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Hier folgt die Kurzfassung auf Englisch.

1 Einleitung

The standard interface between human and computer has for long years been mouse and keyboard. But with the advance of technology, new interfaceing methods were developed in the last few years.

Touch technology for interfacing with mobile devices and desktop computers has become a reliable technology and has been integrated into our everyday lives. Advances in capabilites of CPU as well as GPU hardware has build a foundation for the use of advanced AR and VR Technology. 3D and Stereoscopic rendering can now be accomplished even by mobile hardware (with some limitations)without the need of specifi Hardware. For An intensly immersive experience VR Googles are used to explore digitally created worlds.

But with this level of immerivenes, a touch device or even a mouse and keyboard setuop is rather hindering the user experience. First attempts of solving this problem came with the introduction of tracked controllers for the interaction with the digital world, but these can also only supply a fration of the capabilities of our natural interaction devices, namely the human hands.

2 Description of problem

The usage of the human hands as interaction devices has been a topic of research and most solution concentrate on the tracking of the human hand itsself. Most solutions only did rudimentary integration testing of their developed systems with an VR application.Some of the Solutions are even not capable of tracking the hands in real time.

This thesis will focus on building an Tracking solution for tracking a physical object and the human hand in "real" space. The tracking data is then used in the "virtual" Space to diplay these two objects correctly and allow the user to get a physical feedback when grabbing the real object in the virtual world.

Therefore it will first give an Overview of how the human hand can be displayed in the digital realm. furtermore it will give an overview of the possible Tracking algorithms with ttheir pros and cons. In the next step an testing setuo for evaluation will be described.

3 Description of hand in digital space

Tracking of the human hand has always been a challenging Problem. In comaprison to other larger bodyparts like the Arm or the head, the human hand itself contains a large variety of smaller parts, namely bones and muscles. These components have to be taken into acount when trying to replicate the natural motion of the hand in digital space.

3.1 Physiological structure of the human hand

[5] describes the human hand as "an articulated structure with about 30 degrees of freedom [which] changes shape in various ways by its joint movemnents."
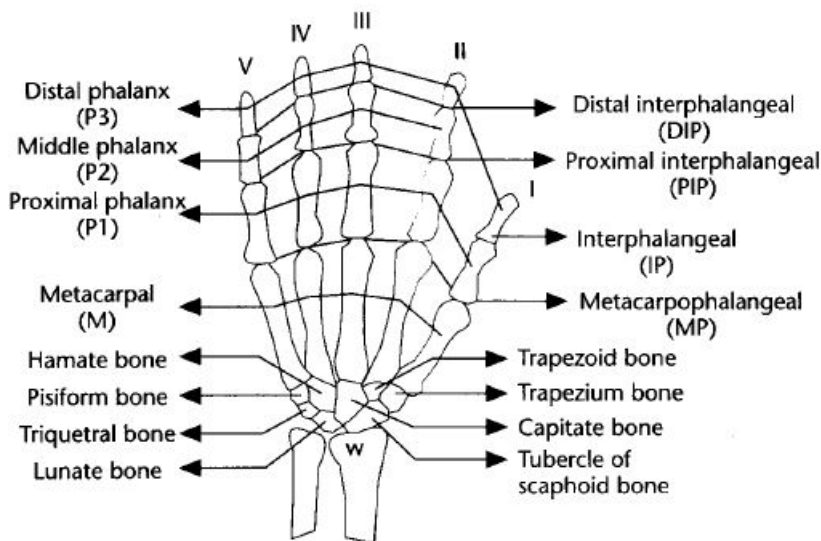

Figure 3.1: Bone structure of the human left hand ([5])

All of the hand components are connected to at least one neighboring component via a joint. Teh joints affect the position of the connected components. To describe the movement of the hand components, we can use the roation angles of the joints to correlate to a specific position.

To do so, we define a local coordinate system for each of the exiting hand joints. By doing so, we achieve a sequence of rotaions in the local coordinate systems of the joints. Such a sequence can then be used to describe a specific movement and/or position of

a component. Not all of the joints in the human hand have equal degrees of freedom. Their functionality can be classified in the amount of DOFs (Degrees of freedom)[4]

- 1 DOF
  - A joint movement that can perfom a **flexion** or **twist** in one direction

- 2 DOF
  - A joint movement that can perform **flexion** in more than one direction (**directive**)

- 3 DOF
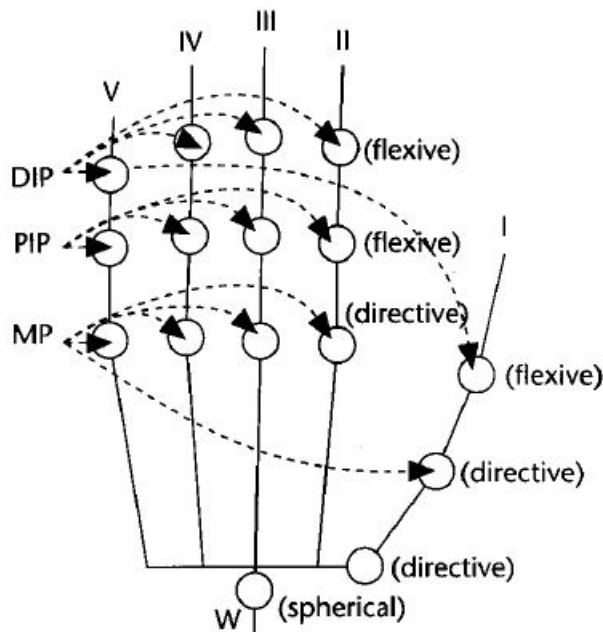 - A joint movement that permits simultaneous **directive** and **twist** movements.(**spherical**)

Figure 3.2: Representation of the DOFs of the human hand

When looking at the DOFs diplayed in Figure 3.2, each finger (II-V) sums up to 4 DOFs and the thumb to 5 DOFs. Also considering 6 DOFs for the rotation and position of the whole and itsself, the result gets us to 27 DOFs for the human hand.

3.1.1 Constraints in Hand Motion

A full usage of all the declared DOFs would lead to al large amount of possible combination. Since the hand is not only made up of bones but also Muscles and the skin, we can impose some constraints([3]) to the movement of the joints. Ling, Wu and Huang([6]) propsed following classification for the constrainsts:

- **Type I constraints**

  -A constraint that limits the range of finger motions based on hand anatomy

- **Type II constraints**

  - A constraint that the position of the joints during finger movement

- **Type III constraints**

  -A constraint that limits position based on natural hand motions

The **Type I** and **Type II** constarints rely on the physiological and mechanical properties of the humand.**Type III** constraints are results of common and natural movements and can be differing form person to person. As these movements are to some degree simular for everyone, a broad grouping can be applied. The curling of the fingers at the sane time when forming a fist is way more natural than curling each finger by itsself. Here the motion of the hand is quite simular between different persons, but the constraints cannot be described in a mathematical form.

A **Type I** constraint example would be that the position of the fingertip is kimited by the length of the other finger segments and therby can only reach as far as the combined length.

An example for **Type II** constraints would be that, for your fingertip to touch your hand palm, all joints in the finger have to be bend to achieve this position. The following inequalities can be used to describe these constraints:

Type I:

$$0° \leq \Theta_{MP\_flex} \leq 90°$$
$$0° \leq \Theta_{PIP\_flex} \leq 110°$$
$$0° \leq \Theta_{DIP\_flex} \leq 90°$$
$$-15° \leq \Theta_{MP\_abduct/adduct} \leq 15°$$

(3.1)

A further constraint that is specific to the middle finger is, that this fingers MP normally does not abduct and adduct much. Therefore we can infer an approximation and thereby remove 1DOF from the model:

$$\Theta_{MP\_abduct/adduct} = 0°$$

(3.2)

The same behavior can be seen in the combination of hand parts labeled W(the connection point between hand and lower arm). This approximation allso eliminates one DOF on the connected thumb:

$$\Theta_{W\_abduct/adduct} = 0°$$

(3.3)

Since the DIP,PIP and MP jonts of our index, middle, ring, and little fingers only have 1DOF for flexion, we can further asume that their motion is limited to movement in one plane.

Type II:

The **Type II** constraints can be split into interfinger and intrafinger constraints. Regarding intrafinger constraints between the joints of the same finger, human hand anatomy implies that to bend the DIP joints on either the index, middle, ring or little fingers,the corresponding PIP joints of thath finger must also be bent. The approximation for this relation[7] can be described as :

$$\Theta_{DIP} = \frac{2}{3}\Theta_{PIP} \tag{3.4}$$

Interfinger constraints can be imposed between joints of adjacent fingers. Interfinger constraints describe that the bending of an MP joint in the index finger forces the MP joint in the middle finger to bend as well.

When combinig the constraints described in the above equations, the starting number 21 DOF's of the human hand can be reduced to 15. Inequalities for these cases, obtained through empiric studies, can be found in [5].

3.2 Kinematics

The preceeding sections gave an overview of how we can describe a model of the human hand and introduced some limiting constraints. With the model and the constraints, we can now start to build a kinematic system for the animation of the model.

Kinematic systems contain so called *kinematic chains*, which consist of a *starting point* or *root*, kinematic elements like *joints*, *links* and an *endpoint*, also called *end effector*. Applied to the human hand, the whole hand model represents the kinematic system. This system contains several *kinematic chains*, namely the fingers of the hand with the fingertips beeing the *end effectors* of each of these chains.

As we begin to move our hands, the states of the kinemtic chains begin to change. Joint angles and end effector positions are modified until the end position is reached. To represent the new position and agnle dataset of our physical hand with our kinematic system, two major paths for achieving a solution can be taken.

3.2.1 Forward Kinematics

Forward Kinmatics (FK) uses the knowledge of the new angles and positions after the application of known transformations to the kinematic chain. The data of the *joints* and *links* between the *root* and the *end effector* is then used to solve the problem of finding the *end effector's* position.

We can denote the exisiting end effectors relative postion to an origin as $s_1, ..., s_k$. The s_i positon is the result of th combination of all the joint angles in the corresponding kinemtaic chain. Respectively, we define the target positon of the end effectors as $t_1, ..., t_i,$

with t_i beeing the target positiojn for the end effector s_i. The required positional change
for the end effector can now be described as $e_i = t_i - s_i$. In systems with more than one
end effector, like our hand system, the components can be written as vectors.

$$\vec{s} = (\mathbf{s}_1, ..., \mathbf{s}_n)^T$$
$$\vec{t} = (\mathbf{t}_1, ..., \mathbf{t}_n)^T \tag{3.5}$$
$$\vec{e} = \vec{t} - \vec{s}$$

As the vector components of $\vec{s}$ are reults of the chain joint angles $\theta_1, ..., \theta_n$ and therefore
are effected by them, we define

$$\vec{s}_i = f_i(\boldsymbol{\theta})$$
$$\vec{s} = f(\boldsymbol{\theta}) \tag{3.6}$$

with $\boldsymbol{\theta}$ beeing the column vector $\boldsymbol{\theta} = (\theta_1, ..., \theta_n)^T$. The second vector equation displayed
in (3.6) is also callled the *Forward Kinematics*(FK) solution.
The advantage of an FK solution is that there is always an unique solution to the prob-
lem. In consequence, this approach is commonly used in the field of robotics, where the
information on the chain elements is easily available.
The tracking of the human hand and all if its chain components is rather compli-
cated.Therefore a solution which takes a known position of the *end effektor* and cal-
culates the parameters for the rest of the cain would be more desireable.

3.2.2 Inverse Kinematics

> Inverse Kinematics (IK) is a method for computing the posture via estimating
> each individual degree of freedom in order to satisfy a given task [1, S. 14]

The concept of *Inverse Kinematics* (IK)already describes it's principle in it's name. It
take the reversed approach in comparison to the FK principle in chapter 3.2.1. Instead
of knowing the states of the chain elements and calculating the resulting position of the
end effector, we take the position of the *end effector* and try to retrieve the possible
states of the other chain elements.

$$\boldsymbol{\theta} = f^{-1}(\vec{s_d}) \tag{3.7}$$

The reult of this equation is the vector $\boldsymbol{\theta}$ for which the values of $\vec{s}$ coincide to the desired
configuration $\vec{s_d}$. In the case of an optimal result, this configuration would have the same
position values as the target positions.
The main problem with this method occurs in the calulaton of the f^{-1} function, due to it
beeing a highly non linear operator which is not easily invertible.Some of the approaches
that are used to counter this problem will be displayed later on in this chapter.

In contrary to having a unique solution with the FK approach, the IK approach can end at the point of not finding a suitable solution. Figure 3.3 diplays three possible outcomes for the IK approach.
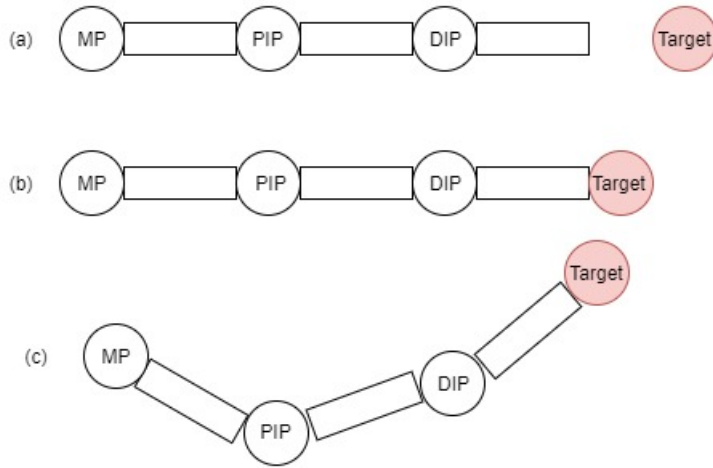

Figure 3.3: Possible solution for an IK problem of a human finger:

      (a)The given target position of the end effector can not be reached. (b) The given target can only be reached by one solution.(c)

      The target position can be reached with multiple different solutions.

Nonlinear Programming

Jacobian Inverse

3.2.3 FABRIK Algorithm

A more recent approach in the kinematics field is the **FABRIK** algorithm proposed by Aristidou and Lasenby[2].As shown in section 3.2.2, these approaches all depend on computational intensive matrix operation like calculating an inverse and may have problems with matrix singularity.

The **FABRIK** algorithm does not depend on these matrix operations as is solves for the position of a point on a line to retrieve the new joint positions. This is done in an forward and also inverse solving approach, itterating these steps until the calculated position converges towards the target position from the tracking data.

Figure 3.4 illustrates the steps

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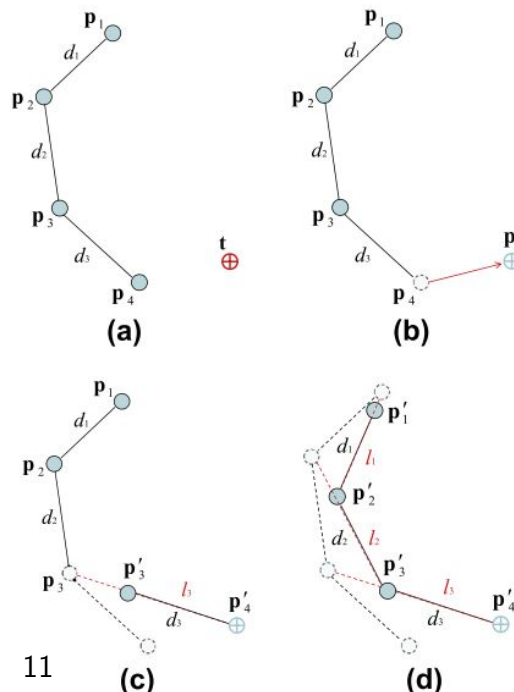
that are contained in one itera-
tion step. The chain joints are
denoted as $\mathbf{p}_i$ with the distance
$\mathbf{d}_i$ being $|\mathbf{p}_{i+1} - \mathbf{p}_i|$. The tar-
get point for the end effector
is denoted as $\mathbf{t}$. Step **(a)** dis-
plays the starting pont of the it-
eration. The joint positions are
taken from either a previous it-
eration or from an initial calibra-
tion.

But before calculations can be-
gin, the algorithm has to check
whether the intended target
point $\mathbf{t}$ is reachable for the end
effector. This is done by mea-
suring the distance between the
root of the kinamtic chain and
the target point $\mathbf{t}$. This value is then compared with the sum of the distances $\mathbf{d}_i$.

$$dist_{t,d_1} < \sum_{k=1}^{i} d_i \tag{3.8}$$

The inverse calculation step is the first step, which is diplayed in **(b)** and **(c)**.The cal-
culation is started at the end effector, moving to the root of the chain. If the summed
distance is greater, then the $\mathbf{t}$ is within the reach of the system and the calculation can
continue, otherwise the calculation has to be aborted and the error has to be manged oth-
erwise. Assuming this requirement to be met, we can now begin with the first calculation.
Therefore we assume that the new position $\mathbf{p}'_n$ is equal to $\mathbf{t}$.

$$\mathbf{p}'_n = \mathbf{t} \tag{3.9}$$

From this new point, we can construct a line that goes through $\mathbf{p}'_n$ and $\mathbf{p}_{n-1}$.

$$A = \mathbf{p}'_n$$
$$B = \mathbf{p}_{n-1} \tag{3.10}$$
$$\mathbf{l}_{n-1} = \overline{AB}$$

The resultng position of the new $\mathbf{p}'_{n-1}$ point is located in this line with the distance of
$\mathbf{d}_{n-1}$ from $\mathbf{p}'_n$ (see **(c)**).

$$\mathbf{p}'_{n-1} = \mathbf{p}'_n + (\overline{AB} \cdot \mathbf{d}_{n-1}) TODOcorrect \tag{3.11}$$

Consecutively, this is done with the remaining joints until the root joint is reached(see **(d)**). This finishes the first halv of the iteration step.With the calculated positions, we now perform a forard calculation, starting from the root until we reach the end effector. Since the root of the system normally does not move from it's initial position, we have to reset the root jont to this value before starting to calculate the new positions of the subsequent joints(see**(e)**).

Analogous to the procedure in the inverse step, we construct the lines between the points and determine the new positon values of the joints. The end result of this step is shown in (f). At this point, we can decide if the result position of the end effector is appropriate in comparison to the value of **t**. A simple threshold value for this case could be the position difference between these two points.

3.3 Digital hand models

4 Fazit

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Max Mustermann