (e.g. 0.1). In our example, we will demonstrate an intervention with a persistent effect over time that is administered during the halfway mark of our observed timeline.

Simulation: Nonlinear Change with a Persistent External Shock (Continuous Time)

In our data generating block, we now include an input variable `M`, which directly influences the state of our latent intervention process `InputState`. To understand how this works let us begin from the equation that defines the `InputState` at each time step: `InputState <- InputState + dInput * 1/Nsteps`. So the `InputState` at a given time step, is given by the `InputState` at the prior time step, plus the rate of change `dInput * 1/Nsteps`.

The rate of change in our latent intervention process `dInput` is given by the previous value of `InputState` multiplied by an autoregressive coefficient, `dInput <- AM*InputState`. Because the autoregressive coefficient is 0 in the case of a persistent input effect, the rate of change is also 0, until the observed intervention occurs.

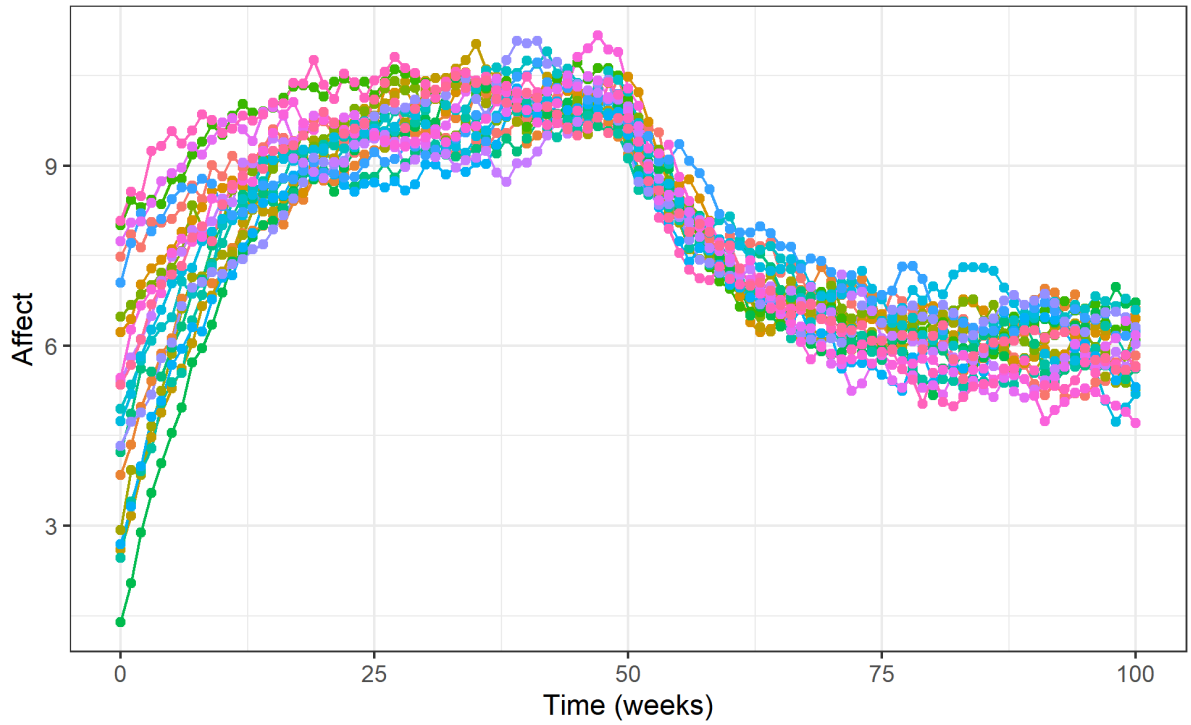
At the time of the intervention, week 50, the input effect `M` is added to the equation for the rate of change `dInput <- AM*InputState + M`. This raises the `InputState` to the value of `M`.

After week 50, the rate of change becomes zero again. Because the autoregressive parameter is zero. Thus, since `InputState` equals its own prior state + (zero) change, the state of the latent intervention process `InputState` will not change; reflecting a persistent input process.

Finally, to model the impact of our latent intervention process on our affect process, we make the rate of change in affect dependent on the state of the intervention process at the current moment `dAffect <- A*AffectState + B + InputState`.

```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=100, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)
A <- -.1 #continuous time state dependence
B <- 1 #continuous intercept
G <- .2 #system noise coefficient
M <- -0.4 #input variable
AM <- 0 #latent input process autoregression
inputTime <- times[ceiling(length(times)/2)] #intervention after ~ 1/2 of time window passed

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect = rep(NA,NSubjects*Nobs))

Nsteps <- 100 #number of steps in time to compute between each observation (increased precision)

row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    if(obsi==1){
      AffectState <- initialAffect[subi] #if first time point, set to initial affect
      InputState <- 0 # initialize latent input process
```

```
    }
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation

        # Compute intervention effect
        dInput <- AM*InputState # deterministic slope of our intervention at earlier time point
        if(times[obsi]==inputTime) dInput <- dInput + M # add input effect if intervention time

        InputState <- InputState + dInput * 1/Nsteps # update state using slope and time step

        # Compute Affect state
        dAffect <- A*AffectState + B + InputState # deterministic slope at earlier time point
        AffectState <- AffectState + dAffect * 1/Nsteps + # update state using slope and time step
          G * rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) # and add system noise

      }
    }
    data$Affect[row] <- AffectState #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Subject[row] <- subi #input subject data
    data$Input <- ifelse(data$Time == inputTime, 1, 0) #input effect data
    data$InputState[row] <- InputState #input latent intervention process data
  }
}

data$Affect <- data$Affect + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data, # Plot the data
  aes(x = Time, y = Affect, color = as.factor(Subject))) +
  geom_line() +
  geom_point() +
  theme_bw()+
    labs(x = "Time (weeks)", y = "Affect")+
  theme(legend.position = "none")
```



Fitting a model: Nonlinear Change with a Persistent External Shock (Continuous Time)

We want to specify a latent intervention process that only captures the effect of our observed intervention variable, without any extra noise or baseline effects. To do this, we set all the extra influences on the latent intervention process, that do not come directly from the observed intervention variable, to 0.

Thus, we set the random fluctuations (DIFFUSION) to zero for our latent intervention process. We also set its starting value to 0, by fixing the TOMEANS and TOVAR to zero for our latent intervention process. Finally, we fix its continuous intercept to zero CINT since there is no constant growth in the latent intervention process.

Next, we set the cross-effect of our latent process to 1 using our DRIFT matrix (adding a 1 in row 1, column 2 of the matrix). This, specifies a direct effect of the current state of the latent intervention process on the rate of change in our affect process.

Lastly, we set the effect of the observed intervention variable on our latent affect process to zero, and estimate its direct effect on our latent intervention process (TDPREDEFFECT = matrix(c(0,"LatentInput"), nrow=2, ncol=1)). Thus, our observed intervention directly impact the latent intervention process, which in turn directly impacts our latent affect process.

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  manifestNames = "Affect", #names of observed variables in dataset
  latentNames = c("Affect","LatentInput"), #names of latent processes
  TDpredNames = 'Input', #names of time dependent predictors in dataset
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  MANIFESTVAR = 'residualSD', #sd of the residual / measurement error
  LAMBDA = matrix(1,nrow=1,ncol=2), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT=c('B||FALSE', #continuous intercept with *no* random effects for Affect,
    "0||FALSE"), # and no CINT for latent input
  TDPREDEFFECT = matrix(c(0,"LatentInput"), nrow=2, ncol=1),
  TOMEANS=c("initialAffect||TRUE", #initial affect with random effects,
    "0||FALSE"), # and latent input process starts at 0
  TOVAR=matrix(c("TOVARAffect",0,0,0), nrow=2, ncol=2),
  DRIFT = matrix(c('stateDependence', 1,
    0, 0), nrow = 2, ncol = 2, byrow = TRUE),
  DIFFUSION = matrix(c('systemNoise',0,
    0, 0), nrow = 2, ncol =2, byrow = TRUE))

ctModelLatex(ct_model) #generate LaTeX representation of the model
```

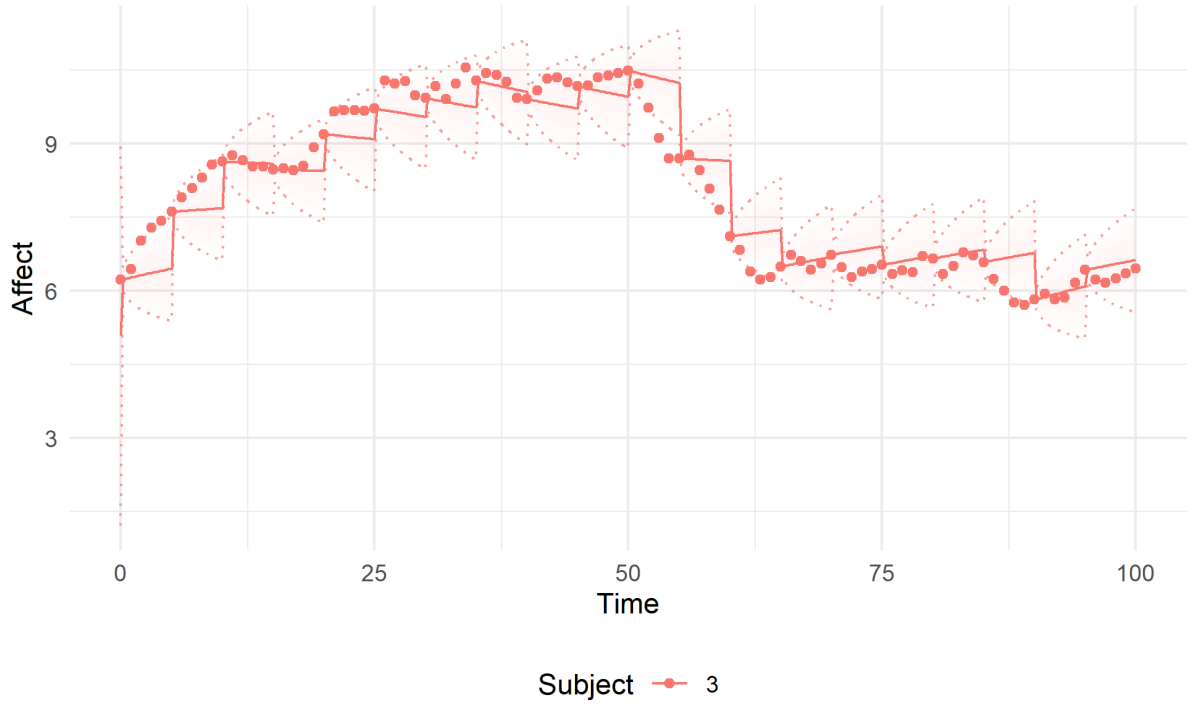
```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #print summary of the fit, some output disabled
```

```
$residCovStd
       Affect
Affect  0.033

$resiCovStdNote
[1] "Standardised covariance of residuals"

$popsd
                mean     sd   2.5%    50%  97.5%
initialAffect 1.9932 0.3324 1.4247 1.9605 2.6971

$popmeans
                   mean     sd    2.5%     50%   97.5%
initialAffect    5.0790 0.4526  4.1644  5.1103  5.9253
stateDependence -0.0241 0.0033 -0.0307 -0.0241 -0.0181
systemNoise      0.2569 0.0040  0.2490  0.2570  0.2642
residualSD       0.0000 0.0000  0.0000  0.0000  0.0000
B                0.1969 0.0261  0.1414  0.1977  0.2446

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] -138.1692

$npars
[1] 6
```

```
$aic
[1] 288.3383

$logposterior
[1] -138.1692

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

```
ctKalman(fit = ct_fit, plot=TRUE, subjects = 3, kalmanvec=c('y','yprior'), removeObs = 5)
```



Model evaluation and comparison

To end this tutorial, we are going to investigate how to evaluate and compare different model structures when we do not know the structure of our observed data. In empirical settings, this can be a very difficult and fascinating problem that requires deep inquiry. To get people started on their journey of model evaluation, we will showcase some tools that can help determine whether a model provides a good representation of the data and whether it is better than any competing explanations (models) we may have. We will begin from a familiar starting place, and then enrich our model evaluation by introducing new tools.

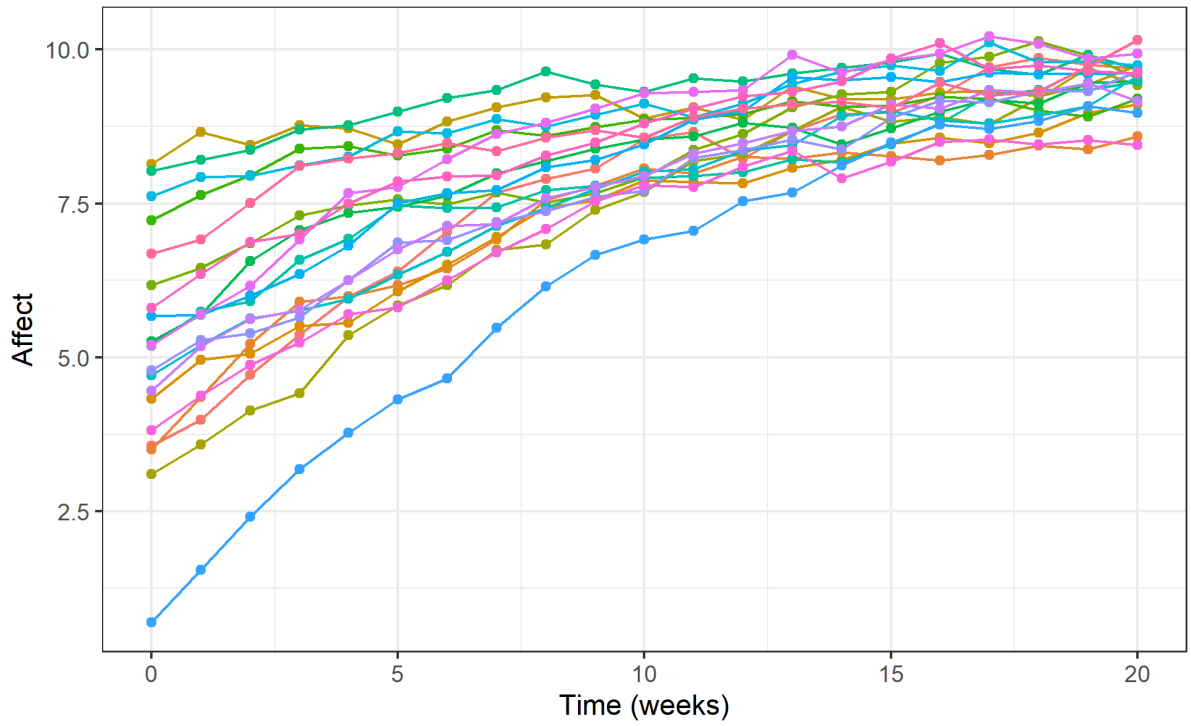
The most common form of model evaluation happens using a very simple method known as the R^2 (Nakagawa & Schielzeth, 2013). The R^2 tells us how much of the total variance in our data is explained by our model by dividing the residual (unexplained) variance ($V\hat{y}$) by the total observed variance(Vy).

So let's imagine that after all the model building we have done, we still think that the best representation of an affect process is a linear model in continuous time. If we have data from 20 patients over 21 weeks, we can use the R^2 estimate to check whether our model explains a substantial amount of variance in our data (what counts as substantial is a topic for another paper). We will generate the data and pretend it is observed, because knowing the answers simplifies the process of understanding model evaluation. So we will generate data using from a continuous-time model with state dependency and random fluctuations.

Generating data

To generate our data we will recycle our code block from earlier (see 'Simulation: Nonlinear Change with Random Fluctuations (Continuous Time)').

```
# Generate data for multiple subjects with individual differences
NSubjects <- 20
times <- seq(from=0, to=20, by=1) #generate sequence of time points when subjects are measured
Nobs <- length(times) #number of observations per subject
initialAffect <- rnorm(n = NSubjects, mean = 5, sd = 2)
A <- -.1 #continuous time state dependence
B <- 1 #continuous intercept
G <- 0.2 #system noise coefficient

#create empty data.frame to fill step by step
data <- data.frame(Subject= rep(NA,NSubjects*Nobs),
  Time = rep(NA,NSubjects*Nobs),
  Affect = rep(NA,NSubjects*Nobs))

Nsteps <- 100 #number of steps in time to compute between each observation (increased precision)

row <- 0 #initialize row counter, to track which row of the data.frame we are on
for(subi in 1:NSubjects){
  for(obsi in 1:Nobs){ #for each observation of a subject
    row <- row + 1
    if(obsi==1) AffectState <- initialAffect[subi] #if first time point, set to initial affect
    if(obsi>1){ #else compute new affect state by taking a sequence of small steps in time
      for(stepi in 1:Nsteps){ #take Nsteps in time between each observation
        dAffect <- A*AffectState + B #compute deterministic slope of affect at earlier time point
        AffectState <- AffectState + dAffect * 1/Nsteps + #update state using slope and time step
          G * rnorm(n=1, mean=0, sd=sqrt(1/Nsteps)) #and add system noise
      }
    }
    data$Affect[row] <- AffectState #input affect data
    data$Time[row] <- times[obsi] #input time data
    data$Subject[row] <- subi #input subject data
  }
}

data$Affect <- data$Affect + rnorm(n=nrow(data), mean = 0, sd = .05) #add measurement error

ggplot(data, # Plot the data
  aes(x = Time, y = Affect, color = as.factor(Subject))) +
  geom_line() +
  geom_point() +
  theme_bw()+
  labs( x = "Time (weeks)", y = "Affect")+
  theme(legend.position = "none")
```



Fitting the wrong model: A linear model in continuous time

We can now specify and fit our linear continuous-time model, with no state-dependency and no system noise.

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  # Specify features of the data
  manifestNames = "Affect", #names of observed variables in dataset
  latentNames = "Affect", #names of latent processes
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  # Specify features of the model
  MANIFESTVAR = 'residualSD', #sd of the residual / measurement error
  LAMBDA = matrix(1,nrow=1,ncol=1), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT='B||FALSE', #continuous intercept with *no* random effects
  TOMEANS='initialAffect||TRUE', #initial affect with random effects
  DRIFT = 0,
  DIFFUSION = 0)

ctModelLatex(ct_model)
```

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #print summary of the fit, some output disabled
```

```
$residCovStd
       Affect
Affect   0.23

$resiCovStdNote
[1] "Standardised covariance of residuals"

$popsd
                mean     sd   2.5%    50%  97.5%
initialAffect 0.7752 0.1267 0.5593 0.7619 1.0591

$popmeans
```

```
                mean     sd   2.5%    50%  97.5%
initialAffect 5.9501 0.1799 5.5790 5.9494 6.2905
residualSD    0.6692 0.0234 0.6247 0.6692 0.7161
B             0.2023 0.0053 0.1925 0.2022 0.2129

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] -459.6372

$npars
[1] 4

$aic
[1] 927.2744

$logposterior
[1] -459.6372

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

Now we can use the R^2 estimate to see how much of the variance in our 'observed' data our model has accounted for. To get the R^2 we first need to extract the residuals. In `ctsem` this is done using the `ctKalman` function to extract model-based estimates and then a sub-setting step to only keep the residuals `k=k[k$Element %in% 'errprior',]`. Then we just use the variance of the residuals and divide it over the variance of our observations, to get the R^2, `R_squared <- 1 - (y_hatVAR / yVAR)`.

```
# Extract residuals
k=ctKalman(ct_fit, subjects=unique(data$Subject)) #get residuals and various estimates
k=k[k$Element %in% 'errprior',] #remove everything except the residuals
k=dcast(data = data.table(k), formula = formula('Subject + Time ~ Row')) #cast to wider format

# estimate R-squared
y_hatVAR = sum(k$Affect^2, na.rm = TRUE)
yVAR <- sum((data$Affect - mean(data$Affect))^2)
R_squared <- 1 - (y_hatVAR / yVAR)
print(R_squared)
```

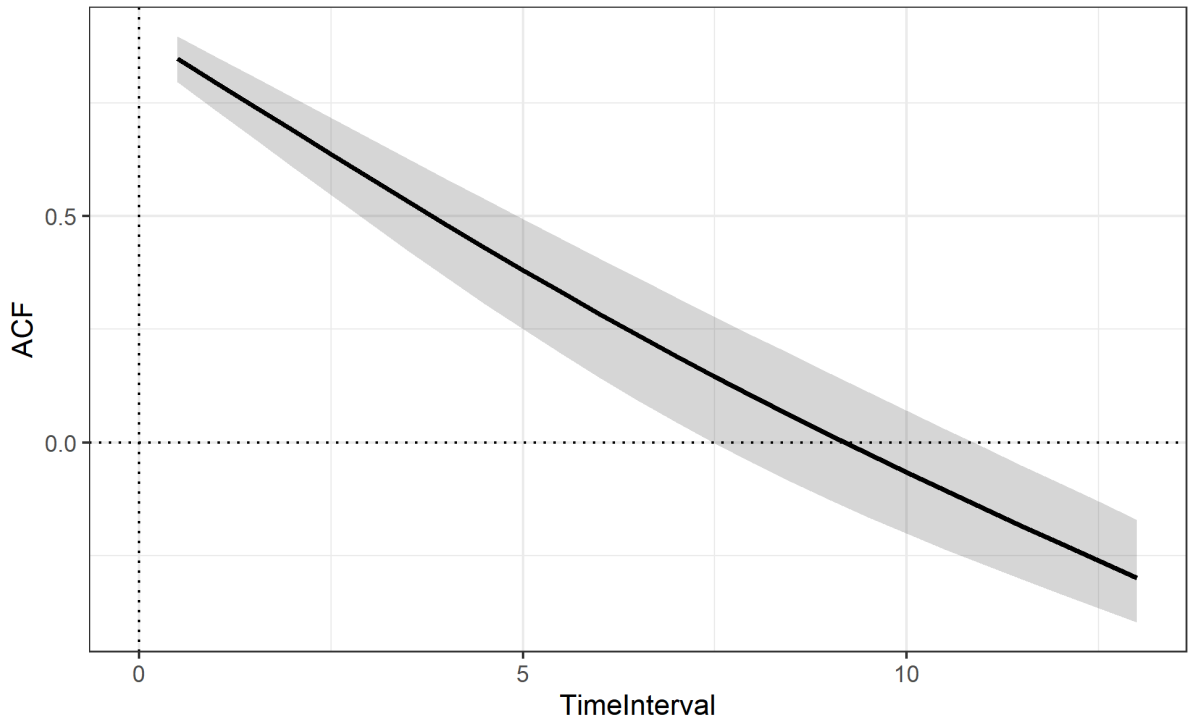
```
[1] 0.7676601
```

We can see that our model explains a very high amount of the variance in our observations. This is because it is almost the same model as the model that generated our data. At this point, in most empirical circumstances we would go home very satisfied with our model. Explaining approximately 75 percent of the variance could mean that the remaining variance is simply noise.

But this can also be assessed. We already extracted the residuals from our model and we can check their autocorrelation. Autocorrelated residuals indicate that our model leaves some predictable structure unexplained (Gelman et al., 1996). While residuals that are not correlated are more likely to just be random noise.

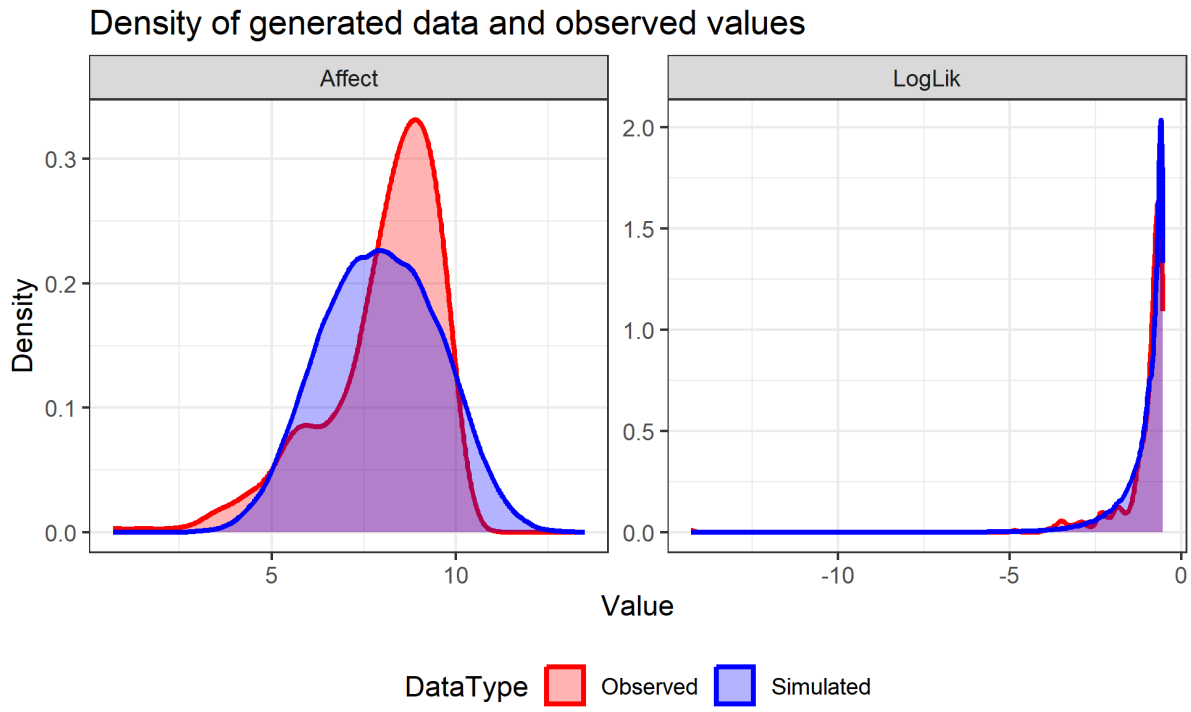
We can create a plot of the autocorrelation between residuals to visualize whether our model is missing any systematic patterns in our data. To do this we use the `ctACFresiduals` function.

```
ctACFresiduals(ct_fit) #plot autocorrelation of residuals
```

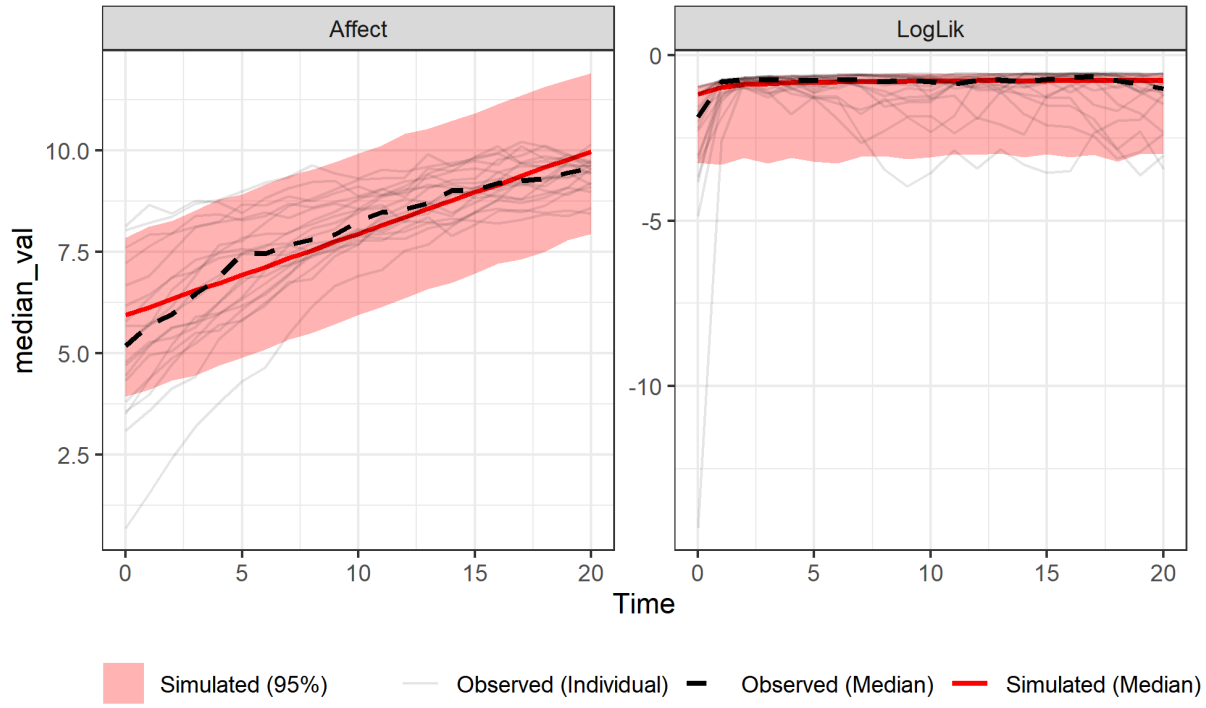


From the plot we can see that there is a high autocorrelation between residuals, about 0.6 between temporally adjacent residuals. So now we know two things: (1) Our model is doing a good job at capturing most of the systematic patterns in our data, (2) there is still room for improvement. The natural follow-up question is what should we improve? To get an idea of model misspecification we can generate data based on the parameter estimates of our model and plot those against our observed data.

```
fit <- ctStanGenerateFromFit(ct_fit, nsamples=200, #add generated data to the fit object
  fullposterior = F, cores = 2)
postpred <- ctPostPredPlots(ct_fit) #generate and store posterior predictive plots
print(postpred[[1]]) #print first plot -- overall density plots of likelihood / variables
```



```
print(postpred[[2]]) #print second plot -- compares expectations / variation over time
```



By looking at the model implied expectations versus the empirical, it is quite clear that we are fitting a linear model to a nonlinear trajectory. Our mode also seems to underestimate the between-subject variance at earlier time points while overestimating the variance at later observations. But in which way can we improve our model to better account for our observations?

By taking a closer look at the individual growth trajectories, we can see there seems to be a dependency between people's initial affect values and their rate of change in affect. That is, people who start with very high affect values have an almost flat growth curve, while people with a low initial level have a very steep growth curve which slowly plateaus as they reach higher values of affect. Thus, it seems that we should add a state-dependency parameter to our model.

Finally, since people largely have the same post-therapy baseline in affect (i.e. they plateau at similar values) we should keep the continuous intercept fixed across our population. So, let's go fit our adjusted model to our data.

Fitting a better model: Adding state-dependence in continuous time

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  # Specify features of the data
  manifestNames = "Affect", #names of observed variables in dataset
  latentNames = "Affect", #names of latent processes
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  # Specify features of the model
  MANIFESTVAR = 'residualSD', #sd of the residual / measurement error
  LAMBDA = matrix(1,nrow=1,ncol=1), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT='B||FALSE', #continuous intercept with *no* random effects
  TOMEANS='initialAffect||TRUE', #initial affect with random effects
  DRIFT = 'stateDependence',
  DIFFUSION = 0)

ctModelLatex(ct_model)
```

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #print summary of the fit, some output disabled
```

```
$residCovStd
       Affect
Affect  0.101

$resiCovStdNote
[1] "Standardised covariance of residuals"

$popsd
                mean     sd   2.5%   50% 97.5%
initialAffect 1.8367 0.3081 1.3066 1.814 2.531

$popmeans
                    mean     sd    2.5%     50%   97.5%
initialAffect    5.1813 0.4187  4.3543  5.1891  5.9603
stateDependence -0.1042 0.0033 -0.1108 -0.1041 -0.0981
residualSD       0.3201 0.0112  0.2983  0.3197  0.3419
B                1.0471 0.0269  0.9971  1.0472  1.1007

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] -169.4929

$npars
[1] 5

$aic
[1] 348.9857

$logposterior
[1] -169.4929

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

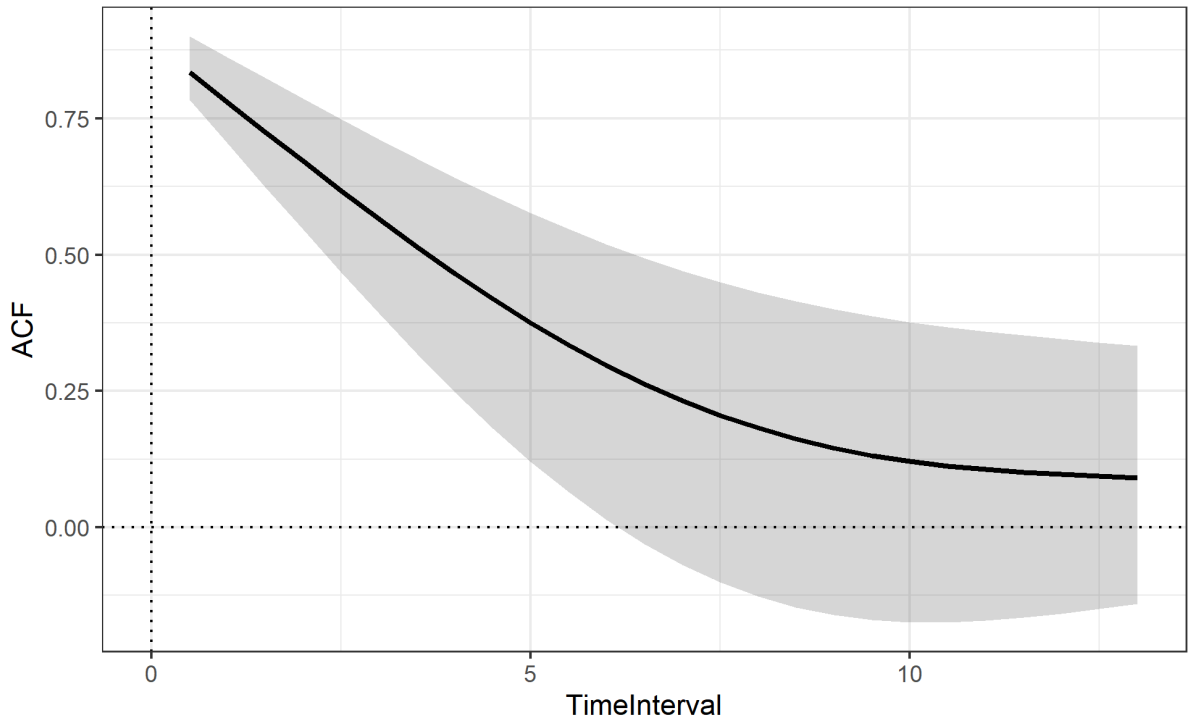
Now we can again see if adding this state-dependence term has helped us explain more variance in our data by computing the R^2.

```
# Extract residuals
k=ctKalman(ct_fit, subjects=unique(data$Subject)) #get residuals and various estimates
k=k[k$Element %in% 'errprior',] #remove everything except the residuals
k=dcast(data = data.table(k), formula = formula('Subject + Time ~ Row')) #cast to wider format

# estimate R-squared
y_hatVAR = sum(k$Affect^2, na.rm = TRUE)
yVAR <- sum((data$Affect - mean(data$Affect))^2)
R_squared <- 1 - (y_hatVAR / yVAR)
print(R_squared)
```

```
[1] 0.8990757
```

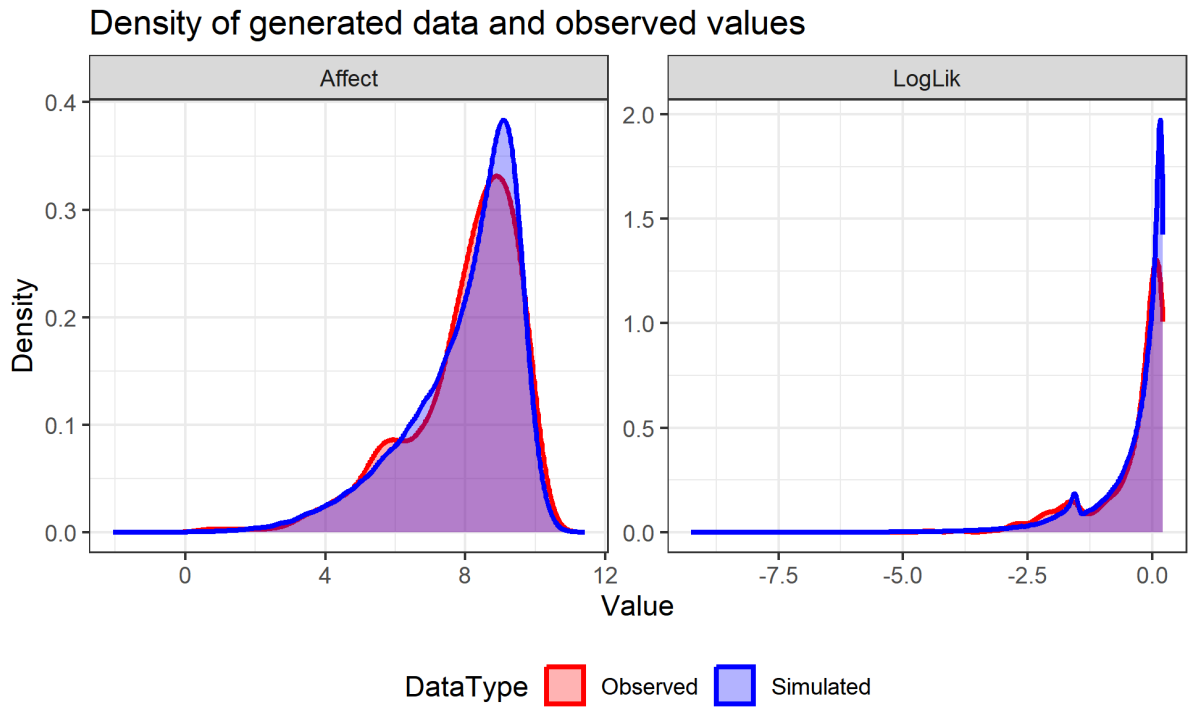
Indeed, we can see that our model explains 89 percent of the variance in our data. That is 15 percent more than before! So now we can go view our autocorrelation plot to check if there is still information left in the residuals that our model could explain.

```
ctACFresiduals(ct_fit) #plot autocorrelation of residuals
```

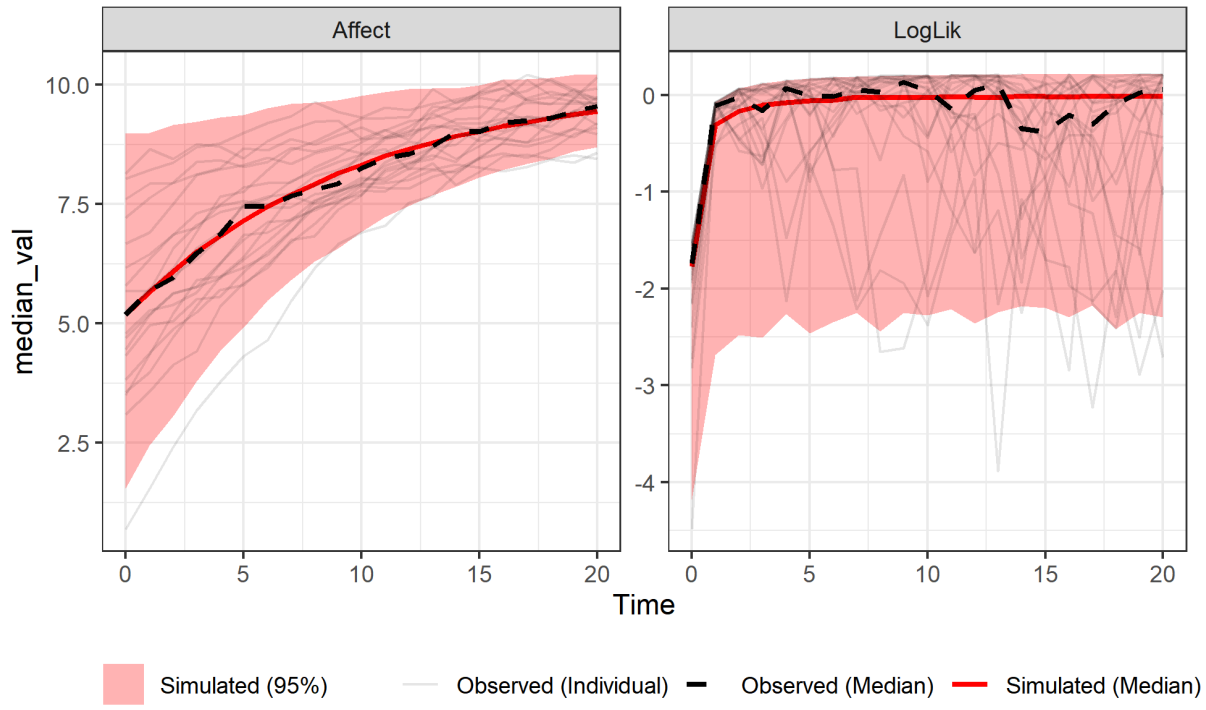


We can see that the autocorrelation has also dropped substantially, but there is still a moderate amount of autocorrelation in our residuals. Which is rightly telling us that there is more predictable variation that our model can leverage. So let's try to find out what it is by plotting the model generated data over our observed data.

```
fit <- ctStanGenerateFromFit(ct_fit, nsamples=200, #add generated data to the fit object
  fullposterior = F, cores = 2)
postpred <- ctPostPredPlots(ct_fit) #generate and store posterior predictive plots
print(postpred[[1]]) #print first plot -- overall density plots of likelihood / variables
```



```
print(postpred[[2]]) #print second plot -- compares expectations / variation over time
```



This time we see that our model implied trajectory almost perfectly fits our observed trajectory. It is not so easy to determine what information we should add to our model. We can reason through domain knowledge (but mostly because we generated the data) that affect processes are often inherently noisy. That is the growth of affect is influenced by many random life events which can push its rate of growth up and down at each moment. The black lines in our plot also indicate that our observed trajectories are noisy. This could be measurement error or system noise. We can add a system noise term to find out.

Fitting the true model: Adding state-dependence and system noise in continuous time

```
# Fit continuous time structural equation model
ct_model <- ctModel( #define the ctsem model
  # Specify features of the data
  manifestNames = "Affect", #names of observed variables in dataset
  latentNames = "Affect", #names of latent processes
  time = 'Time', #name of time column in dataset
  id = 'Subject', #name of subject column in dataset
  type='ct', #use continuous time / differential equation model (dt for discrete-time)
  # Specify features of the model
  MANIFESTVAR = 'residualSD', #sd of the residual / measurement error
  LAMBDA = matrix(1,nrow=1,ncol=1), #relating latent process to observed variables
  MANIFESTMEANS=0, #no measurement intercept (1 observed variable relates directly to latent)
  CINT='B||FALSE', #continuous intercept with *no* random effects
  TOMEANS='initialAffect||TRUE', #initial affect with random effects
  DRIFT = 'stateDependence',
  DIFFUSION = 'systemNoise')

ctModelLatex(ct_model)
```

```
ct_fit <- ctStanFit(datalong = data, ctstanmodel = ct_model) #fit the model to our data
```

```
summary(ct_fit, parmatrices=FALSE) #print summary of the fit, some output disabled
```

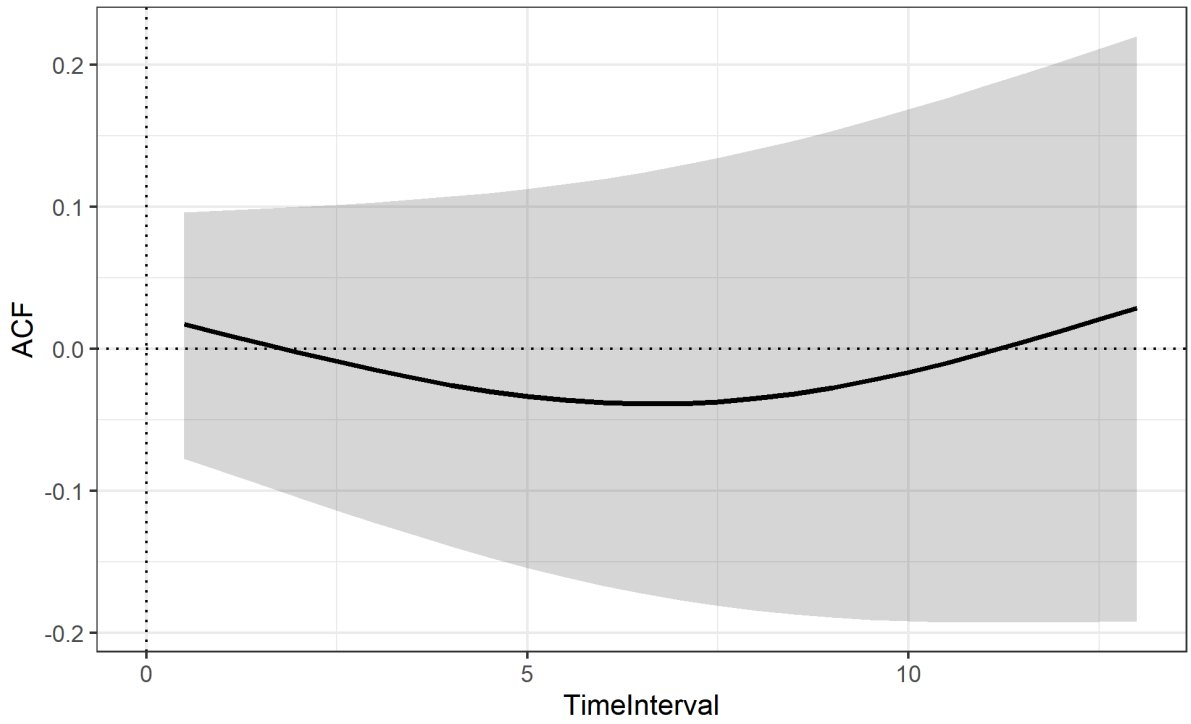
```
$residCovStd
       Affect
```

```
Affect  0.074

$resiCovStdNote
[1] "Standardised covariance of residuals"

$popsd
                mean     sd   2.5%    50%  97.5%
initialAffect 1.8177 0.3088 1.2973 1.7903 2.5101

$popmeans
                    mean     sd    2.5%     50%   97.5%
initialAffect    5.1946 0.4018  4.4534  5.1878  5.9688
stateDependence -0.1041 0.0066 -0.1180 -0.1038 -0.0919
systemNoise      0.1926 0.0127  0.1687  0.1922  0.2198
residualSD       0.0530 0.0290  0.0182  0.0461  0.1259
B                1.0440 0.0532  0.9402  1.0430  1.1534

$popNote
[1] "covariance pars in sd / unconstrained cor form, see $parmatrices for cor/cov!"

$loglik
[1] 50.55521

$npars
[1] 6

$aic
[1] -89.11043

$logposterior
[1] 50.55521

$parmatNote
[1] "For additional summary matrices, use argument: parmatrices = TRUE"
```

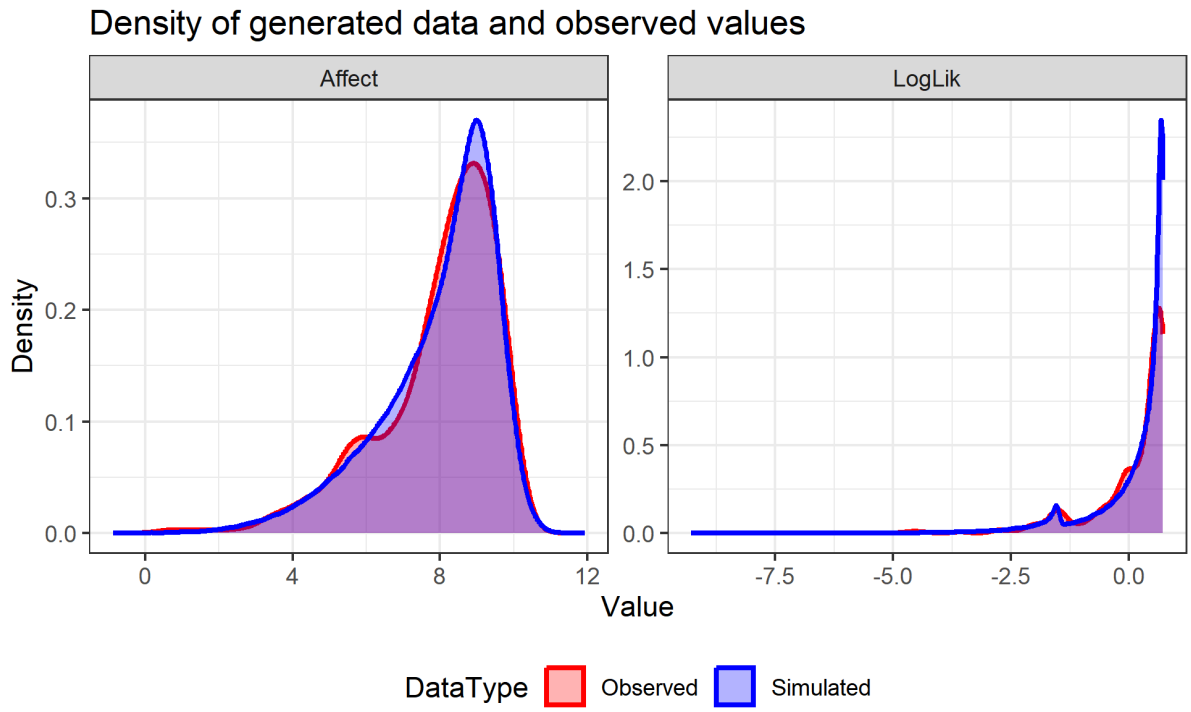
```r
# Extract residuals
k=ctKalman(ct_fit, subjects=unique(data$Subject)) #get residuals and various estimates
k=k[k$Element %in% 'errprior',] #remove everything except the residuals
k=dcast(data = data.table(k), formula = formula('Subject + Time ~ Row')) #cast to wider format

# estimate R-squared
y_hatVAR = sum(k$Affect^2, na.rm = TRUE)
yVAR <- sum((data$Affect - mean(data$Affect))^2)
R_squared <- 1 - (y_hatVAR / yVAR)
print(R_squared)
```

```
[1] 0.9256217
```

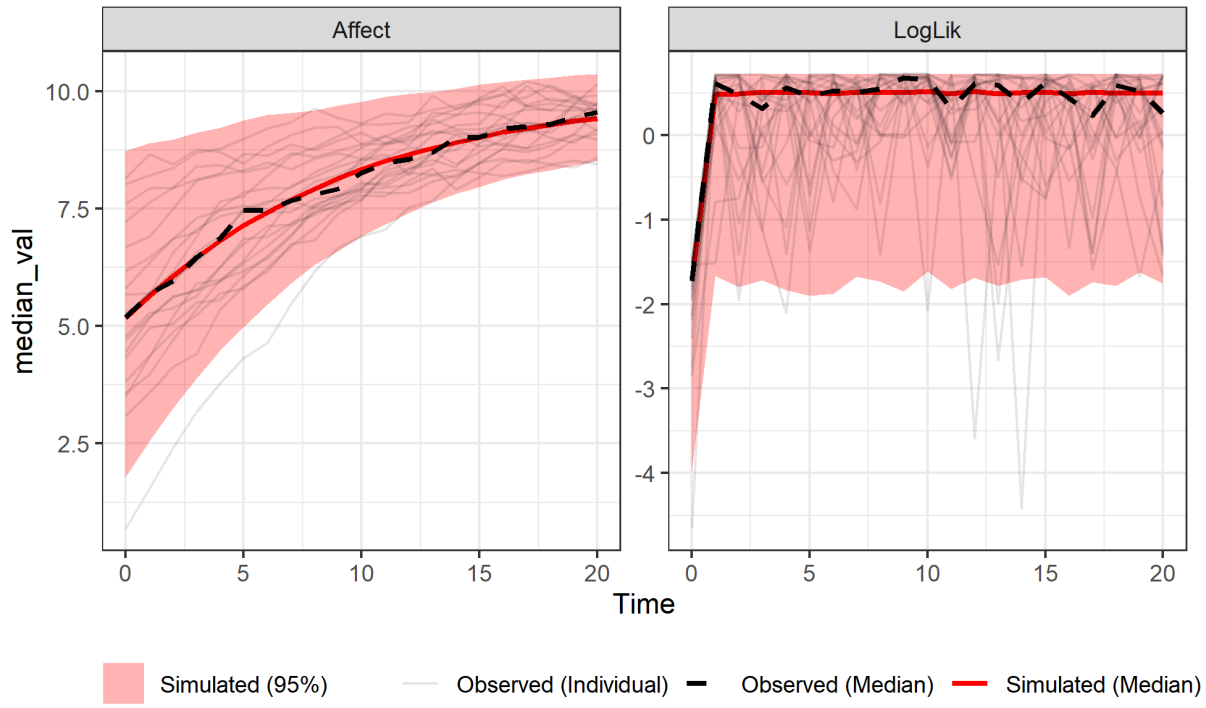
```r
ctACFresiduals(ct_fit) #plot autocorrelation of residuals
```




```
fit <- ctStanGenerateFromFit(ct_fit, nsamples=200, #add generated data to the fit object
  fullposterior = F, cores = 2)
postpred <- ctPostPredPlots(ct_fit) #generate and store posterior predictive plots
print(postpred[[1]]) #print first plot -- overall density plots of likelihood / variables
```




```
print(postpred[[2]]) #print second plot -- compares expectations / variation over time
```



Overall, we can see that fitting the model to the data it generated leads to a greater R^2, a near-zero autocorrelation between residuals, and a model-implied trajectory that maps as perfectly as we can wish for onto the observed trajectory.

In empirical contexts, this process is going to be more complicated and a data-driven method to iterative model improvement runs the risk of making model modifications that explain chance characteristics of the data. Thus, raising questions about generalizability to other samples and the population of interest. To mitigate such concerns, tools to circumvent overfitting can be used, such as iteratively building a model using a subsample of the data and then evaluating the model on unseen data (for more examples see Yarkoni and Westfall (2017)).

Conclusion

Modern computational tools and software packages such as `ctsem` simplify the process of building intricate statistical models to meet the surge of interest in intensive longitudinal data. However, the interpretation of complicated models still remains challenging despite the increasing ease of their implementation. In this tutorial, we have provided psychological researchers a set of tools to aid in the fit and interpretation of complex model structures, with flexibility to approximate many different theoretical structures of human dynamic systems.

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