

**What are “arms” in REDCap?**

In REDCap an “arm” is a construct that allows study events to be grouped into a sequence. A REDCap project has one arm by default although this is only evident if your study is longitudinal.

**Why would I use arms in  REDCap?**

Traditionally study arms (in a clinical trial for example) represent different sequences of assessments or treatments undertaken by the study participants. For example, in a clinical trial:

1. The intervention group may have a different study visit schedule from the control group.
2. The control group may not be subject to the same clinical procedures as the intervention group.

Both these scenarios would be handled by creating two different arms in REDCap and defining their event sequence and/or event CRFs to be different in the two arms.

**What are the differences between REDCap arms and traditional study arms?**

1. In a traditional study design participants would normally be randomized into one of the treatment arms. However, REDCap does not link the ramdomization module to arms. As a result, if randomization to an arm is required, the randomization can be performed in REDCap but the assignment to the study arm must be performed manually during data entry.
2. Normally a participant would be assigned to a single study arm, or at least would only exit in one arm at any particular time point. However, REDCap allows a participant ID to be present in each arm simultaneously. REDCap displays a warning if a participant ID is present in more than one arm.

**What else can I do with study arms?**

We recently used study arms to model the relationship between patients and their caregivers in a pediatric study. This study required the patient to answer a set of forms both before and after treatment. The patient’s parents also needed to answer the same forms before and after treatment.

* We created two study arms, one called “patient” and the other “parent”.
* Each study arm contained “before” and “after” events.
* Each study form was then allocated to each event in each arm.

Each patient/parent pair was allocated a study ID and this ID was used to perform data entry for both the patient and their parent. When the data was exported for analysis the parent and the patient were each represented by a row of data and the two rows for the pair could be linked by the study ID.