Chapter 2

Physiological mechanical system

INTRODUCTION

This chapter deals with the mechanical block of the human motor control scheme (figure 2.1). It relates the forces or moments of force to the movement of the skeletal system, depending on the mechanical properties of the skeletal system. In order to do so, we have to formulate how the properties of the skeletal system are described in a mathematical model, how the movement is defined and how the forces relate to both. The part of (bio)mechanics that studies this is called *rigid body dynamics* and is explained more extensively in the courses *Biomechanics* and *Human Motion Control*. In this chapter some basic concepts are presented.



Figure 2.1 Schematic block diagram of the human motor control system. Subject of this chapter is the skeletal system.

OBJECTIVES

This chapter will show:

- the assumptions in modeling human movement;
- the differences between medical and technical descriptions of movement;
- the general way to describe rigid body motion with a translation vector and a rotation matrix;
- some alternatives in 3-D to derive rotation angles from the rotation matrix, e.g. Euler angles and helical axes;
- the concepts of inverse dynamics and direct (or forward) dynamics;
- how to derive the equations of motion for a system of rigid bodies in the Newton-Euler or Lagrange formulation.

CONTENTS

2.1 Rigid body dynamics

The human body consists of a more or less rigid structure (the bones of the skeleton) to which soft tissues (muscles, fat, organs etc.) attach. A structure is considered rigid when under practical loading situations the structure does not noticeable deform, i.e. the mechanical stiffness seems to be infinite. The description of the movement of a human body is, in a mechanical sense, equal

to the description of the deformation of the body. Since the soft tissues are not rigid and do deform in practical loading situations, a mechanical description of human movement would involve the description of the displacement of each volume element of the human body. Each volume element interacts with neighboring elements and is subject to the laws of motion and the force of gravity, so the description of this system would involve a very complex and large finite element approach. This approach is only feasible in some very specific applications, for example to study the effect of car crash impacts on brain damage. As is it also not possible to measure all deformations, some assumptions are made be able to study human movement at all. The most important assumption is that the deformations only occur in a limited number of positions of the human body and nowhere else. The deformations may be very large, obviously it makes sense to choose the positions at the joints of the human body. The structure in-between the joints are rigid and called segments. So, it is assumed that the human body behaves like a segments model: A linked system of rigid bodies. Apart from the enormous reduction of complexity, this viewpoint has other advantages as well: Within segments, the interaction forces between volume elements cancel each other out and do not contribute to the movement of the segment. The laws of motion, applied to the entire segment, are sufficient to describe the dynamics. Of course, the interaction forces between the segments (at the joints) cannot be neglected. Rigid body dynamics describes the kinematics (movement) and dynamics (forces) of a given segments model. The equations of motion are the link between these two, which is a set of second-order (or two first-order) nonlinear differential equations. For a given segments model the forces and movements provide interchangeable information: The forces can be calculated when the movement is known (i.e. inverse dynamics approach) and the movement can be calculated when the forces are known (i.e. direct or forward dynamics approach).

The segments model, kinematics and dynamics are subject of later sections in this chapter. First, the medical terminology of motion description is provided.

2.2 Medical motion description

Two bones can move with respect to each other by virtue of the joint in between. Although in the human body more types of joints are discerned, only the synovial joints allow for large rotations. In principle, a bone has six Degrees-of-Freedom (DOF) of motion with respect to the other bone: three rotations and three translations. The motions of the joint are limited by passive structures like the articular surfaces and the ligaments. These passive structures pose *restraints* to the joint motions: Though motions in the direction of the restraint are still possible, these motions will be very small. For example, cartilage can be compressed a few millimeters. Most of the time these small motions are neglected, and the motion is said to be *constrained*. For each constraint the number of DOF diminishes by one. As soon as constraints are coming into the picture, one has already started modeling the joint. In figure 2.2 all combinations of (constrained) rotations and translations are shown. Many of them are merely hypothetical, and will not be found in the human body.

Traditionally, joints have been studied (e.g. by Fick, 1911) by comparing them with standard revolute joints: Hinges, spherical joints, ellipsoidal joints, saddle joints (see figure 2.3). In the human body joints can be found which motions quite resemble these standardized revolute joints. The shoulder joint and the hip joint behave approximately as spherical joints only permitting three rotational

DOF. The elbow joint and finger joints can be regarded as hinge joints with one rotational DOF. The first thumb joint and the ankle joint resemble a saddle joint, having two non-intersecting rotational axes. But many times one can not derive the potential motions from the shape of the articular surfaces.

ROTATION



Figure 2.2 Combinations of rotations and translations in joints. Many joints shown are hypothetical and are not found in the human body.



Figure 2.3 Examples of standard revolute joints (Fick, 1911).

Since physicians were the first to study joint motions, medical definitions still dominate the way joint motions are described. The goals of the medical definitions is to distinguish between pathological and normal motion, and to evaluate the outcome of treatments: Is there improvement in the range of motion or not.

Anatomic position As a starting position the *anatomical position* is used: a well-defined¹ position of the human body (figure 2.4). From this position the motion is defined for each

single rotation apart. For spherical joints the rotation axes are defined along the axis of the global coordinate system: A vertical axis and two horizontal axes, pointing backward-forward and medial-lateral (from the center of the body to the left or right outside). Often used terms are flexion-extension (bending and stretching a joint), abduction-adduction (rotations about a backward-forward axis outside and inside, respectively), anteflexion-retroflexion (rotations about a medial-lateral axis, forward and backward respectively), endorotation-exorotation (rotation about a vertical axis, towards and away from the body respectively). A problem occurs if the motion is not about just one of the standardized axis, but is a combination of rotations. The order of rotations is not defined, and it is not clear whether the rotation axes move with the bone or not. This still results in much confusion about rotation angles, and makes the comparison between studies often impossible.

¹ The anatomical position is officially defined in the Nomina Anatomica: A kind of dictionary of anatomical terms and concepts.



Figure 2.4 The anatomical position.

2.3 The segments model

All models to analyze or simulate human movement are based on segments models. These are coupled systems of rigid bodies, with dimensions and inertial properties that are deduced from the dimensions and inertial properties of the human body. Initially, these segments models were used to dimension the dummies used in experiments (e.g. Clauser, McConville and Young, 1969) and were therefore based on averaged data of human bodies. With the introduction of the segments models to computer simulations, a wider variety became possible. The segments models became scaleable, with inertial properties usually depending on local segment dimensions and total body weight. In this way, the segments model could be matched to fit each individual (e.g. Chandler et al., 1975).

The choice of the number of segments should be large enough to simulate the movement adequately. Too large a number of segments, however, would lead to unnecessary complexity and larger computational efforts. To simulate walking, segments models varying from 3 segments (McMahon, 1984) up to 17 segments (Hatze, 1981) have been proposed. To further reduce complexity, symmetry

between right and left leg is often assumed (e.g. Brand et al., 1982) and the movement is often restricted to the sagittal plane (dividing the left and right of the body) only.

In a model for normal walking there are segments for the upper legs, lower legs and feet. The head, arms and trunk (HAT) and the pelvis are modeled as two separate segments. The segments are connected to each other in the joints (figure 2.5). Although it is possible to have more than two joints on a segment (e.g. the pelvis), each joint is connecting exactly two segments. The point of contact between foot and floor is modeled as if it were a joint. In this view, the floor is a segment with zero velocity and infinite mass. The advantage of this view is that the ground reaction forces are treated in the same way as the joint forces.

To define the position of the segments in space, an absolute or reference frame is attached to the floor, with the x-axis pointing in the walking direction, the y-axis pointing upward and the z-axis perpendicular to the xy-plane in the lateral direction. Figure 2.5 shows the 8-segmental model with the numbering of the segments, the joints and the definition of the reference frame. It should be noted that the shape of the segments is of no importance as long as the positions of the joints and the mass properties are well defined. In each segment a local frame is defined, standardized with the help of some bony landmarks on the segment.



Figure 2.5 The segments model for the body at rest: Numbering of segments and joints, definition of the reference frame, definition of local frames and positions of the centers of mass.

The segments model must include the following definitions, that are dependent on individual characteristics: The dimensions and positions of the segments in space, the positions of the joints, and the mass properties of the segments (mass, position of the center of mass and moment of inertia tensor). Other properties, such as the ranges of motion of the joints, the maximal joint angular accelerations, the maximal moments of force that can be exerted in the joints, and muscle models, may also be included (Koopman et al., 1995).

2.4 Kinematics

The segments model is the basis for a sound technical description of human movement. In general, a movement of a rigid body is defined as the displacement and orientation of the local frame relative to the reference frame or another local frame. Therefore, any description of a (joint) rotation implicitly assumes that some kind of segments model is defined, otherwise the rotation has no unique meaning (see also section 2.1). One can only measure the local deformation of soft tissue, when measured at another position on the segment the result would be different. Only when linked to the local frame position and orientation, the measurement becomes meaningful. As the offset position for the segments model, i.e. the position where the rotations are defined to be zero, usually the anatomical position is taken.



Figure 2.6 Transformation of position vector ${}^{A}\mathbf{p}$ from local coordinate system A to position vector ${}^{G}\mathbf{p}$ in the global coordinate system G.

rotation matrix translation vector Mathematically, the motion of a body with respect to another body can be described unambiguously by a [3x3] *rotation matrix* \mathbf{R} and a *translation vector* $\underline{\mathbf{t}}$ (see Figure 2.6):

$$\begin{pmatrix} {}^{G}\mathbf{\underline{p}} - {}^{G}\mathbf{\underline{t}} \end{pmatrix} = {}^{GA}\mathbf{R} \cdot \begin{pmatrix} {}^{A}\mathbf{\underline{p}} - {}^{A}\mathbf{\underline{t}} \end{pmatrix}$$

$$\begin{pmatrix} {}^{G}\mathbf{\underline{p}} = {}^{G}\mathbf{\underline{t}} + {}^{GA}\mathbf{R} \cdot {}^{A}\mathbf{\underline{p}} \end{pmatrix}$$

$$(2.1)$$

Bold capitals are used to denote matrices; underlined lowercase characters are used to denote vectors. ${}^{G}\mathbf{p}$ is the position vector of point *P* in the global coordinate system *G*, ${}^{A}\mathbf{p}$ is the position vector of point *P* in the local coordinate system *A*. ${}^{G}\mathbf{t}$ is the translation vector from the origin of *A* expressed in coordinate system *G*. Obviously ${}^{A}\mathbf{t}$, the origin of *A* expressed in coordinates of *A* equals the zero vector $\mathbf{0}$. ${}^{GA}\mathbf{R}$ is the rotation matrix that describes the rotation from the local coordinate system *A* to the coordinate system *G* (the global coordinate system). In other words, when ${}^{A}\mathbf{p}$ would be a base vector of *A* in equation (2.1), then (${}^{G}\mathbf{p}$ - ${}^{G}\mathbf{t}$) would be the same base vector but transformed to coordinate system *G*. When **A** is the matrix of base vectors of coordinate system *A*, it follows that (since ${}^{A}\mathbf{A}$ is the unity matrix **I**):

$$\mathbf{F} \mathbf{A} = \mathbf{G}^{A} \mathbf{R} \cdot \mathbf{A} = \mathbf{G}^{A} \mathbf{R}$$
(2.2)

Or the rotation matrix ^{*GA*}**R** equals the base vectors of *A* expressed in *G*. Rotation matrices are orthonormal matrices, hence $\mathbf{R}^{-1} = \mathbf{R}^{\mathrm{T}}$ (^T means transposed). When ^{*AG*}**R** is the inverse rotation of ^{*GA*}**R**, it can easily be shown that

$${}^{A}\mathbf{A} = {}^{AG}\mathbf{R} \cdot {}^{G}\mathbf{A} = \mathbf{I}$$

$${}^{GA}\mathbf{R} \cdot {}^{AG}\mathbf{R} = {}^{GA}\mathbf{R} \cdot {}^{GA}\mathbf{R}^{-1} = \mathbf{I}$$

$${}^{GA}\mathbf{R} = {}^{AG}\mathbf{R}^{\mathrm{T}}$$
(2.3)

Element-wise, equation (2.1) looks like

$$\begin{bmatrix} G \\ p_x \\ G \\ p_y \\ G \\ p_z \end{bmatrix} = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix} \cdot \begin{bmatrix} A \\ p_x \\ A \\ p_y \\ A \\ p_z \end{bmatrix} + \begin{bmatrix} G \\ t_x \\ G \\ t_y \\ G \\ t_z \end{bmatrix}$$
(2.4)

in which the elements of the rotation matrix are cosines of the angles between the axes of the global and local coordinate system (see figure 2.6):

$${}^{GA}\mathbf{R} = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix} = \begin{bmatrix} \cos(\theta_{11}) & \cos(\theta_{12}) & \cos(\theta_{13}) \\ \cos(\theta_{21}) & \cos(\theta_{22}) & \cos(\theta_{23}) \\ \cos(\theta_{31}) & \cos(\theta_{32}) & \cos(\theta_{33}) \end{bmatrix}$$

$$\theta_{11} = \angle({}^{A}\mathbf{\underline{x}}, {}^{G}\mathbf{\underline{x}}), \qquad (2.5)$$

$$\theta_{21} = \angle({}^{A}\mathbf{\underline{x}}, {}^{G}\mathbf{\underline{y}}), \quad etc.$$

	<u>Euler angles</u> Though the rotation matrix contains 9 elements, there are only three independent variables present. Together with the three elements of the translation vector, these six variables describe the potential 6 DOF motion between two bones. Often, the translation vector is not used, since its values depend on the individual dimensions of the bones. The rotation matrix does not need scaling and permits comparisons between subjects. For a better imagination of the motion and comparison between subjects, the rotation matrix is decomposed in three successive rotations about the axes of the first or intermediate coordinate.
Euler angles	system: <i>Euler angles</i> . This can be imagined as three hinge joints in succession.
	Rotation of the first hinge will change the orientation of the second and third, rotation of the second hinge will change the orientation of the third hinge, and rotation about the third hinge will result in the desired orientation of the local coordinate system.
Cardan angles	In Biomechanics, usually <i>Cardan angles</i> are used, which are Euler angles with successive rotations about the local x -, y - and z -axes. Instead of the order x - y - z any other combination of these rotations could have been chosen. Since matrix multiplication is not a commutative operation, each combination of rotations will result in other values of the angles. In figure 2.7 is demonstrated that reversing the order of rotation indeed results in a different position.
	<u>Helical axis</u>
	combination of a rotation about an axis and a translation along the same axis. There is only one unique axis for which this is true. This axis is called the
helical axis	<i>helical axis</i> or <i>screw axis</i> (see figure. 2.8). More precisely, this is called the
screw axis	Finite Helical Axis (FHA). In contrast, the Instantaneous Helical Axis (IHA) describes the angular velocity vector ω of the moving rigid body at a certain time t. If the time interval Δt between the two positions of the FHA approaches zero, the FHA will approach the IHA. The FHA is characterized by 6 independent parameters and describes all 6 DOE of the motion between two
	positions of the distal bone with respect to the proximal bone. These 6
	parameters are the unit direction vector \mathbf{n} (two independent parameters since the basely is a lower basely and the maximum data and the second s
	length is given), the position vector \underline{s} (two independent parameters since \underline{s} is defined perpendicular to \mathbf{n}), rotation ϕ and translation t. These parameters can
	be calculated from the rotation matrix ${}^{GA}\mathbf{R}$ and the translation vector ${}^{G}\underline{\mathbf{t}}$











The sequence dependence of the Euler angles and the occurrence of gimbal lock positions resulted in a search for other parameterizations of the rotation matrix. From the FHA the *helical angles* ϕ_x , ϕ_y , ϕ_z have been derived which are defined by the 'vector' $\phi = \phi \cdot \mathbf{n} = [\phi_x \phi_y \phi_z]^T$. Advantage of this description is the complete symmetry of the vector components. Disadvantage is the missing physical interpretation of the ϕ , since it is defined in a nonlinear vector space which does not permit vector addition.

helical angles

2.5 Dynamics

The next step after defining the movement of rigid bodies is to apply the equations of motion. This results, depending on the application, in either an inverse dynamics or a direct dynamics formulation of the system, derived in most cases with a Newton-Euler approach or a Lagrange approach. The application of the equations of motion to human movement requires the human body to be described as a linked system of rigid bodies, the so-called segments model.

2.5.1 NEWTON-EULER EQUATIONS, INVERSE ANALYSIS

Newton formulated the equations of motion for systems of mass particles. Euler recognized that a rigid body is a special case for such a system: The positions of the particles are constrained with respect to each other. This leads to the notion that the internal forces (the forces acting between the particles) do not perform work and do not contribute to the equations of motion for the entire system, the rigid body. Since a rigid body has six *degrees of freedom (DOF)*, there must be six equations describing the relation between forces and motion. This leads to

the formulation of the Newton-Euler equations of motion for each segment:

$$\underline{\mathbf{F}}_{CM} = \underline{\mathbf{p}}_{CM} = m\underline{\mathbf{r}}_{CM}$$

$$\underline{\mathbf{M}} = \underline{\mathbf{h}} = \frac{\mathbf{d}(\mathbf{J}_{CM}\underline{\mathbf{0}})}{dt}$$
(2.6)

Where $\underline{\mathbf{F}}_{CM}$ is the resulting external force acting on the center of mass (*CM*) of the rigid body, $\underline{\mathbf{p}}_{CM}$ is the momentum of *CM*, which equals (with a constant mass *m*) the product of mass and velocity of *CM*. Any force, acting on the rigid body, can be divided in a force, acting on *CM*, and a moment of force $\underline{\mathbf{M}}$. When no moments of force act on the rigid body the angular momentum $\underline{\mathbf{h}}$ is conserved. $\underline{\mathbf{h}}$ is the product of the rotation inertia tensor \mathbf{J}_{CM} and the angular velocity vector $\underline{\mathbf{\omega}}$. Unlike the mass *m*, \mathbf{J}_{CM} is in general not constant in each coordinate system. This leads to considerable complications in 3-D; in 2-D \mathbf{J}_{CM} reduces to a single constant component. However, since the body is rigid, \mathbf{J}_{CM} expressed in local body coordinates must be constant tensor. In global coordinates, \mathbf{J}_{CM} depends on time. Also, $\underline{\mathbf{\omega}}$ does not behave like a regular velocity vector: The time integral of $\underline{\mathbf{\omega}}$ does not have a physical meaning. As is shown in section 2.4, rotations cannot be considered as a vector since they do not commute. However, in 2-D $\underline{\mathbf{\omega}}$ can be considered a scalar (it is always perpendicular to the plane of action) and its integral is the rotation angle.

Consider now the 2-D situation of a segment *A* with mass *m* and moment of inertia J_A . A local frame is attached to the center of mass with an angle θ to the global (inertial) frame *G*. The segment connects to another segment in joint *P* (figure 2.9). Of course, the other segment applies some connection forces on the segment, the joint force $\underline{\mathbf{F}}_P$ and joint moment of force M_P . When all vectors are expressed in global coordinates, equation (2.6) reduces to 3 scalar equations:

degrees of freedom (DOF)



Figure 2.9 Free body diagram of a rigid body A with joint P.

Note that *g* is the acceleration of gravity constant. The expression between brackets in the moment of force equation is the product of force and moment arm. Note also that the vector ${}^{A}\mathbf{\underline{r}}_{AP}$ is a constant but ${}^{G}\mathbf{\underline{r}}_{AP}$ depends on the angle θ (and thus on time) as defined by equation (2.1).

When the movement of the segment is known the second derivatives of the position and rotation coordinate may be calculated. Equation (2.7) may than be used to calculate the (unknown) joint forces and moments of force. Likewise, when an additional joint is present with known forces, equations similar to (2.7) may be derived to compute the unknown forces at the other joint. For example, in an inverse analysis of the walking movement, the measured ground reaction forces are known in the equations of motion for the foot segment. These are then used to calculate the ankle forces. From these and the equations of motion of the lower leg segment, the knee forces are calculated, and so on.

2.5.2 LAGRANGE EQUATIONS, DIRECT DYNAMICS

The Lagrange equations of motion can be derived from the Newton-Euler equations or the principle of d'Alembert: The virtual work done on the system by external forces must lead to a similar increase of the system's kinetic or potential energy. The main difference is that the movement is expressed in independent (generalized) coordinates, equal to the number of degrees of freedom of the system. For a single segment system in 2-D both Newton-Euler and Lagrange result in (the same) 3 scalar equations of motion. For a linked 2-segment system, however, Newton-Euler needs 6 equations whereas Lagrange needs 4 equations. For increasing numbers of segments this difference becomes larger. When simulating a movement in a forward dynamics approach (calculating the movement by integrating the equations of motion) it is obvious that the smallest number of equations is preferable. However, the joint forces that are related to the dependent coordinates are not calculated. Also, it is quit cumbersome to derive the Lagrange equations for large systems.

Roughly, the derivation of the Lagrange equations requires the following steps to be taken:

1. Define the Lagrangian from the system's kinetic and potential energy, and

express it in the generalized coordinates.

- 2. Determine the generalized forces from the external forces on each rigid body that perform (virtual) work.
- 3. Derive the Lagrange equations.
- As an example, the equations for the system of figure 2.9 will be derived.

<u>1. Define the Lagrangian from the system's kinetic and potential energy</u> The kinetic energy T_A of a rigid body A is composed of the translational and rotational kinetic energy:

$$T_{A} = \frac{1}{2} \dot{\underline{\mathbf{r}}}_{A}^{\mathrm{T}} \cdot \underline{\mathbf{p}}_{A} + \frac{1}{2} \underline{\omega}_{A}^{\mathrm{T}} \cdot \underline{\mathbf{h}}_{A} = \frac{1}{2} m \dot{\underline{\mathbf{r}}}_{A}^{\mathrm{T}} \cdot \dot{\underline{\mathbf{r}}}_{A} + \frac{1}{2} \underline{\omega}_{A}^{\mathrm{T}} \cdot \mathbf{J}_{A} \cdot \underline{\omega}_{A}$$
(2.8)

Note that T_A is a scalar; it does not matter whether the vectors are expressed in local or global coordinates, as long as these are not mixed within each term. In most applications, it is useful to derive the translational kinetic energy in global coordinates for a simple relation with generalized coordinates and the rotational kinetic energy in local coordinates because J_A is a constant tensor then. The potential energy V_A may include all contributions from forces that can be derived from a potential, such as gravitational forces, spring forces etc. However, this is not a necessity, since in principal these forces may also be included in the generalized forces, as long as these are not included twice. The gravitational potential energy is defined as:

$$V_A = -m^G \underline{\mathbf{r}}_A^{\mathrm{T}} \cdot^G \underline{\mathbf{g}} = mg^G r_{Ay}$$
(2.9)

With a natural choice for the generalized coordinates $\mathbf{q} = [{}^{G}r_{Ax} {}^{G}r_{Ax} \theta]^{T}$ the Lagrangian *L* becomes

$$L = T_A - V_A = \frac{1}{2}m({}^G\dot{r}_{Ax}^2 + {}^G\dot{r}_{Ay}^2) + \frac{1}{2}J_A\dot{\theta}^2 - mg^G r_{Ay} (2.10)$$

2. Determine the generalized forces

The generalized forces are calculated by calculating the virtual work of each of the external forces that are not derivable from a potential. For the virtual displacement connected to external force $\underline{\mathbf{F}}_{p}$ we can write (see also equation 2.1):

$${}^{G}r_{Px} = {}^{G}r_{Ax} + {}^{A}r_{APx}\cos(\theta) - {}^{A}r_{APy}\sin(\theta)$$

$${}^{G}r_{Py} = {}^{G}r_{Ay} + {}^{A}r_{APx}\sin(\theta) + {}^{A}r_{APy}\cos(\theta)$$
(2.11a)

$${}^{G}\dot{r}_{Px} = {}^{G}\dot{r}_{Ax} - {}^{A}r_{APx}\dot{\theta}\sin(\theta) - {}^{A}r_{APy}\dot{\theta}\cos(\theta)$$

$${}^{G}\dot{r}_{Py} = {}^{G}\dot{r}_{Ay} + {}^{A}r_{APx}\dot{\theta}\cos(\theta) - {}^{A}r_{APy}\dot{\theta}\sin(\theta)$$
(2.11b)

$$\begin{bmatrix} \delta r_{P_X} \\ \delta r_{P_y} \end{bmatrix} = \begin{bmatrix} 1 & 0 & -^A r_{AP_X} \sin(\theta) - ^A r_{AP_y} \cos(\theta) \\ 0 & 1 & +^A r_{AP_X} \cos(\theta) - ^A r_{AP_y} \sin(\theta) \end{bmatrix} \cdot \begin{bmatrix} \delta r_{A_X} \\ \delta r_{A_y} \\ \delta \theta \end{bmatrix}$$
$$\delta \mathbf{\underline{r}}_P = \mathbf{D}_P(\mathbf{\underline{q}}) \cdot \delta \mathbf{\underline{q}}$$
(2.11c)

Where $\mathbf{D}_{P}(\mathbf{q})$ is a [2×3] matrix. The virtual rotation associated with the moment

of force M_P is already one of the generalized coordinates. From the virtual work done on the system of figure 2.9, the generalized force **Q** follows:

$$\delta W = \underline{\mathbf{F}}_{P}^{\mathrm{T}} \cdot \delta \underline{\mathbf{r}}_{P} + M_{P} \cdot \delta \boldsymbol{\theta} = \underline{\mathbf{Q}}^{\mathrm{T}} \cdot \delta \underline{\mathbf{q}}$$
(2.12)

Since this holds for any virtual displacement $\delta \underline{\mathbf{q}}$, this will eventually result in the three components of $\underline{\mathbf{Q}}$, each associated with one of the generalized coordinates.

3. Derive the Lagrange equations

For each of the generalized coordinates q_i , an equation of motion is now derived according to:

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{q}_i} \right) - \frac{\partial L}{\partial q_i} = Q_i; \quad i = 1, \dots, n$$
(2.13)

It is left to the reader to prove that these equations are equal to equation (2.7).

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